The H19G5 transcript is expressed in the heart. H19G5 polypeptides and
polynucleotides are useful for preventing or treating a cardiac disease,
such as congestive heart failure, dilated congestive cardiomyopathy,
hypertrophic cardiomyopathy, restrictive cardiomyopathy, mitral valve
disease, aortic valve disease or tricuspid valve disease, angina
pectoris, myocardial infarction, cardiac arrhythmia, pulmonary, arterial
or rhenovascular hypertension, arteriosclerosis, atherosclerosis and
cardiac tumours in humans. The polypeptide is also useful for detecting
the expression of a protein capable of regulating signal transduction or
the expression of a protein capable of acting as a donor or acceptor
molecule of a phosphate group. The monoclonal antibodies can be used as
probes for detecting discrete antigens expressed by tissue or cell
samples, and therefore used in humans for localization and monitoring of
microbial infection

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SQ   Sequence 5007 BP; 946 A; 1722 C; 1541 G; 798 T; 0 U; 0 Other;

Query Match           94.4%;   Score 4915.8;   DB 5;   Length 5007;
Best Local Similarity 99.9%;   Pred. No. 0;
Matches 4920;   Conservative   0;   Mismatches   7;   Indels   0;   Gaps   0;

Qy    258  CCCAGGGCCCCATCCATGCAGGTAACCATCGAGGATGTGCAGGCACAGACAGGCGGAAC  317
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     81  CGCACGGGCCCCATCCATGCAGGTAACCATCGAGGATGTGCAGGCACAGACAGGCGGAAC  140

Qy    318  GGCCCAATTCGAGGCTCATCATTGAGGGCGACCCACAGCCCTCGGTGACCTGGTACAAGGA  377
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    141  GGCCCAATTCGAGGCTCATCATTGAGGGCGACCCACAGCCCTCGGTGACCTGGTACAAGGA  200

Qy    378  CAGCGTCCAGTGGTGGACAGCACCCGGCTTAGCCAGCAGCAAGAAGGCACCACCATACTC  437
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    201  CAGCGTCCAGTGGTGGACAGCACCCGGCTTAGCCAGCAGCAAGAAGGCACCACCATACTC  260

Qy    438  CCTGGTGCTGAGGCATGTGGCCTCGAAGGATGCGGGGGTTACCTCGCCTGGCCCAAAA  497
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    261  CCTGGTGCTGAGGCATGTGGCCTCGAAGGATGCGGGGGTTACCTCGCCTGGCCCAAAA  320

Qy    498  CACTGGTGGCCCAGGTGCTCTGCAAGGCACGAGCTGCTGGTGCTTGGGGGGACAATGAGCC  557
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    321  CACTGGTGGCCCAGGTGCTCTGCAAGGCACGAGCTGCTGGTGCTTGGGGGGACAATGAGCC  380

Qy    558  GGACTCAGAGAGCAAAGCCACCGGAGGAAGTGCACTCCTTCTATGAGGTCAAGGAGGA  617
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    381  GGACTCAGAGAGCAAAGCCACCGGAGGAAGTGCACTCCTTCTATGAGGTCAAGGAGGA  440

Qy    618  GATTGAAGGGCGGTGTTGGCTTGGCTTCGTAAAAAGAGTGCAGCACAAGGAAACAAGATCTT  677
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    441  GATTGAAGGGCGGTGTTGGCTTGGCTTCGTAAAAAGAGTGCAGCACAAGGAAACAAGATCTT  500

Qy    678  GTGCGCTGCCAAGTTCATCCCCCTACGGAGCAGAACTCGGGCCCAGGCATACAGGGAGCG  737
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    501  GTGCGCTGCCAAGTTCATCCCCCTACGGAGCAGAACTCGGGCCCAGGCATACAGGGAGCG  560

Qy    738  AGACATCTGGCCGGCCTGAGCCCCTGGTCACCGGGTCGCTGACCAGTTGAGAC  797
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    561  AGACATCTGGCCGGCCTGAGCCCCTGGTCACCGGGTCGCTGACCAGTTGAGAC  620

Qy    798  CCGCAAGACCCTCATCCTCATCCTCGGAGCGTGCTCATCCGAGGAGCGTGCTGGACCGCCT  857
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    621  CCGCAAGACCCTCATCCTCATCCTCGGAGCGTGCTCATCCGAGGAGCGTGCTGGACCGCCT  680

Qy    858  GTACAGGAAGGGCGTGGTGACGGAGCGCCGAGGTCAAGGTCTCATCCGAGCTGGTGGA  917
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    681  GTACAGGAAGGGCGTGGTGACGGAGCGCCGAGGTCAAGGTCTCATCCGAGCTGGTGGA  740

Qy    918  GGGGCTGCACTACCTGCACAGCCATGGCGTTCCACCTGGACATAAAGCCCTCTAACAT  977
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    741  GGGGCTGCACTACCTGCACAGCCATGGCGTTCCACCTGGACATAAAGCCCTCTAACAT  800

Qy    978  CCTGATGGTGCATCCTGCCCGGAAGACATTAAAATCTGCGACTTTGGCTTTGCCCAGAA  1037
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    801  CCTGATGGTGCATCCTGCCCGGAAGACATTAAAATCTGCGACTTTGGCTTTGCCCAGAA  860
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(Left column)

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Qy   4878  GTCCGGGGGGGCCGGTGGCCTTCCTGCGCAGCACTCTGTGCCCCCAGCCCTGGGCCGGCC  4937
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  23750  GTCCGGGGGGGCCGGTGGCCTTCCTGCGCAGCACTCTGTGCCCCCAGCCCTGGGCCGGCC  23809

Qy   4938  CTGCCGTCCAGTGCCTGCAGTGCCGTGGCTAACAGAGGAGGGCCCGCCTGTTCGCG  4997
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  23810  CTGCCGTCCAGTGCCTGCAGTGCCGTGGCTAACAGAGGAGGGCCCGCCTGTTCGCG  23869

Qy   4998  GCCCGCGCCCGTGACCTTCCTACCGCGCGGCTGCCGGTCTTCTGTGCGCAATGCGCGAGAA  5057
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  23870  GCCCGCGCCCGTGACCTTCCTACCGCGCGGCTGCCGGTCTTCTGTGCGCAATGCGCGAGAA  23929

Qy   5058  GAGACGCGCGCTGCTGTACAAGAGAGCACAACCTGGCCCAGGTGCCGCTGAAGGGTCGCCCCG  5117
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  23990  GAGACGCGCGCTGCTGTACAAGAGAGCACAACCTGGCCCAGGTGCCGCTGAAGGGTCGCCCCG  23989

Qy   5118  GCCACACCCTTGGTCTCCCCGCTGGGGGTCGCTGCAGACGCGCCAATAAAAACGCACAGC  5177
           ||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db  23990  GCCACACCCTTGGTCTCCCCGCTGGGGGTCGCTGCAGACGCGCCAATAAAAACGCCCCAGC  24049

Qy   5178  CGGGCGAGAAAAAAAAAAAAAAAAAAAA  5207
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Db  24050  CGGGCGAGAAAAAAAAAAAAAAAAAAAA  24079
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RESULT 6
AAC62286

ID   AAC62286 standard; cDNA; 5007 BP.
XX
AC   AAC62286;
XX
DT   19-MAR-2001  (first entry)
XX
DE   cDNA encoding a full length human signal transduction polypeptide.
XX
KW   Signal transduction; H19G5; kinase; cardiac disease; angina pectoris;
KW   congestive heart failure; dilated congestive cardiomyopathy;
KW   hypertrophic cardiomyopathy; restrictive cardiomyopathy; hypertension;
KW   mitral valve disease; aortic valve disease; tricuspid valve disease;
KW   myocardial infarction; cardiac arrhythmia; arteriosclerosis;
KW   atherosclerosis; cardiac tumour; microbial infection; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             97..4929
FT                   /*tag= a
FT                   /product= "signal transduction polypeptide H19G5"
XX
PN   WO200063381-A1.
XX
PD   26-OCT-2000.
XX
PF   11-APR-2000; 2000WO-US009488.
XX
PR   16-APR-1999; 99US-0129553P.
XX
PA   (SCIO-) SCIOS INC.
XX
PI   Zeng W, Stanton L, Kong H;
XX
DR   WPI; 2001-007013/01.
DR   P-PSDB; AAB30568.
XX
PT   Novel h19G5 polypeptides capable of regulating signal transduction and
PT   exhibiting kinase activity useful for identifying antibodies to treat
PT   cardiac diseases, and additional mediators of signal transduction.
XX
PS   Claim 4; Page 59-61; 81pp; English.
XX
CC   The present sequence encodes a human protein with putative function in
CC   signal transduction. The polypeptide is designated H19G5. The protein is
CC   capable of regulating signal transduction and exhibits kinase activity.

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Qy  1038  CATCACCCCAGCAGAGCTGCAGTTCAGCCAGTACGGCTTCCCCTGAGTTCGTCTCCCCGA  1097
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   861  CATCACCCCAGCAGAGCTGCAGTTCAGCCAGTACGGCTTCCCCTGAGTTCGTCTCCCCGA   920

Qy  1098  GATCATCCAGCAGCAGAACCCTGTGAGCGAAGCCTTCGACATTTGGCCATGGGGTGTCATCTC  1157
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   921  GATCATCCAGCAGCAGAACCCTGTGAGCGAAGCCTTCGACATTTGGCCATGGGGTGTCATCTC   980

Qy  1158  CTACCTCAGCCTGACCTGCTCATCCCATTTGCCGCGAGAGTGACCGTGCCACCCTCCT  1217
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   981  CTACCTCAGCCTGACCTGCTCATCCCATTTGCCGCGAGAGTGACCGTGCCACCCTCCT  1040

Qy  1218  GAACGTTCCTGGAGGGGCGCGTGTCATGGAGCAGCCCATGGCTGCCACCCTCCAGGCAAGA  1277
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1041  GAACGTTCCTGGAGGGGCGCGTGTCATGGAGCAGCCCATGGCTGCCACCCTCCAGGCAAGA  1100

Qy  1278  CGCCAAAGACTTCATCAAGGCTACGGCTGCAGAGAGCCCTCAGGCCCGGCCCTAGTGCGGC  1337
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1101  CGCCAAAGACTTCATCAAGGCTACGGCTGCAGAGAGCCCTCAGGCCCGGCCCTAGTGCGGC  1160

Qy  1338  CCAGTGCCTCTCCCACCCTGGTTCCTGGAGGGACTGCCGGAGGAGCCCACTTCAT  1397
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1161  CCAGTGCCTCTCCCACCCTGGTTCCTGGAGGGACTGCCGGAGGAGCCCACTTCAT  1220

Qy  1398  CAACACCAAGCAGCTCAAGTTCCTCCTGGCCCGGAAGTCGTCTGCAGGTTCCCTGATGAG  1457
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1221  CAACACCAAGCAGCTCAAGTTCCTCCTGGCCCGGAAGTCGTCTGCAGGTTCCCTGATGAG  1280

Qy  1458  CTACAAGTCCATCCTGTGATGCGCTCCATCCCTGAGCTGCTCGCGGGGGCCCACCCGACAG  1517
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Db  1281  CTACAAGTCCATCCTGTGATGCGCTCCATCCCTGAGCTGCTCGCGGGGGCCCACCCGACAG  1340

Qy  1518  CCCCTCCTCGGGGTAGCCCGGCACTCCGGACACTCGGTTGCTCTCCGAGGACACTCCAGTTCCTC  1577
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1341  CCCCTCCTCGGGGTAGCCCGGCACTCCGGACACTCGGTTGCTCTCCGAGGACACTCCAGTTCCTC  1400

Qy  1578  CTCCTCCTGCAACGAGCTCGCCCCATTTGCCCGGCTAAGTCACTGCCACCCCCC  1637
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1401  CTCCTCCTGCAACGAGCTCGCCCCATTTGCCCGGCTAAGTCACTGCCACCCCCC  1460

Qy  1638  GGTGACACACTCACCACTGTCTGCACCCCCGGGGCTTCTGCGCCCTCGGCCAGCCTGCC  1697
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Db  1461  GGTGACACACTCACCACTGTCTGCACCCCCGGGGCTTCTGCGCCCTCGGCCAGCCTGCC  1520

Qy  1698  TGAGGAAGCCGGAGGCGCTCACCGGCCAGTGAGGGCTCGGCCCCAGTCCGGCTCGCTGATCCCCGA  1757
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1521  TGAGGAAGCCGGAGGCGCTCACCGGCCAGTGAGGGCTCGGCCCCAGTCCGGCTCGCTGATCCCCGA  1580

Qy  1758  GGGTGCCGGGCCCACCGGGCGGGGGCTGAGCACACGGGCCCTGGCCCGGGGAGCAGGCG  1817
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1581  GGGTGCCGGGCCCACCGGGCGGGGGCTGAGCACACGGGCCCTGGCCCGGGGAGCAGGCG  1640

Qy  1818  GTTCTACCACCAGGCGGGCGGGGGTGAGAGCGGCCCTGGCCGGGGCGTACATTGCGGGG  1877
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1641  GTTCTACCACCAGGCGGGCGGGGGTGAGAGCGGCCCTGGCCGGGGCGTACATTGCGGGG  1700

Qy  1878  GCACCCACTTGGCCCCTGGCCACAGCCACTCCCTGGAAGGGCGGGCCCAGGGCGCTGCCAGG  1937
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1701  GCACCCACTTGGCCCCTGGCCACAGCCACTCCCTGGAAGGGCGGGCCCAGGGCGCTGCCAGG  1760

Qy  1938  CCTGCGCGGAGCCACTGATGAGCACCGGCGTCGGCCAAAGCCTGCCCTCGGCCTGCCTGG  1997
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1761  CCTGCGCGGAGCCACTGATGAGCACCGGCGTCGGCCAAAGCCTGCCCTCGGCCTGCCTGG  1820

Qy  1998  GGCCCACCCTCCTGCCCAAAGCCCCTCATTGGCCCCTCATTCGAGACTGTGCCTCCTGG  2057
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1821  GGCCCACCCTCCTGCCCAAAGCCCCTCATTGGCCCCTCATTCGAGACTGTGCCTCTG  1880

Qy  2058  CACCCACTTGGCCCCTGGCCCTGGCCACAGCCACTCCCTGGAACATGACTCTCCGAGCACCCCCG  2117
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1881  CACCCACTTGGCCCCTGGCCCTGGCCACAGCCACTCCCTGGAACATGACTCTCCGAGCACCCCCG  1940

Qy  2118  CCCCTCCTCGGAGGCCTGCGGTGAGGCACAGCCGACTGCCTTCAGCCCGCGGGGGGGGC  2177
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db  1941  CCCCTCCTCGGAGGCCTGCGGTGAGGCACAGCCGACTGCCTTCAGCCCGCGGGGGGGGC  2000

Qy  2178  CCCATCAGGGACATGGGGCACGTGGCACCTCAAAGCAGCTTCCATCCACTGGTGGCCA  2237
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2001  CCCATCAGGGACATGGGGCACCTCAAAGCAGCTTCCATCCACTGGTGGCCA  2060

Qy  2238  CCCAGGCACTGCTCAGCCAGAGAGCCCATCCCGACAGCCAGCCAGCCC  2297
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db  2061  CCCAGGCACTGCTCAGCCAGAGAGCCCATCCCGACAGCCAGCCAGCCC  2120

Qy  2298  TTTCTGCCACCCAAGCAGCAGGGTTCGCCCCCCCAGGAGGGCTGAGCCCCACCCAGCAGT  2357
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2121  TTTCTGCCACCCAAGCAGCAGGGTTCGCCCCCCCAGGAGGGCTGAGCCCCACCCAGCAGT  2180

Qy  2358  TGCCCCATGCCTCCTGGCTTCCTTCCCTCCAGGATCTTGCAAAGAGCCCCCTAGTACC  2417
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2181  TGCCCCATGCCTCCTGGCTTCCTTCCCTCCAGGATCTTGCAAAGAGGGCCCCCTAGTACC  2240

Qy  2418  CTCAAGCCCCTTCTTGGACAGCCCCAGGCACCCCCTGCCCCTGCCAAAGCAAGCACCCCCC  2477
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2241  CTCAAGCCCCTTCTTGGACAGCCCCAGGCACCCCCTGCCCCTGCCAAAGCAAGCAGCCCCC  2300

Qy  2478  ATTGGACTCTAAGATGGGGCCTGAGAGACATCTCTTCTCCTGGGAGGCCAAAACCCGGCCC  2537
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2301  ATTGGACTCTAAGATGGGGCCTGAGACATCTCTTCTCCTGGGAGGCCAAAACCCGGCCC  2360

Qy  2538  CTGCAGTTCCCCAGGTCAGCCTCCCAGGGCTCTTCCCAGCGGCGGGCTCCCTCAGGGT  2597
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Db  2361  CTGCAGTTCCCCAGGTCAGCCTCCCAGCGGTCTTCCCAGCGGCGGGCTCCCTCAGGGT  2420

Qy  2598  GGGTCCTCCTCCCAGGTGGCACAGAGCTCGGCCCCTCCGATGCGGAGGGCTGACCCA  2657
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2421  GGGCTCCTCCCAGGTGGCACAGAGCCTGGCCCCTCCGATGCGGAGGGCTGACCCA  2480

Qy  2658  GGAGGCTGAGGATCTGTCCGACTCCACACCCACCTTGCGAGCGGCTCAGGAACAGGTGAC  2717
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2481  GGAGGCTGAGGATCTGTCCGACTCCACACCCACCTTGCGAGCGGCTCAGGAACAGGCGAC  2540

Qy  2718  CATGCGCAAGTTCTCCCTGGTGTGTCGCGGGCGTACGCAGCGGTGGCTATGGCAC  2777
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2541  CATGCGCAAGTTCTCCCTGGTGTGTCGCGGGCGTACGCAGCGGTGGCTATGGCAC  2600

Qy  2778  CTTTGCCTTGGTGGAGATGCAGGGGGCATGCTGGGGCAGGGGCAGGAGGGGCCAGGAT  2837
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Db  2601  CTTTGCCTTGGTGGAGATGCAGGGGGCATGCTGGGGCCAATCGGGGCCAGGAGGGGCCAGGAT  2660

Qy  2838  AGCCTGGGCTGTGTCCCAGTCGGAGGAGCAGGAGAGCCCAGGGGCTGAGTCCCA  2897
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2661  AGCCTGGGCTGTGTCCCAGTCAGAGGAGCAGGAGAGCAGGAGGGGCTGAGTCCCA  2720

Qy  2898  GTCGGAGCAGCAGGGTGTGAGAGCCCAGGGCTCCCAGGTCAGTGCAAGGCC  2957
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2721  GTCGGAGCAGCAGGGTGTGAGAGCCCAGGGTCAGTCAGTGCAAGGCC  2780

Qy  2958  TGTGCCTGGAGGTCGGTGCAGATCCGGACCTGTCAGTGATGCGGAGGAGGA  3017
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2781  TGTGCCTGAGGTCGGTGCAGATCCGGACCTGTCAGTGATGCGGAGGAGGA  2840

Qy  3018  CATCGGGCAGGTTCCCCTGGTCAGATCCGGGACCTCAGACTCTCAGACCTGTA  3077
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Db  2841  CATCGGGCAGGTTCCCCTGGTCAGATCCGGGACCTCAACCTCTCAGACCTCGA  2900

Qy  3078  CACAATATCCCTGGACATTCCGAGGTGGACACCCGGCTACCCTCAACCTCTGTA  3137
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2901  CACAATATCCCTGGACATTCCGAGGTGGACACCCGGCTACCTCAACCTCTGTA  2960

Qy  3138  CGATATCAAGTACCTCCCATTGGAGTTTATGATCTTCAGGAAAGTCCCGTCA  3197
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Db  2961  CGATATCAAGTACCTCCCATTGGAGTTTATGATCTTCAGGAAAGTCCCGTCA  3020

Qy  3198  GCCAGAGCCGCCCGCCCTTGCGGGTGAGGCACAGCCGACTGCCTTCAGCCCGCCACGTG  3257
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Tue Apr 27 10:11:33 2004

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Db   3021 GCCAGAGCCGCGCCCTCCCCATGGCTGAGGAGGAGCTGGCCGAGTTCCCGAGCCCACGTG 3080

Qy   3258 GCCCTGCAGTGAACTGGGCCCCACGCAGCGGCCTGAGGATCACAGAGGAGTCAGAGGA   3317
          ||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||
Db   3081 GCCCTGCAGTGAACTGGGCCCCACGCAGGCCCCTCAAGGGACCTGCGCCACCCGGCCC    3140

Qy   3318 TGTGGACGGCCTGCGTTGCGCAGAGGCTGCCGTGGGCAGGAAGCGCAAGTGGTCCTCGCCGTC 3377
          |||| ||||||||||||||||||||||||||||||||  ||||| ||||||||||||||||
Db   3141 TGTGGACGCGCTGCTGGCCAGAGCGTGCCGTGGGCAGGACGCGCAAGTGGTCCCTCGCCGTC  3200

Qy   3378 ACGCAGCCTCTTCCACTTCCTGGAGGAGGCACCTGCCGCGGATGAGCCTGCGAGAGCTGGG 3437
          |||||||||||||||||||| |||||||||||||||||||||||||||| |||||||||||
Db   3201 ACGCAGCCTCTTCCACTTCCCGGAGGAGGCACCTGCCGCGGATGAGCCTGCGAGAGCTGGG  3260

Qy   3438 GCTGCGTGAGAGAGTGAAGGCCTCCGTGGAGCACATCTCCGGATCTTGAAGGGCAGGCC   3497
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Db   3261 GCTGCGTGAGAGAGTGAAGGCCTCCGTGGAGCACATCTCCGGATCCTGCGAAGGGCAGGCC  3320

Qy   3498 GGAAGGTCTCGAGAAGGAGGGGGCCCCCAGGAGAAGCCAGGCCTTGCTTCCTTCCGGCT   3557
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Db   3321 GGAAGGTCTCGAGAAGGAGGGGGCCCCCAGGAGAAGCCAGGCCTTGCTTCCTTCCGGCT    3380

Qy   3558 CTCAGGTCTGAAGAGCTCTAAGGAGAGCTTCAGATGAGAC                      3617
          |||||||||||||||||||||||||||||||||||||||||
Db   3381 CTCAGGTCTGAAGAGCTGGACCGAGCGCCGAGCGCCCGACAC                    3440

Qy   3618 TGTGGTTCCTGGGCCAGTCAGTGACACTGGCCTGCCAGTGTCAGCCCAGCCAGCTGCCCA  3677
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Db   3441 TGTGGTCCTGGGCCAGTCAGTGACACTGGCCTGCCAGTGTCAGCCCAGCCAGCCGCCCA    3500

Qy   3678 GGCCACCTGGACAAAGACCGGAGCCCCCCGGAGCAGCAGCCCGTGTCCTCATCCTCTGC   3737
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3501 GGCCACCTGGACAAAGACCGGAGCCCCCCGGAGCAGCAGCCCGTGTCCTCATCCTCTGC    3560

Qy   3738 CACCCTCAAGAACTTCCAGCTTCTGACCATTCCGGTGGTGGTGGCTGAGGGACCTGGGTGT 3797
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Db   3561 CACCCTCAAGAACTTCCAGCTTCTGACCATTCCGGTGGTGGTGGCTGAGGGACCTGGGTGT  3620

Qy   3798 GTACACCTGAGCGTGAGCAGCGTGAATGGCGTGGGAATCCTACGGCCCTGTGACCACCAC  3857
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3621 GTACACCTGAGCGTGAGCAGCGTGAATGGCGTGGGAATCCTACGGCCCTGTGACCACCAC  3680

Qy   3858 GGCAGAGCGCCCCTCATCTTCGCCATGCCCGGATATCGGGGAGGTGTACGGCGGATGGGGT 3917
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3681 GGCAGAGCGCCCCTCATCTTCGCCATGCCCGGATATCGGGGAGGTGTACGGCGGATGGGGT  3740

Qy   3918 GCTGCGTGGTCTGGAAGCCCGTGGAATCCTACGGCCCTGTGACCATTGTGCAGTGCAG    3977
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3741 GCTGCGTGGTCTGGGAAGCCCGTGGAATCCTACGGCCCTGTGACCATTGTGCAGTGCAG   3800

Qy   3978 CCTAGAAGGGCGGCAGCTGACCACACTGGCCTCCGACATCTTTGACTGCTGCTACCTGAC  4037
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3801 CCTAGAAGGGCGGCAGCTGACCACACTGGCCTCCGACATCTTTGACTGCTGCTACCTGAC  3860

Qy   4038 CAGCAAGCTCTCCCGGGGTGGCACTTCGCACGGCATGTGTCAGCAAGGCAGG         4097
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Db   3861 CAGCAAGCTCTCCCGGGGTGGCACTTCGCACGGCATGTGTCAGCAAGGCAGG         3920

Qy   4098 AATGGGGTCCCTACAGCAGCCCTCGGACGCAAGTCCTCCTGGGAGGGGCCCAGCCACCTGGC 4157
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3921 AATGGGGTCCCTACAGCAGCCCTCGGACGCAAGTCCTCCTGGGAGGCGCCCAGCCACCTGGC  3980

Qy   4158 CTCTGAGGAGGAGCAGGCCAGGGCGTCAGCCCAACCCTGCCCAGCGCACAAAGACCTTCGC 4217
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Qy   4278 CAGCGGCGGGCGGCCTGGCCCCGGCCAAGATCATCCCCACCACCCCAAGGACAAGACAGCAGT 4337
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Qy   4518 GCAGATGTTGAGTGCCACCCAGTACCTGCCACAACCAGCACAATCCTGCACCTGGACCTGCGAG 4577
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Db   4401 GTCCGAGAACATGATCATCACCGAATACAACCTGCTCAAGAGTCGTGGCAATGC           4460

Qy   4638 ACAGAGCCTCAGCCAGGAGAAGTGCTGCCCTCAGACAAGTTCAAGGACTACTAGAGAC      4697
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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OM nucleic - nucleic search, using sw model

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GenCore version 5.1.6

Run on: April 26, 2004, 06:40:08 ; Search time 13028 Seconds
(without alignments)
17323.241 Million cell updates/sec

Title: US-10-697-263-1
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Sequence: 1 cagcacgaggaactccttct........aaaaaaaaaaaaaaaaa 5207

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 2167151 6995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
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| 1 | 5207 | 100.0 | 5207 | 6 | AR255867 | AR255867 Sequence |
| 2 | 5207 | 100.0 | 5207 | 6 | AX430856 | AX430856 Sequence |
| 3 | 5207 | 100.0 | 5207 | 6 | AX430858 | AX430858 Sequence |
| 4 | 5173.6 | 99.4 | 5454 | 6 | AX504255 | AX504255 Sequence |
| 5 | 4915.8 | 94.4 | 5007 | 6 | AX039410 | AX039410 Sequence |
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| 7 | 4885.2 | 93.8 | 4936 | 6 | AX207401 | AX207401 Sequence |
| 8 | 4146.6 | 79.6 | 4175 | 6 | AX039409 | AX039409 Sequence |
| 9 | 4020.2 | 77.2 | 4041 | 6 | AB046859 | AB046859 Homo sapi |
| 10 | 3197.8 | 61.4 | 3225 | 6 | AX642969 | AX642969 Sequence |
| 11 | 2067.2 | 39.7 | 62164 | 9 | AL670729 | AL670729 Human DNA |
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| c 16 | 827.4 | 15.9 | 260998 | 2 | AC099089 | AC099089 Rattus no |
| c 17 | 756.8 | 14.5 | 1183 | 10 | BC046431 | BC046431 Mus muscu |
| c 18 | 639.8 | 12.3 | 250087 | 2 | AC096931 | AC096931 Rattus no |
| 19 | 613.8 | 11.8 | 164766 | 2 | AC026657 | AC026657 Homo sapi |
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| 21 | 358.4 | 6.9 | 382 | 9 | AX315962 | AX315962 Sequence |
| 22 | 327.6 | 6.3 | 6726 | 9 | AB037718 | AB037718 Homo sapi |
| 23 | 327.6 | 6.3 | 7710 | 6 | AX056397 | AX056397 Sequence |
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| 33 | 175 | 3.4 | 2055 | 9 | AB022341 | AB022341 Homo sapi |
| 34 | 175 | 3.4 | 2079 | 6 | BD127287 | BD127287 Primer fo |
| 35 | 175 | 3.4 | 2079 | 9 | AK074799 | AK074799 Homo sapi |
| 36 | 173.4 | 3.3 | 1514 | 10 | RNO6971 | RNO6971 Rattus no |
| 37 | 173.4 | 3.3 | 1560 | 10 | BC062076 | BC062076 Rattus no |
| 38 | 173.4 | 3.3 | 2105 | 6 | BD176607 | BD176607 Method of |
| 39 | 173.4 | 3.3 | 2105 | 9 | AB007144 | AB007144 Homo sapi |
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| 41 | 173.4 | 3.3 | 2132 | 6 | AR124102 | AR124102 Sequence |
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ALIGNMENTS

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DEFINITION  Sequence 1 from patent US 6482624.
ACCESSION   AR255867
VERSION     AR255867.1  GI:27305065
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 5207)
  AUTHORS   Wei,M.-H., Ketchum,K.A., Di Francesco,V. and Beasley,E.M.
  TITLE     Isolated human kinase proteins, nucleic acid molecules encoding
            human kinase proteins, and uses thereof
  JOURNAL   Patent: US 6482624-A 1 19-NOV-2002;

Pred. No. is the number of results predicted by chance to have a

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                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Query Match          100.0%;  Score 5207;  DB 6;  Length 5207;
Best Local Similarity 100.0%;  Pred. No. 0;
Matches 5207;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;
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Qy       1 CAGCACGAGGAACTCCTTCTGATCACCTGGCCAGCTGAGGTCAGAGTGGGAGAGGCAGTG 60
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Db       1 CAGCACGAGGAACTCCTTCTGATCACCTGGCCAGCTGAGGTCAGAGTGGGAGAGGCAGTG 60

Qy      61 GTTCCATTGAAGGAGTACTCCTAACTGTCAGAAGCCTGGGCGGTCAGGATGGGGTGCTGT 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 GTTCCATTGAAGGAGTACTCCTAACTGTCAGAAGCCTGGGCGGTCAGGATGGGGTGCTGT 120

Qy     121 CGCTTGGCTGCGGGGGGTGTTCAGTTGCCCACAGTGTATCTCAGGGTCTCACCAACCAT 180
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Db     121 CGCTTGGGCTGCGGGGGGTGTTCAGTTGCCCACAGTGTATCTCAGGGTCTCACCAACCAT 180

Qy     181 CCAAGCATGGTAGGCTGTGCTGGCACCCAGGGTTGTGTTGGCTGAGGTGGTGGTGGTGGTCTCCAC 240
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Qy  2401  GAGGCCCCTTAGTACCCTCAAGCACCCCTTCTTGGACAGCCCCAGCAGCCCCTGCCCT    2460
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Qy  2461  GCCAAAGCAAGCCCCCATTGACTCTAAGATGGGGCCTGAGACATCTTCTTCTTCCTGGG   2520
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Db  2461  GCCAAAGCAAGCCCCCATTGACTCTAAGATGGGGCCTGAGACATCTTCTTCTTCCTGGG   2520

Qy  2521  AGGCAAAACCCGCCCAGTTCCCGCTCAGCCCTGGAGCTCTTCCCAA              2580
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Qy  2581  GTGAGCTCCCTCAGGGTGGGCTTCCTCCCAGGTGGGCACAGAGCCTGGCCCCTCCCTGGAT 2640
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Qy  2641  GCGGAGGGCTGGACCCAGGAGGCTGAGGATCTGTCCGACTTCCACACCCACCTTGCAGCGG 2700
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Qy  2701  CCTCAGGAACAGGTGACCATGCGCAAGTTCTCCCTGGGTGGTCGGGGGGCTACCGGAGC   2760
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Qy  2821  CCCATGTGGGCCAGGATAGCCTGGGCTGTGTCCAGTCGGAGGAGGAGCAGGAGCAGGAGAG 2880
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Db  2821  CCCATGTGGGCCAGGATAGCCTGGGCTGTGTCCAGTCGGAGGAGGAGCAGGAGCAGGAGAG 2880

Qy  2881  GCCAGGGCTGAGTCCAGTCGGAGGAGCAGCAGGAGGCCGCAGGGCTCCCACTGCCC     2940
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Qy  3241  TTCCGGAGCACCCAGTGCCCTGGCCCCAGGTGAACTGGCCCCCACCAGGCCTGGAGATC   3300
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Qy  3301  ACAGAGGAGTCAGAGGATGTGGACGGCGTCGGTGGGCGACAGAGGTGCCGTGGCAGGAGCGC 3360
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Qy  3961  TACATTGTGCAGTGCAGCCAGCGGCGCAGTGTCCTCACAGCAGCCCCACTGCCTTCCGACACACTCTTT 4020
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Qy  4081  TGTGTCAAGGCACCAGAATGGGTCCCTACAGCAGCCCCTGGGAGCAGGTCTCCTGGGA      4140
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Qy  4141  GGGCCCAGCCACCTGCCCAACCCCTGCCCCGGGGGCGGTCAGCCAAGGGGTCAGCCGACACTTC 4200
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Db  4141  GGGCCCAGCCACCTGCCCAACCCCTGCCCTCAGGAGGAGAGCCACGGCGGGTCAGCCCGACACTTC 4200

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KEYWORDS       .
SOURCE         Homo sapiens (human)
  ORGANISM     Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1
  AUTHORS      Ketchum,K., Beasley,E.M., Wei,M.H. and di Francesco,V.
  TITLE        Isolated human kinase proteins, nucleic acid molecules encoding
               human kinase proteins, and uses thereof
  JOURNAL      Patent: WO 0240683-A 1 23-MAY-2002;
               PE CORP NY (US)
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ORIGIN

Query Match           100.0%;  Score 5207;  DB 6;  Length 5207;
Best Local Similarity 100.0%;  Pred. No.0;
Matches 5207;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

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Db     1 CAGCACGAGGAACTCCTTCTGATCACCTGGCCAGCTGAGGTCAGAGTGGGAGGAGGCAGTG 60

Qy    61 GTTCCATTGAAGGAGTACTCCTAACTGTCAGAAGCCTGGGCGGTCAGGATGGGGTGCTGT 120
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Db   121 CGCTTGGGCTCGGGGGGGTGTTCAGTTGCCACAGTGTATCTCAGGGTCTCACCAACCAT 180

Qy   181 CCAAGCATGGTAGGCTGTGCTGGCACCCAGGGTTGTGTGGCTGGGGAGGTGGTGCTCCAC 240
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Db   181 CCAAGCATGGTAGGCTGTGCTGGCACCCAGGGTTGTGTGGCTGGGGAGGTGGTGCTCCAC 240

Qy   241 AGTTCCTCCCTGCCCTCCCAGGGCCCCATCCATGCAGGTAACCATCGAGGATGTGCAG 300
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Db   241 AGTTCCTCCCTGCCCTCCCAGGGCCCCATCCATGCAGGTAACCATCGAGGATGTGCAG 300

Qy   301 GCACAGACAGGCGGAACGGCCCATTCGAGGCTATCATTGAGGCGACCCACAGCCCTCG 360
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Qy   361 GTGACCTGGTACAAGGACAGCGTCCAGCTGGTGGCATGGGCCTGGTAACAGAGGAG 420
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Qy   421 GAAGGCACCACCATACTCCCGGTGCTGCAAGGCATGGGCCTGCGAAGGATGCCGGCGTTTAC 480
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Db  4201 AGCACAAAGACCTTCGCATTCCAGACACAGATCCAGAGGGGCCGCTTCAGCGTGGTGCGG 4260

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Qy  4381 CTGGCCCAGCTGCACGCAGCCTCACCTCAGCCCCCGCACCTGGTGCTCATCTTGGAGCTG 4440
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Qy  4741 ACAGACATCTGGGCCATCGGTGTGACAGCCTTCATCATGCTGAGCGCCGAGTACCCGGTG 4800
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Qy  4801 AGAGCGGAGGGTGCACGCGACCTGCAGAGAGGACTGCGCAAGGGGCTGGTCCGGCTGAGC 4860
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RESULT 2
AX430856
LOCUS       AX430856              5207 bp    DNA     linear      PAT 28-JUN-2002
DEFINITION  Sequence 1 from Patent WO0240683.
ACCESSION   AX430856
VERSION     AX430856.1  GI:21655921
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Db 1561  GGCTCCTCCAGTTCCTCCTCTCGACAACGAGCTCGCCCCATTTGCCCGGGCTAAG  1620

Qy 1621  TCACTGCCACCCTCCCCGGTGACACTCACCACTGCTCGCACCCCGGGGTTCCTGCGCG  1680
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1621  TCACTGCCACCCTCCCCGGTGACACATGACCATCACCACTGCTCGCACCCCGGGCTTCCTGCGGG  1680

Qy 1681  CCCTCGGCCAGCCAGCCTCGGGCCGAGAGCGCAGCCGGCCAGTGAGCGCTCCACCGAGGCCCCAGCT  1740
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1681  CCCTCGGCCAGCCAGCCTCGGGCCGAGAGCGCAGCCGGCCAGTGAGCGCTCCACCGAGGCCCCAGCT  1740

Qy 1741  CCGCCTGATCCTCCCGAGGGTGCCGGGGCACCGCGCCCTGTCCCCGGGAC  1800
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Db 1741  CCGCCTGATCCTCCCGAGGGTGCCGGGGCACCGCGCCCTGTCCCCGGCAC  1800

Qy 1801  AGCGTCATCCGCAGCCTGTTTACCACCGGCCGGCTGGAGCACGGGGGCCTG  1860
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1801  AGCGTCATCCGCAGCCTGTTTACCACCGGCCGGCTGGAGCACGGGGGCCTG  1860
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Qy 1861  GCCCCGGGGAGCAGCAGCGGCACCCCGGCCGGGGCGGGCCCCGGCCACCTGCTGCTGGAAGGGCGGCTACATT  1920
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Db 1861  GCCCCGGGGAGCAGCAGCGGCACCCCGGCCGGGGCGGGCCCCGGCCACCTGCTGCTGGAAGGGCGGCTACATT  1920

Qy 1921  GCGGGGGCGCTTGCCAGGCCTGCGCGGCAGCCACCGTGATGGAGCACCGCCGTGCTGGAGGAGGAG  1980
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1921  GCGGGGGCGCTTGCCAGGCCTGCGCGGCAGCCACTGATGGAGCACCGCCGTGCTGGAGGAGGAG  1980

Qy 1981  GCCGCCAGGAGGAGGAGCAGGCAGGCCACCCTCCTGCCCAAGAGCCCCCTCATTCGAGACTGCCCTC  2040
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Db 1981  GCCGCCAGGAGGAGGAGCAGGCAGGCCACCCTCCTGCCCAAAGCCCCCTCATTCGAGACTGCCCTC  2040

Qy 2041  CGGCTGCCTGCCTCTGGCACCCCACTTGGCCCCTGGCCACAGCCACTCCCTGGAACATGAC  2100
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Db 2041  CGGCTGCCTGCCTCTGGCACCCCACTTGGCCCCTGGCCACAGCCACTCCCTGGAACATGAC  2100

Qy 2101  TCTCCGAGCACCCCGCCCTGCGGTGGAGGCCTGCGGTGAGGCACAGGGACTGCCTTCA  2160
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2101  TCTCCGAGCACCCCGCCCTGCGGTGGAGGCCTGCGGTGAGGCACAGGGACTGCCTTCA  2160

Qy 2161  GCCCCCTCCGGGGGGCCCCTATCAGGACATGGGCCAGCAGCTGCTCAGCCGAGGCCATCCCCGGACAGCCCT  2220
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Db 2161  GCCCCCTCCGGGGGGCCCCTATCAGGACATGGGCCAGCAGCTGCTCAGCCGAGGCCATCCCCGGACAGCCCT  2220

Qy 2221  CCATCCACTGTGGCCACCAGGACTGCTCAGCCGACTGCTCAGCGAGAGTCCCCGGACAGCCCCT  2280
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Db 2221  CCATCCACTGGTGGCCACCAGGACTGCTCAGCCGACTGCTCAGCGAGAGTCCCCGGACAGCCCCT  2280

Qy 2281  TGGGGGCAGCCAGCCCCTTCTGCCACCCAAGCAGGTTCTGCCCCCCAGGAGGGCTGC  2340
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2281  TGGGGGCAGCCAGCCCCTTCTGCCACCCAAGCAGGTTCTGCCCCCCAGGAGGGCTGC  2340

Qy 2341  AGCCCCACCCAGCAGTGCCCCATGCCCTCCTGGCTCCTTCCCTCCCTCCCGGATCTTGCAAA  2400
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Db 2341  AGCCCCACCCAGCAGTGCCCCATGCCCTCCTGGCTCCTTCCCTCCCTCCCGGATCTTGCAAA  2400

Qy 2401  GAGGCCCCCTTAGTACCCTCAAGCCCCTTCTTGGACTCCGCCCTTCTTCCGCCCCT  2460
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Db 2401  GAGGCCCCCTTAGTACCCTCAAGCCCCTTCTTGGACAGCCCCCTTCTTCCGCCCCT  2460

Qy 2461  GCCAAAGCAAGCCCCAGAGGCTCTAAGATGGGCCTGAGACTCGTGTCCGAGATCTGTCCGAGCTCTTCCTGGG  2520
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2461  GCCAAAGCAAGCCCCAGAGGCTCTAAGATGGGCCTGAGACTCGTGTCCGAGATCTGTCCGAGCTGTCCTGGG  2520

Qy 2521  AGGCCAAAACCCGGCCCTGCAGTTCCCAGGGTCAGCCTCCAGGGTGGTGCGGGGCTCTTCCCAA  2580
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2521  AGGCCAAAACCCGGCCCTGCAGTTCCCAGGGTCAGCCTCCAGGGTGGTGCGGGGCTCTTCCCAA  2580

Qy 2581  GTGAGCTCCCTCAGGGTGGGCTCCTCCCAGTGGCACAGAGCCTGGCCCCTCCTGGAT  2640
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2581  GTGAGCTCCCTCAGGGTGGGCTCCTCCCAGTGGCACAGAGCCTGGCCCCTCCTGGAT  2640

Qy 2641  GCGGAGGGCTGGACCCAGAGGCTGAGGATCTGTTCCGACTCGTCACACCACCCTTGCAGCGG  2700
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2641  GCGGAGGGCTGGACCCAGAGGCTGAGGATCTGTTCCGACTCGTCCACACCACCCTTGCAGCGG  2700

Qy 2701  CCTCAGGAACAGGTGACCATGCGCAAGTTCTCCCCGGGGGTCTCGCGGCTACGCAGC  2760
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2701  CCTCAGGAACAGGTGACCATGCGCAAGTTCTCCCCGGGGGTGTCGCGGCTACGCAGC  2760

Qy 2761  GTGGCTGGCTATGGCCAGGAGCACCTTTGCCCTTGGGAGATGCAGGGGCATGCTGGGGCAGGGG  2820
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Db 2761  GTGGCTGGCTATGGCCAGGAGCACCTTTGCCCTTGGGGGGATGCAGGGGCATGCTGGGGCAGGGG  2820

Qy 2821  CCCATGTGGGCCAGGATAGCCTGGGCCGTGTCCCAGTGGGCAGGAGGAGCAGGAGGAGGAG  2880
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2821  CCCATGTGGGCCAGGATAGCCTGGGCCGTGTCCCAGTGGGCAGGAGGAGCAGGAGGAGGAG  2880

Qy 2881  GCCAGGCTGAGTCCCAGTCGGAGGAGCAGCAGGAGGCCCAGGGCTGAGAGCCCACTGCCC  2940
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2881  GCCAGGGCTGAGTCCCAGTCGGAGGAGCAGCAGGAGGCCCAGGGCTGAGAGCCCGACTGCCC  2940

Qy 2941  CAGGTCAGTGCAAGGCGTGCCTGAGGTCGGCAGGGCTCCCACCAGGAGCTCTCCAGAG  3000
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Qy  4021 GACTGCTGTCTACCTGACCAGCAAGCTCTCCCGGGGTGGCGACCTACACCTTCCGCACGGCA 4080
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Qy  4081 TGTGTCAGCAAGGCAGAGAATGGGTCCCTACAGAGCAGCCCTCGGAGCAGCGCCTCCTGGGA 4140
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Qy  4201 AGCACAAAGACCTTCGCATTCCAGACACAGATCCAGAGCAGATCCAGGAAA 4260
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Db  4261 CAATGCTGGGAGAAGGCCAGCGGCGGCGCGGCCTGCGCCGGCGCCCTCAAGGGCCTGCGCCGCCCAAGATCATCCCTACCACCCC 4320

Qy  4321 AAGGACAAGACAGCAGTGCTGCGCAATACGAGCCCCCGGCACCTGTGCTCATCTTGGAGCTG 4380
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Db  4321 AAGGACAAGACAGCAGTGCTGCGCAATACGAGCCCCCGGCACCTGTGCTCATCTTGGAGCTG 4380

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Qy  4441 TGCTCTGGGCCCGAGCTGTCTCCCCTGCTGGGCAGGGCCACCTGCCGCTGGAT 4500
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Qy  4501 GTGAAGGACTACCTGTGGCAGATGTTGAGTGCCACCCAGTACCTGCACAACCAGCACATC 4560
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4501 GTGAAGGACTACCTGTGGCAGATGTTGAGTGCCACCCAGTACCTGCACAACCAGCACATC 4560

Qy  4561 CTGCACCTGACCTGAGGTCCGGAGAACATGATCATCCGGAATACAACCTGCTCAAGGTC 4620
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Db  4561 CTGCACCTGACCTGAGGTCCGGAGAACATGATCATCCGGAATACAACCTGCTCAAGGTC 4620

Qy  4621 GTGGACCTGGCAATGCACAGACCTCAGCCCAGGAGAAGGTGCTGCCCTCAGACAAGTTC 4680
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Db  4621 GTGGACCTGGCAATGCACAGACCTCAGCCCAGGAGAAGGTGCTGCCCTCAGACAAGTTC 4680

Qy  4681 AAGGACTACCTAGAGACCATGGCTTCCAGAGCTTCATCATGCTGAGCGCCGAGTACCCGGTG 4740
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy  4741 ACAGACATCTGGGACCTGCACGCAGCTGGGCAAGGGCCAGAGGGCTGGTCCGGCTGAGC 4800
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Qy  4801 AGCAGCGGAGGGTGCACGGCCAAGGGCCAAGGCTGGTCCGGCTGTGAGC 4860
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Qy  3001 CCCACCCCATGGGAGACATCGGGCAGGTCTCCCGGTGCAGATCCGGACCTGTCAGGT 3060
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Db  3061 GATGCCGGAGGCGGCGACACAATATCCCTGACATTTCCGAGGTGACCCGCCTACCTC 3120

Qy  3121 AACCTCTCAGACCTGTACGTACGATATCAAGTACCTCCCATTCGAGTTTATGATCTTCAGGAAA 3180
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Db  3121 AACCTCTCAGACCTGTACGATATCAAGTACCTCCCATTCGAGTTTATGATCTTCAGGAAA 3180

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Db  3181 GTCCCCAAGTCCGCTCAGCCAGAGCCGCCCTCCCCATGGCTGAGGAGGAGCTGGCCGAG 3240

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Qy    5161  CAATAAAAACGCACAGCCGGGCGGGGAGAAAAAAAAAAAAAAAAAAA 5207
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RESULT 3
AX430858
LOCUS       AX430858              5207 bp    DNA        linear   PAT 28-JUN-2002
DEFINITION  Sequence 3 from Patent WO0240683.
ACCESSION   AX430858
VERSION     AX430858.1  GI:21655922
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Ketchum,K., Beasley,E.M., Wei,M.H. and di Francesco,V.
  TITLE     Isolated human kinase proteins, nucleic acid molecules encoding
            human kinase proteins, and uses thereof
  JOURNAL   Patent: WO 0240683-A 3 23-MAY-2002;
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ORIGIN

Query Match             100.0%;  Score 5207;  DB 6;  Length 5207;
Best Local Similarity   100.0%;  Pred. No. 0;
Matches 5207;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

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Db       1  CAGCACGAGGAACTCCTCTGATCACCTGGCCAGCTGAGGTCAGAGTGGGAGGAGGCAGTG   60

Qy      61  GTTCCATTGAAGGAGTACTCCTAACTGTCAGAAGCCTGGCCGGTCAGGATGGGGTGCTGT  120
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Qy     121  CGCTTGGGCTGCGGGGGGTGTTCAGTTGGCCACCAGTGTATCTCAGGGTCTCACCAACCAT  180
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Db     121  CGCTTGGGCTGCGGGGGGTGTTCAGTTGGCCACCAGTGTATCTCAGGGTCTCACCAACCAT  180

Qy     181  CCAAGCATGGTAGGCTGCGTGGCTGGCACCCAGGGTTGTGTGGCGTAACCATGCAGGATGTGCAG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181  CCAAGCATGGTAGGCTGCGTGGCTGGCACCCAGGGTTGTGTGGCGTAACCATGCAGGATGTGCAG  240

Qy     241  AGTTCCCTCCCTGCCCTCCCAGGGCCCCATCCATGCAGCCCCACCAGCCCCTCG  300
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Db     241  AGTTCCCTCCCTGCCCTCCCAGGGCCCCATCCATGCAGCCCCACCAGCCCCTCG  300

Qy     301  GCACAGAGCAGGCCGAACGGCCACCGCCGTCCAGCTCATTGAGGCCTATCATTGAGGGGCACCCAGCAGCCCCACAGCCCCTCG  360
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Db     301  GCACAGAGCAGGCCGAACGGCCACCGCCGTCCAGCTCATTGAGGCCTATCATTGAGGGGCACCCAGCAGCCCCACAGCCCCTCG  360

Qy     361  GTGACCTGGTACAAGGACAGCAGCGTCCCAGCTGGTGGACGCACCCGGCTTAGCCGCAGCAA  420
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Qy     421  GAAGGCACCACATACTCCCGTGTGCTGAGGCATGTGGCCTCGAAGGATGCCGGCGTTTAC  480
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Qy     541  GGGGGGCAATGAGCCGGACTCAGAGAGCAAAGCCACCGAGGAAGCTGCACTCCTTC  600
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Qy     601  TATGAGGTCAAGGAGGAGATTGGAAGGGGCGTGTTTGGCTTCGTAAAAGAGTGCAGCAC  660
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Db     601  TATGAGGTCAAGGAGGAGATTGGAAGGGGCGTGTTTGGCTTCGTAAAAGAGTGCAGCAC  660

Qy     661  AAAGGAAACAAGATCTTGTCGCGTCGCTCCCAGTTCATCCCCTACGGACGAGAACTCGGGCC  720
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Db     661  AAAGGAAACAAGATCTTGTCGCGTCGCTCCCAGTTCATCCCCTACGGACGAGAACTCGGGCC  720

Qy     721  CAGGCATACAGGGAGCGGAGACATCTGGCCGCGGTCCGCTGAGCCACCGCCGGTCACGGGGCTG  780
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Db     841  GAGCTGCTGACCGCCTGTACAGGAAGGGCGTGGTGACGAGGGCCGAGGTCAAGGTCTAC  900

Qy     901  ATCCAGCAGCTGGTGGAGGGGCTGCACTACCTGCACAGCCAGCATGGCGTTCTCCACCTGGAC  960
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Qy    1201  GACCGTGCCACCCTCCTGAACGTCCTGGAGGGCCGCGTGTCATGGAGCAGCCCCATGGCT 1260
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Db  2041  CGGCTGCCTCTGGCACCCCACTTGGCCCCTCCTGGAACATGAC  2100

Qy  2101  TCTCCGAGACACCCCGCCCCCGCCCTCCTGGAGGCCTGCGGTGAGGCACAGCGACTGCCTTCA  2160
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Db  2221  CCATCCACTGGTGCCACCCAGGGACACTGCTCAGCCAGGAGGCCATCCCGGACAGCCCT  2280

Qy  2281  TGGGGGCAGCCAGCCCCTTTCTGCCACCCCAAGCAGAGGGTTCTGCCCCCAGGAGGGCTGC  2340
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Db  2281  TGGGGGCAGCCAGCCCCTTTCTGCCACCCCAAGCAGGGTTCTGCCCCCAGGAGGGGCTGC  2340

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Qy  2581  GTGAGCTCCCTCAGGGTGGGCTCCTCCAGTGGGCTCCTCCACCCCACCCTGCAGCGG  2640
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Qy  3001  CCCACCCCATGGAGGACATCGGGCAGGTCTCCCTGGTGCAGATCCGGACCTGTCAGGT  3060
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Db  3001  CCCACCCCATGGGAGGACATCGGGACAGTCTCCCTGGTGCAGATCCGGACCTGTCAGGT  3060

Qy  3061  GATGCGGAGGCGGCCGACACAATATCCCTGGACATTTCCGACGTGAGCCCGCCTCACCTC  3120
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Qy  3181  GTCCCCAAGTCCGCTCAGCCGCAGAGCCGCCCCTCCCCATGGCTGAGGAGGAGCTGGCCGAG  3240
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AUTHORS     Gururajan,R., Baughn,M.R., Walia,N.K., Elliott,V.S., Xu,Y.,
            Arvizu,C., Yao,M.G., Ramkumar,J., Ding,L., Tang,Y.T., Hafalia,A.J.,
            Nguyen,D.B., Gandhi,A.R., Lu,Y., Yue,H., Burford,N., Bandman,O.,
            Tribouley,C.M., Lal,P.G., Recipon,S.A., Lu,D.A., Borowsky,M.L.,
            Thornton,M., Swarnaker,A., Thangavelu,K., Khan,F.A. and Ison,C.H.
TITLE       Human Kinases
JOURNAL     Patent: WO 0233099-A 44 25-APR-2002;
            Incyte Genomics, Inc. (US)
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ORIGIN

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Best Local Similarity   99.8%;  Pred. No. 0;
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Qy  63 TCCATTGAAGGAGTACTCCTAACTGTCAGAGCCTGGGCGGTCAGGATGGGGTGCTGTCG 122
Db 327 TCCATTGAAGGAGTACTCCTAACTGTCAGAGCCTGGGCGGTCAGGATGGGGTGCTGTCG 386

Qy 123 CTTGGGCTGCGGGGGTGTTCAGTTGCCCACCAGGGTCTCTCAGGGTCTCACCACCATCC 182
Db 387 CTTGGGCTGCGGGGGTGTTCAGTTGCCCACCAGGGTCTCTCAGGGTCTCACCACCATCC 446

Qy 183 AAGCATGGTAGGCTGTGGCTGGCACCCAGGGTTGTGTGGCTGGCGGGGAGGTGGTCTCCACAG 242
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Qy    603  TGAGGTCAAGAGGAGATTGAAAGGGGCGTGTTTGGCTTCGTAAAAAGAGTGCAGCACAC  662
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Db    867  TGAGGTCAAGAGGAGATTGAAAGGGGCGTGTTTGGCTTCGTAAAAAGAGTGCAGCACAA  926

Qy    663  AGGAAACAAGATCTTGTGCGCTGCCAAGTTCATCCCCTACGGAGCAGAACTCGGGGCCA  722
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    927  AGGAAACAAGATCTTGTGCGCTGCCAAGTTCATCCCCTACGGAGCAGAACTCGGGGCCCA  986

Qy    723  GGCATACAGGAGGAGGACGACTCTGGCCGCGGACTCCTGGCCCCGTGGTCACGGGGCTGCT  782
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    987  GGCATACAGGAGGAGGACGAGACATCCTGGCCGCGGCCTGAGCCACCCGCTTGGTCACGGGGCTGCT  1046

Qy    783  GGACCAGTTTGAGACCCGGCAAGACCCTCATCCTGGAGCTGTGCTCATCCGAGGA  842
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1047  GGACCAGTTTGAGACCCGGCAAGACCCTCATCCTGGAGCTGTGCTCATCCGAGGA  1106

Qy    843  GCTGCTTGGACCGCCTTGTACAGGAAGGGCGTGGTGACGAGGCCGAGTCAAGTTCTACAT  902
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1107  GCTGCTTGGACCGCCTTGTACAGGAAGGGCGTGGTGACGAGGCCGAGTCAAGTTCTACAT  1166

Qy    903  CCAGCAGCTGGTGGAGGGGCTGCACTACTTGCACAGCCATGGCCGTTCTTCCCACCTGACAT  962
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1167  CCAGCAGCTGGTGGAGGGGCTGCACTACTTGCACAGCCATGGCCGTTCTTCCCACCTGACAT  1226

Qy    963  AAAGCCCTCTAACATCCTGCTTGATGTGCATCCTGCCCGGGAAGACATTAAAATCTGCGACTT  1022
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1227  AAAGCCCTCTAACATCTCTGCTTGATGTGCATCCTGCCCGGGAAGACATTAAAATCTGCGACTT  1286

Qy   1023  TGGCTTTGCCCAGAACATCACCCCAGAGAGTTCAGCCAGTTACGGCGCTCCCCTGA  1082
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1287  TGGCTTTGCCCAGAACATCACCCCAGAGAGTTCAGCCAGTTACGGCGCTCCCCTGA  1346

Qy   1083  GTTCGTCTCCCCGAGATCATCCAGCAGAACCCTGTGAGCGGAAGCCTTCCGACATTTGGGC  1142
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1347  GTTCGTCTCCCCCGAGATCATCCAGCAGAACCCTGTGAGCGGAAGCCTTCCGACATTTGGGC  1406

Qy   1143  CATGGGTGTCATCTCCTACCTCAGCTGCTCATCCCATTTGCCGGCGGAGAGTGA  1202
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1407  CATGGGTGTCATCTCCTACCTCAGCTGCTCATCCCCATTTGCCGGCGGAGAGTGA  1466

Qy   1203  CCGTGCCACCCTCCTGAACGTCTCTGGAGGGCGCGGTGTCATGGAGCAGCCCCATGGCTGC  1262
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1467  CCGTGCCACCCTCCTGAACGTCTCTGGAGGGCGCGGTGTCATGGAGCAGCCCCATGGCTGC  1526

Qy   1263  CCACCTCAGCGGAAGACGCCAAAGACCTTCATCAAGGCTACGCTGCAGAGGAGCCCCTCAGGGC  1322
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1527  CCACCTCAGCGGAAGACGCCAAAGACTTCATCAAGGCTACGCTGCAGAGGAGCCCCTCAGGGC  1586

Qy   1323  CCGGCCTAGTTGCGGCCCAGTCCTCTCCCACCCCTGGTTCCTGAAATCCATGCCTGCGGCA  1382
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1587  CCGGCCTAGTTGCGGCCCAGTCCTCTCCCACCCCTGGTTCCTGAAATCCATGCCTGCGGCA  1646

Qy   1383  GGAGGCCCACTTCATCAACAACACCAGCAGCTTCAAGTTCCTCTGGCCCGGCCCGCTGGCA  1442
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1647  GGAGGCCCACTTCATCAACAACACCAGCAGCTTCAAGTTCCTCTCGGCCCGGCCCGCTGGCA  1706
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Qy   1443  GCGTTCCCTGATGAGCTACAAGTCCATCCTGGTCATGCCGCTCCATCCTGAGTGCTGCG  1502
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1707  GCGTTCCCTGATGAGCTACAAGTCCATCCTGGTCATGCCGCTCCATCCTGAGTGCTGCG  1766

Qy   1503  GGGCCACCCCGACAGCCCTCCCTTCGGGGTAGCCGGCACCTGTCAGGCACACTGGTGG  1562
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1767  GGGCCACCCCGACAGCCCTCCCTTCGGGGTAGCCGGCACCTGTCAGGCACACTGGTGG  1826

Qy   1563  CTCCCTGCCAGTTCCTCTCCTCTCTGACAAACGAGCTCGCCCATTGCCGGGCTAAGTC  1622
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1827  CTCCTCCAGTTCCTCTCCTCTCCTGACAACGAGCTCGGCCCATTGCCGGGCTAAGTC  1886

Qy   1623  ACTGCCACCCTCCCGGTGACACTCACCACTGCTGCCCCGGGCTTCCTGCGCGC  1682
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1887  ACTGCCACCCTCCCGGTGACACTCACCACTGCTGCCCCGGGCTTCCTGCGGCC  1946

Qy   1683  CTCGGCCAGCTGCCTGAGGAAGCCGAGGCCAGTGAGCGGCTCACCCAGGCCCCAGTCC  1742
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1947  CTCGGCCAGCTGCCTGAGGAAGCCGAGGCCAGTGAGCGGCTCACCCAGGCCCCAGTCTC  2006

Qy   1743  GCCTGCATCTCCGAGGGGTGCGGCCACCGGGGTGCGTGCCCGGCACAG  1802
           |||||||||||||||||||||||||||||||||||||||||||||||
Db   2007  GCCTGCATCTCCGAGGGGTGCGGCCACCGGGGTGCGTGCCCGGCACAG  2066

Qy   1803  CGTCATCCGCAGCCTGTTCTACACCAGGCGGTGAGAGCCTGAGCACGGGCCCTGGC  1862
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2067  CGTCATCCGCAGCCTGTTCTACACCAGGCGGTGAGAGCCTGAGCACGGGCCCTGGC  2126

Qy   1863  CCCGGGGAGCAGAGGGAGCCACCCGGCCCCGGCGGCCGGCACTGCGAAAGGGCGGCGGTACATTGC  1922
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2127  CCCGGGAGCAGAGGGAGCCACCCGGCCCCGGCGGCCGGCACTGCGAAAGGGCGGCGGTACATTGC  2186

Qy   1923  GGGGGCGCGTGCCAGGCCTGCGAGCCACTGATGGGAGCCACCGCGTGCTGGACGAGGAGGC  1982
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2187  GGGGGCGCGTGCCAGGCCTGCGAGCCACTGATGGGAGCCACCGCGTGCTGGACGAGGAGGC  2246

Qy   1983  CGCCAGGGAGGAGGAGGCCACCCCTCCTCTGCGCCAAAAGCCCCCTCATTGGAGACTGCCCCCG  2042
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2247  CCGCCAGGGAGGAGGAGGCCACCCCTCCTCTGCGCCAAAAGCCCCCTCATTGGAGACTGCCCCCG  2306

Qy   2043  GCTGCCTGCCTCTGGCACCCACTTGGCCGCCCCTGGCCACAGCCACTCCCTGGAACATGACTC  2102
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2307  GCTGCCTGCCTCTGGCACCCACTTGGCCGCCCCTGGCCACAGCCACTCCCTGGAACATGACTC  2366

Qy   2103  TCCGAGCACCCCCGCGGAGGCCTGCGGTGAGGCACCCAACGACTGCCTTCAGC  2162
           |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2367  TCCGAGCACCCCCGCGGAGGCCTGCGGTGAGGCACCCAACGACTGCCTTCAGC  2426

Qy   2163  CCCCTCCGGGGGCCCCTATCAGGGACATGGGGCCCTCAGGGCTCCAAGCAGCTTCC  2222
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2427  CCCCTCCGGGGGCCCCTATCAGGGACATGGGGCCCTCAGGGCTCCAAGCAGCTTCC  2486

Qy   2223  ATCCACTGGTGGCCACCCAGGACACTGCTCAGCCAGAGGCCATCCCGGACAGCAGCCCTTG  2282
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2487  ATCCACTGGTGGCCACCCAGGACACTGCTCAGCCAGAGGCCATCCCGGACAGCAGCCCTTG  2546

Qy   2283  GGGGGCAGCCAGCCCCTTTCTGCCACCCCAAGCAGGGTTCTGCCCCCAGAGGGGCTGCAG  2342
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2547  GGGGGCAGCCAGCCCCTTTCTGCCACCCCAAGCAGGGTTCTGCCCCCAGGAGGGGCTGCAG  2606

Qy   2343  CCCCACCCAGCAGTTGCCCATGCCCTCCTGGCTCTTCTTCGGGATCTTGCAAAGA  2402
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2607  CCCCACCCAGCAGTTGCCCATGCCCTCCTGGCTCTTCTTCGGGATCTTGCAAAGA  2666

Qy   2403  GGCCCCTTAGTACCTCAAGACCCTCGGTTCCTGAAATCCATGGCTCGCGAA  2462
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2667  GGCCCCTTAGTACCTCAAGGCCCTCTTGGGACACCCCCTGCCCCTGC  2726

Qy   2463  CAAAGCAAGCCCCCCATTGGACTTCTAAGATGGGCCTGGAGACATCTCTTCCTGGGAG  2522
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2727  CAAAGCAAGCCCCCCATTGGACTTCTAAGATGGGCCCGGAGACATCTCTTCCTGGGAG  2786

Qy   2523  GCCAAAACCCGGCCCGCCCCTGCAGTTCCCCAGGGTCAGCTCCCAGGCGAGCTCTTCCCAAGT  2582
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Db  2787 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         GCCAAAACCCGGCCCGGCTCAGCTCCCAGGGTCAGCTTCCCAGGGGAGCTCTTCCCAAGT 2846

Qy  2583 GAGCTCCCTCAGGGTGGGCTCCTCCCAGGTGGGCACAGAGCCTGCCCCTCGCCCTCCTCCC
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2847 GAGCTCCCTCAGGGTGGGCTCCTCCCAGGTGGGCACAGAGCCTGCCCCTCGCCCTCCTGGATGC 2906

Qy  2643 GGAGGGCTGGACCCAGGAGAGGCTGAGGATCTGGCGACTCCAGCACCTGCAGCGCGGC
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2907 GGAGGGCTGGACCCAGGAGAGGCTGAGGATCTGGCGACTCCAGCACCTTGCAGCGCGCC 2966

Qy  2703 TCAGGAACAGTGACCATGCCGCAAGTTCTCCCTGGGTGGTCGCGGGGCTACGCAGGCGT
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2967 TCAGGAACAGTGACCATGCCGCAAGTTCTCCCTGGGTGGTCGCGGGGCTACGCAGGCGT 3026

Qy  2763 GGCTGGCTATGGCACCTTTGCCTTTGGTGTGGAGATGCAGGGGGCATGCTGGGGCAGGGGC
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3027 GGCTGGCTATGGCACCTTTGCCTTTGGTGTGGAGATGCAGGGGGCATGCTGGGGCAGGGGC 3086

Qy  2823 CATGTGGGCCAGGATAGCCTGGGCTGTGTCCAGTGGCTGTGTCCTGGTGGTCCAGTCGTCCCAGTC
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3087 CATGTGGGCCAGGATAGCCTGGGCTGTGTCCAGTGGCTGTGTCCTGGTGGTCCAGTCGTCCCAGTC 3146

Qy  2883 CAGGGGCTGAGTCCCAGTCGGAGGAGCAGGAGGCAGGGCTGAGAGCCCACTGCCCCA
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3147 CAGGGGCTGAGTCCCAGTCGGAGGAGCAGGAGGCAGGGCTGAGAGCCCACTGCCCCCA 3206

Qy  2943 GGTCAGTGCAAGGCCTGGTCGAGGGTCGGCAGGAGGCTCCCACCAGGAGGCTCTCAGAGCC
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3207 GGTCAGTGCAAGGCCTGTGCCTGAGGCTCCCACCAGGAGGCTCTCAGAGCC 3266

Qy  3003 CACCCCATGGGAGGGACATCGGGCAGTCTCCCTGGTCGAGATCCCGGGACCTGTCAGTGA
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3267 CACCCCATGGGAGGGACATCGGGCAGTCTCCCTGGTCGAGATCCCGGGACCTGTCAGTGA 3326

Qy  3063 TGCGGAGGCGGCCGACAATATCCCTGGACATTCCGGAGGTGGACCCGGCCTACCTCAA
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3327 TGCGGAGGCGGCCGACAATATCCCTGGACATTCCGGAGGTGGACCCGGCCTACCTCAA 3386

Qy  3123 CCTCTCAGACCTGTACGATATCAAGTACTTCCCATTCGAGTTTATGATCTTCAGGAAAGT
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3387 CCTCTCAGACCTGTACGATATCAAGTACTTCCCATTCGAGTTTATGATCTTCAGGAAAGT 3446

Qy  3183 CCCCAAGTCCGCTCAGCCGAGGGCGCGCCCTCCCCCAGGGCTGCCGTGGCGCTGAGGCCGAGTT
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3447 CCCCAAGTCCGCTCAGCCGAGGGCGCGCCCTCCCCCAGGGCTGCCGTGGCGCTGAGGCCGAGTT 3506

Qy  3243 CCCGGGAGCCCACGTGGGCCTGCCTGAGCTGGCCCCCGTGGAACTGGGCCCCAGTGAACTGAGATCAC
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3507 CCCGGGAGCCCACGTGGGCCTGCCTGAGCTGGCCCCCGTGGAACTGGGCCCCAGTGAACTGAGATCAC 3566

Qy  3303 AGAGGAGTCAGAGGATGTGACGGCCCGGAAGTGTGAGAAGAGGAGGAGCGCGCTCTTGGAGAAGCCGCAA
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3567 AGAGGAGTCAGAGGATGTGACGGCCCGGAAGTGTGAGAAGAGGAGGAGCGCGCTCTTGGAGAAGCCGCAA 3626

Qy  3363 GTGGTCCTCGCCGCTCACGCAGCCTCTTCCACTTCCGACTCCGCTGATGA
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3627 GTGGTCCTCGCCGCTCACGCAGCCTCTTCCACTTCCGACTCCGCTGGACGA 3686

Qy  3423 GCCTGCAGAGCTGGGGCTGGGGGCTGGCTGAGAGAGTGAAGGCCGTGAGAGCACATCTCCCGGAT
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3687 GCCTGCAGAGCTGGGGCTGGGGGCTGGCTGAGAGAGTGAAGGCCGTCCGTGAGCACATCTCCCGGAT 3746

Qy  3483 CCTGAAGGGCAGGCCGGAAGTGTGAGAAGGAGGGCGCCCCCAGGAGAAGCCAGGCCT
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3747 CCTGAAGGGCAGGCCGGAAGTGTGAGAAGGAGGGCGCCCCCAGGAGAAGCCAGGCCT 3806

Qy  3543 TGCTTCCTTCCGGCTTCAGGTCTTGAAGAGCTGGACCGAGCCGAGCGCCGACATTCCTAAGGGA
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3807 TGCTTCCTTCCGGCTTCAGGTCTTGAAAGAGCTGGACCGCCGAGCCGACATTCCTAAGGGA 3866

Qy  3603 GCTCTCAGATGAGACTGTGGTCCTGGCCAGTGACACTGGCCTGCCAGGTGTCAGC
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db  3867 GCTCTCAGATGAGACTGTGGTCCTGGGCCAGTGACACTGGCCTGCCAGGTGTCAGC 3926

Qy  3663 CCAGCCAGCTGCCCAGCCGAGCCACCTGGAGCAAAGACGGAGCCCCCTGCCCCCTGGGAGAGCAGCAGCACCG
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3927 CCAGCCAGCTGCCCAGCCACCTGGAGCACAGACGGAGCCCCCTGCCCCCTGGAGAGCAGCAGCAGCACCG 3986

Qy  3723 TGTCCTCCATCTCTGCCACCCTCAAGAACTTCCAGGTTCGACCATCCTGGTTGGTGGTGGC
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3987 TGTCCTCCATCTCTGCCACCCTCAAGAACTTCCAGCTTCGACCATCCTGGTTGGTGGTGGC 4046

Qy  3783 TGAGGACCTGGGTGGTGTACACCTGCAGCAATGGCGTGGGCAGTGAGTGACCACAC
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4047 TGAGGACCTGGGTGGTGTACACCTGCAGCGTGAGCAATGGCGTGGGCAGTGAGTGACCACAC 4106

Qy  3843 GGGCGTCCTCCCGAAGCAGAGCGCCCCTCATCTTCGCCATGCCCGATATCGGGGAGGT
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4107 GGGCGTCCTCCCGAAGCAGAGCGCCCCTCATCTTCGCCATGCCCGATATCGGGGAGGT 4166

Qy  3903 GTACGCCGATGGGCGTGCTGGTCTGGAAGCCCGTGGAATCCTACGGCCCTGTGACCTA
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4167 GTACGCCGATGGGCGTGCTGGTCTGGTCTGGAAGCCCGTGGAATCCTACGGCCCTGTGACCTA 4226

Qy  3963 CATTGTGCAGTGCAGCCTAGAAGGGGGCAGTGGACCACACTGGCCTCCGACATCTTTGA
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4227 CATTGTGCAGTGCAGCCTAGAAGGGGGCAGTGGACCACACTGGCCTCCGACATCTTTGA 4286

Qy  4023 CTGCTCTACCTGACCAGCAAGCTCTTCCCGGGGTGCACCTACACCTTCCGCACGGCATG
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4287 CTGCTCTACCTGACCAGCAAGCTCTTCCCGGGGTGCACCTACACCTTCCGCACGGCATG 4346

Qy  4083 TGTCAGCAAGGCAGGAATGGGCTCCCTACAGCAGAGGAGAGCCAGGGCGTCAGCCCAACCCCTGCCCAG
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4347 TGTCAGCAAGGCAGGAATGGGTCCCTACAGCAGAGGAGAGCCAGGGCGTCAGCCCAACCCCTGCCCAG 4406

Qy  4143 GCCCAGCCACCTGGCTCTGAGGAGCAGACAGATCCAGAGGGCCGCCGCTTCAGCGTGGTGCGCA
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4407 GCCCAGCCACCTGGCTCTGAGGAGCAGACAGATCCAGAGGGCCGCCGCTTCAGCGTGGTGCGCCAG 4466

Qy  4203 CACAAAGACCTTCGCATTCGATTCAGACACGATTCAGATCGACACTCCTACCACCCCAA
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4467 CACAAAGACCTTCGCATTCGATTCAGACACGATTCAGATCGACACTCCTACCACCCCAA 4526

Qy  4263 ATGCTGGGAGAAGGCCAGCAGCGAGCCTACCTCAGCCCCCGGCCCGAAGATCATCCCTACCACCCCAA
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4527 ATGCTGGGAGAAGGCCAGCAGCGAGCCTACCTCAGCCCCCGGCCCGAAGATCATCCCTACCACCCCAA 4586

Qy  4323 GGACAAGACAGCAGTGCTGCGCGAATACGAGCCCCTCAGGGGCTGCGCCAGGGCTGCGCCACCGACCCT
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4587 GGACAAGACAGCAGTGCTGCGCGAATACGAGCCCCTCAGGGGCTGCGCCAGGGCTGCGCCACCT 4646

Qy  4383 GGCCCAGTGCAGCGAGCCTACCTCAGCCCCCGGCCCTGGAGCTGTGTCATCTTGGAGCTGTG
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4647 GGCCCAGTGCACCGAGCCTACCTCAGCCCCCGGCCTGGTGTCATCTTGGAGCTGTG 4706

Qy  4443 CTCTGGCCCCGAGCTGCTCTCCCCTGCCTGGCGAGAGGGCTCCTCTACTCAGAATCTGAGGT
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Db  4707 CTCTCGGCCCCGAGCTGCTCTCCCCTGCCTGGCGAGAGGGCTCCTCTACTCAGAATCCGAGGT 4766

Qy  4503 GAAGGACTACCTGTGGCAGATGTTGAGTGCCACCCAGTGCCACACAACCAGCACATCCT
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4767 GAAGGACTACCTGTGGCAGATGTTGAGTGCCACCCAGTACCTGCACACAACCAGCACATCCT 4826

Qy  4563 GCACCTGGACCTGAGGTCCGAGAACATGATCATCACCGAATACACCTGCTCAAGGTCGT
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Db  4827 GCACCTGGACCTGAGGTCCGAGAACATGATCATCACCGAATACACCTGCTCAAGGTCGT 4886

Qy  4623 GGACCTGGGCAATGCAGTCGCCCTCAGCCAGGAGGTGCTGCCCTCAGACAAGTTCAA
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4887 GGACCTGGGCAATGCAGTCGCCCTCAGCCAGGAGGTGCTGCCCTCAGACAAGTTCAA 4946

Qy  4683 GGACTACCTAGAGACCATGGCCTCCAGAGCTCCTGGAGGGGCCAGGGGGGCGTGTTCCACAGAC
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4947 GGACTACCTAGAGACCATGGCCTCCAGAGCTCCTGGAGGGGCCAGGGGGGCGTGTTCCACAGAC 5006
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                                                                SAPQEGSPHPAVAPCPPGSPPGSCKEAPLVPSSPFLGQPQAPAPAKASPPLDSKM
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                                                                TYTFRTACVSKAGMGPYSSPSEQVLLGAPSHLASEEESQGRSAQPLPSTKTFAFQTQI
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                                                                "

ORIGIN

        Query Match       94.4%;   Score 4915.8;   DB 6;   Length 5007;
        Best Local Similarity   99.9%;   Pred. No. 0;
        Matches 4920;   Conservative   0;   Mismatches   0;   Indels   7;   Gaps   0;

Qy   258 CCCAGGGCCCCATCCAGGTAACCATCGAGGATGTGCAGGCACAGACAGGCGGAAC  317
             ||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db    81 CGCACGGCCCCCATCCATCGAGGATGTGCAGGCACAGACAGGCGGAAC         140

Qy   318 GGCCCAATTCGAGGTATCATTGAGGGGCGACCCCACAGCCTCGGTGACCTGGTACAAGGA  377
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   141 GGCCCAATTCGAGGTATCATTGAGGGGCGACCCCACAGCCTCGGTGACCTGGTACAAGGA  200

Qy   378 CAGCGGTCCAGCTGGTGGACAGCACCCGGCTTAGCCAGCAGCAAGAAGGCACCACATACTC  437
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Db   201 CAGCGGTCCAGCTGGTGGACAGCACCCGGCTTAGCCAGCAGCAAGAAGGCACCACATACTC  260

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RESULT 5
AX039410

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DEFINITION  Sequence 3 from Patent WO0063381.
ACCESSION   AX039410
VERSION     AX039410.1  GI:11229478
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Zeng,W., Stanton,L. and Kong,H.
  TITLE     Mammalian protein with putative function in signal transduction
  JOURNAL   Patent: WO 0063381-A 3 26-OCT-2000;
            SCIOS INC. (US)
FEATURES             Location/Qualifiers
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Db  3981  CTCTGAGGAGGAGGAGAGCCAGGGCGGTCAGCCCAGCCAGCACAAGAGACCTTCGC  4040

Qy  4218  ATTCCAGACACAGATCCAGAGAGGGGCCGCTTCAGCCTGGTGTGCGGCAATGCTGGGAGGAGGC  4277
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Db  4041  ATTCCAGACACAGATCCAGAGAGGGGCCGCTTCAGCCTGGTGTGCGGCAATGCTGGGAGAAGC  4100

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Db  4101  CAGGCGGCGGCGGCGTGGCCCGCCAGAGTCATCCCTACCACCCCAAGGACAAGAGACAGCAGT  4160

Qy  4338  GCTGCGCGAATACGAGGCCCTCAAGGGCCTGCGCCACCCGCACCTGGCCCAGCTGCACGC  4397
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Qy  4398  AGCTACCTCAGCCCCGGCACTGGTGCTCATCTTGAGCTCATCTTGGAGTCTCTGGGCCCGAGCT  4457
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Qy  4638  ACAGAGCCTCAGCCAGGAGAGTGCTGCCCTCCTCAGAAGTTCAAGGACTACCTAGAGAC  4697
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Qy  4698  CATGGCTCCAGAGTTCCTGGAGGCCCAGGGGCGTGTTCCACAGACAGACATCTGGGCCAT  4757
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Qy  4758  CGGTGTGACAGCCTTCATCATGCTGCAGGAGGGGTGGTCCGGCTGAGCGCTGCTACGCGGGGCT  4817
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Qy  4818  CGACCTGCAGAGAGACTGCGCAAGGGGCGTGGTGTCGGCTGAGCGCTGGGGCT  4877
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Qy  4938  CTGCGGCGTCCAGCTGCCTGCCAGTGCTAACAGGAGGGCCCGGCCTTGTTCGCG  4997
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Qy  5118  GCCACACCCCTTGGTCTCCCCGCGTGGGGGCGCGTCAGCAGCGCGCCAATAAAAACGCACAGC  5177
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RESULT 6
AX039412
LOCUS       AX039412              7928 bp    DNA     linear   PAT 18-NOV-2000
DEFINITION  Sequence 5 from Patent WO0063381.
ACCESSION   AX039412
VERSION     AX039412.1  GI:11229480
KEYWORDS    .
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens

REFERENCE    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1
  AUTHORS    Zeng,W., Stanton,L. and Kong,H.
  TITLE      Mammalian protein with putative function in signal transduction
  JOURNAL    Patent: WO 0063381-A 5 26-OCT-2000;
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ORIGIN

Qy    318  GGCCCAATTCGAGGCTATCATTCATTGAGGGCGACCACCAGCCCTCGGTCGGTACAAGGA  377
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Db   3062  GGCCCAATTCGAGGCTATCATTCATTGAGGGCGACCACCAGCCCTCGGTCGGTACAAGGA  3121

Qy    378  CAGCGTCCAGCTGGTGCAGCACCGGCTTAGCCAGCGGCTTAGCCAGCGCAGCACCACATACTC  437
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Db   3122  CAGCGTCCAGCTGGTGCAGCACCGGCTTAGCCAGCGGCTTAGCCAGCGCAGCACCACATACTC  3181

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Db   3182  CCTGGTGCTGAGGCATGTGGCCTCGAAGGATGCCGGCGTTTACACCTGCGTTACACCTGGCCCAAAA  3241

Qy    498  CACTGGTGGCCAGGTGCTCTGCAAGCAGCAGAGCTGTCGTGGTGCTTGGGGGGGGACAATGAGCC  557
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Qy    558  GGACTCAGAGAAGCAAAGCACCGGAGGAAGCTGACTCCTTCATGAGCAGTTCAAGGAGA  617
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Qy    618  GATTGGAAGGGCGTGTTGGCTTCGTAAAAAGAGTGCAGCACAAGAAACAAGATCTT  677
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Qy    678  GTGCGCGTGCCAAGTTCATCCCCTACGGAGCAGAACTCGGGCCAGGCATCACAGGAGCG  737
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Db   3422  GTGCGCGTGCCAAGTTCATCCCCTACGGAGCAGAACTCGGGCCAGGCATCACAGGAGCG  3481

Qy    738  AGACATCCTGGCCGCACCCGCTGGTCACGGGGTGCTGACCAGTTTGAGAC  797
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Db   3482  AGACATCCTGGCCGCACCCGCTGGTCACGGGGTGCTGACCAGTTTGAGAC  3541

Qy    798  CCGCAAGACCCTCATCCTGGAGCTGTGTCATCCGAGGAGCTGCTGACCGGCCT  857
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Db   3542  CCGCAAGACCCTCATCCTGGAGCTGTGTCATCCGAGGAGCTGCTGACCGGCCT  3601

Qy    858  GTACAGGAAGGCGTGGTGACGGAGGCCGAGTCAAGGTCTCACATCCAGAGCTCGTGGA  917
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Db   3602  GTACAGGAAGGCGTGGTGACGGAGGCCGAGTCAAGGTCTCACATCCAGAGCTCGTGGA  3661

Qy    918  GGGGCTGCACTACCTGCCCTGCCCCGGGAAGACATTAAAATCTGGACTTTTGGCTTTGGCCAGAA  977
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Db   3662  GGGGCTGCACTACCTGCCCTGCCCCGGGAAGACATTAAAATCTGGACTTTTGGCTTTGGCCAGAA  3721

Qy    978  CCTGATGTGTCATCCTGCCCGGGAAGACATTAAAATCTGGACTTTTGGCTTTGGCCAGAA  1037
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Db   3722  CCTGATGTGTCATCCTGCCCGGGAAGACATTAAAATCTGGACTTTTGGCTTTGGCCAGAA  3781

Qy   1038  CATCACCCCAGCAGAGCTGCAGTTGCAGTTCAGCGGCTCCCCGAGTTCGTCTCCCCGA  1097
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Db   3782  CATCACCCCAGCAGAGCTGCAGTTGCAGTTCAGCGGCTCCCCGAGTTCGTCTCCCCGA  3841

Qy   1098  GATCATCCAGCAGAGCAACCCGTGACGAAGCCCGGACATTTGGCGTCATCTC  1157
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Qy   1158  CTACCTCAGCCTGACCTGCTCATCCCATCCCCATTTGCCGGCGAGTGACCGTGCCACCCTCCT  1217
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Qy   1338  CCAGTGCCTCTCCCAACCCTGGTTCCTGAAATCCATGCCTGAAATCCATGCCCACTTCAT  1397
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Query Match   94.4%;   Score 4915.8;   DB 6;   Length 7928;
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Matches 4920;   Conservative   0;   Mismatches   7;   Indels   0;   Gaps   0;

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Qy  1398  CAACACCAAGCAGCTCAAGTTCCTCCTGGCCCGAAGTCGCTGGCAGCGTTCCCTGATGAG  1457
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Db  4202  CTACAAGTCCATCCTGTGATGCGTCCATCCTGAGCTGTGCGGGCCGCCCACCCGACAG    4261

Qy  1518  CCCCTCCTCGGCGTAGCCCGGCACCTCTGAGGACACTGGTGCTCCTCCAGTTCCTC      1577
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Qy  1638  GGTGACACTCACCACTGCTGCGACCCCGGGCTTCTGCGCGCCCTGGCCAGCCTGCC      1697
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Qy  1698  TGAGGAGGCCGGAGGCGCTCCACCGAGCGCGCCCAGCTCCGCCTGCATCCCGA         1757
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Qy  1818  GTTCTACCACCAGGCGGGTGAGAGCCTGGAGCACGGGCCCTGGCCCGGGGAGCAGGCG     1877
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Qy  1878  GCACCCGGCCCGGGGCGGGGCCACCTGCTGCTGCTGAGAGGGCGGCTACATTGCGGGGCGCGCTGCCAGG  1937
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Qy  1938  CCTGGCGCGGAGCCACTGATGAGGAGCCGCGTGTGCTGAGGAGGAGGCGGCCGCAGGGAGGAGCA  1997
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Qy  1998  GGCCACCCTCCTGGCCAAAGCCCCTCATTCGAGACTGCCCTCGGCTGCCTCCTGCCTCTGG      2057
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Qy  2058  CACCCACTTGGCCCCTGGCCACAGCCACTCCCTGGAACATGACTCTCCGAGACACCCCCCG      2117
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Qy  2118  CCCCTCCTCGGAGGCCTGCGGTGAGGCACAGCGGACTGCCTTCAGCCCCCTCCGGGGGGC      2177
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Db  4862  CCCCTCCTCGGAGGCCTGCGGTGAGGCACAGCGGACTGCCTTCAGCCCCCTCCGGGGGGC      4921

Qy  2178  CCCTATCAGGGACATGGGGCACCCTCAGGGCTCCAAGCAGCTTCCATCCACTGGTGGCCA      2237
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Qy  2238  CCCAGGCACTGCTCAGCCAGGAGAGGCCATCCCCGGGCAGCAGCCCCTGGGGCAGCCAGCCCC  2297
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Qy  2298  TTTCTGCCACCCAAGCAGGGTTCTGCCCCCCAGGAGGGCTGCAGCCCCCAGGGCAGACCCCAGCAGT  2357
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Qy  2538  CTGCAGTTCCCCAGGGTCAGCCTCCCGGAGCTCTTCCCAAGTGAGCTCCTCAGGGT      2597
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Db  5282  CTGCAGTTCCCCAGGGTCAGCCTCCCGGAGCTCTTCCCAAGTGAGCTCCTCAGGGT      5341

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Qy  2658  GGAGGGTGAGGATCTGTCCGACTCCACACCACCTTGCAGCGGGCCTCAGGAACAGGTGAC  2717
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Db  5402  GGAGGGTGAGGATCTGTCCGACTCCACACCACCTTGCAGCGGGCCTCAGGAACAGGCGAC  5461

Qy  2718  CATGCGCAAGTTCTCCCTGGGTGGTGCGGGGGCTCACCGCAGGGGCTGGCTGGCCATGGCAC  2777
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Db  5462  CATGCGCCAAGTTCTCCCTGGGTGGTGCGGGGGCTACCGCAGGGGCTGGCTGGCCATGGCAC  5521

Qy  2778  CTTTGCCTTTGGTGAGATGCAGGGGCATGCTGGGGCAGGGGCCCATGTGGGCCAGAT     2837
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Db  5522  CTTTGCCTTTGGTGAGATGCAGGGGCATGCTGGGGCAGGGGCCCATGTGGGCCAGGAT     5581

Qy  2838  AGCCTGGGCTGTGTCCCAGTCGGAGGAGGCCAGGGGCTGAGTCCCA              2897
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Db  5582  AGCCTGGGCTGTGTCCCAGTCGGAGGAGGCCAGGGGCTGAGTCCCA              5641

Qy  2898  GTCGGAGGAGCAGCAGAGGAGGCTGAGAGCCCACTGCCCCAGTTCAGTGCAAGGCC      2957
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Db  5642  GTCGGAGGAGCAGCAGAGGAGGCTGAGAGCCCACTGCCCCAGTTCAGTGCAAGGCC      5701

Qy  2958  TGTGCCTGAGGTCGGCAGGAGTCTCCCTGGTGCAGATCCGGACTGGTGATGGCGGAGGA   3017
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Qy  3018  CATCGGGCAGGTCTCCCTGGTGCAGATCCGGACCTGTCAGGTGAGGCGGCCGA          3077
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Qy  3078  CACAATATCCTGGACATTCCGAGGTGACCCGGCTACCTCAACCTCTCAGACCTGTA       3137
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Qy  3138  CGATATCAAGTACCTCCCATTCGAGTTTATGATCTTCAGGAAAGTCCCCAAGTCCGCTCA    3197
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Qy  3198  GCCAGAGCCGCGCCTCTGAGGCCTGAGGAGGAGGCTGCCGAGTTCCCGGAGCCCACGTG    3257
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Db  5942  GCCAGAGCCGCGCCTCTGAGGCCTGAGGAGGAGGCTGCCGAGTTCCCGGAGCCCACGTG    6001

Qy  3258  GCCCTGGCCAGGTGAACTGGGCCCCCAGGCAGGGAATCACAGAGGAGTCAGAGGA       3317
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Qy  3318  TGTTGGACGCGGCTGCTGCGGCAGAGGCGGGCAGGAAGCCCAAGTGGTCCTCGGCCGTC    3377
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Db  6062  TGTTGGACGCGGCTGCTGCGGCAGAGGCGGGCAGGAAGCCGCAAGTGGTCCTCGGCCGTC    6121

Qy  3378  ACGGAGCCTCTTCCACTTCCCTCTGGGAGGCACTGCCCGTGGAGCTGCTGAGAGCTGGG    3437
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Qy  3438  GCTGCCTGAGAGTGAAGGCTTCCGTGGAGCACATCTCCCGGGACATCTCCGAGACCTGAAGGGGCAGGCC  3497
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Qy  3498  CTCAAGCCCCTTCTTGGGACAGCCCCCGGAAGGTCTGGAGGAGGTGGATCTTGCTTCCTCCGGCT       3557
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Qy  3558  CTCAGTCTCGAAGAGCTGGGACCGAGCGCGACATTCCTAAGGGAGCCTCAGATGAGAC      3617
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Qy   3738 CACCCTCAAGAACTTCCAGCTTCTGACCATCCTGGTTGGTGGTGCTGAGACCTGGGTGT 3797
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Qy   4158 CTCTGAGGAGGAGCCAGGGCGGTCAGCCAACCCCTGCCCAGCACAAAGACCTTCGC 4217
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RESULT 7
AX207401

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DEFINITION  Sequence 14 from Patent WO0155356.
ACCESSION   AX207401
VERSION     AX207401.1  GI:15395213
KEYWORDS
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Plowman,G., Whyte,D., Manning,G., Sudarsanam,S. and Martinez,R.
  TITLE     Human protein kinases and protein kinase-like enzymes
  JOURNAL   Patent: WO 0155356-A 14 02-AUG-2001;
            Sugen, Inc. (US)
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ORIGIN

Query Match             93.8%;  Score 4885.2;  DB 6;  Length 4936;
Best Local Similarity   99.6%;  Pred. No. 0;
Matches 4915;  Conservative 0;  Mismatches  3;  Indels 18;  Gaps  1;

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Qy    328 GAGGCTATCATTGAGGGCGACCCCAGCCCTCCGGTGACCTGGTACAAGGACAGGGTCCAG 387
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GAGGCTATCATTGAGGGCGACCCCAGCCCTCCGGTGACCTGGTACAAGGACAGGGTCCAG 120
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Qy   388  CTGGTGACAGCACCGGCTTAGCCAGCAGCAGCAAGAAGGCACCACATACTCCCTGGTGCTG  447
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Qy   448  AGGCATGGCCTCGAAGGATGCCGGCGTTTACACCTGCTGGCCCAAAACACTGGTGGC      507
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Db   181  AGGCATGGCCTCGAAGGATGCCGGCGTTTACACCTGCTGGCCCAAAACACTGGTGGC      240

Qy   508  CAGGTGCTCTGCAAGGCAGAGCTGCTGGTGTGCTTGGGGCCGCTTCCCACTCCTAGGGGAC  549
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Qy   550  AATGAGCCGGACTCAGAGAAGCAAAGCCACCGGAGGAAGTGCACTCCTTCTATGAGGTC   609
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Qy   850  GACCGGCCTGTACCTCACTCGGGCATCGCACTACCTGCACAGCTGCACTACCTCGAGC   909
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Db   601  GACCCGCCTGTACAGGAAGGGGTGGTGACGGAGGTCAAGGTCTACATCCAGCAG     660

Qy   910  CTGGTGAGGGCTGCACTACCTGCACAGCCATGCGTTCTCCACCTGGACATAAAGCCC   969
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Db   661  CTGGTGAGGGCTGCACTACCTGCACAGCCATGCGTTCTCCACCTGGACATAAAGCCC   720

Qy   970  TCTAACATCCTGATGTGCATCCTGCCCCGGAACGCATTCCCCATTGCCCGGACTTTGGCTTT  1029
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Db   721  TCTAACATCCTGATGTGCATCCTGCCCCGGAACGCATTCCCCATTGCCCGGACTTTGGCTTT  780

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Qy  1090  TCCCCGAGATCATCCAGCAGAGAACCCTGTGAGCGAAGCCTCCGACATTGGGCCATGGGT   1149
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Db   901  GTCATCCTCACCTGACCTGCATCCTGACCTCGGCGGGCCGGAGAGTTGACCGTGCC    960

Qy  1210  ACCCTCCTGAACGTCCTGGAGGGGCCGCGTGTCATGGAGGCAGCCCACATGGCTGCCCACCTC  1269
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Qy  1270  AGCGAAGACGCCAAAGACTTCATCAAGGCTACGCTGCAGAGAGCCCCGGCCT     1329
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Db  1021  AGCGAAGACGCCAAAGACTTCATCAAGGCTACGCTGCAGAGAGCCCCGGCCT     1080

Qy  1330  AGTGCGGCCCAGTGCCTCTCCACCCTGGTTCCTGAAATCCATGCGTGCCGAGGAGGCC    1389
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Qy  1390  CACTTCATCAACACCAAGCAGCTCAAGTTCCTCCTGGCCGAAGTCGCTGGAGCGTTCC     1449
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Db  1141  CACTTCATCAACACCAAGCAGCTCAAGTTCCTCCTGGCCGAAGTCGCTGGAGCGTTCC     1200

Qy  1450  CTGATGAGCTACAAGTCCATCCTGGTGATGCGCTCCATCCCTGAGCTGCTGCGGGGGCCCA  1509
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Db  1201  CTGATGAGCTACAAGTCCATCCTGGTGATGCGCTCCATCCCTGAGCTGCTGCGGGGGCCCA  1260
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Qy        CCCGACAGCCCTCCTCGGCGTAGCCCGGCACCTCTGCAGGACACACTGGTGCTCCTCC  1569
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Qy        AGCAGGCGGCCTGCGCGGCCACCTGATGAGCACCGCGTCGTGCTGGAGGAGGCCGCCAGG  1929
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Qy        GGTGCCACCCAGGACTGCTCACGACAGCCCCTTGCCCGAGAGTTGACCGTGCAG  2289
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1981  GGTGCCACCCAGGACTGCTCACGACAGCCCCTTGCCCGAGAGTTGACCGGCAG  2040

Qy        CCAGCCCCTTTCTGCCACCCAAGCAGGGTTCTGCCCCGGAGGAGGCTGCAGCCCCAC  2349
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2041  CCAGCCCCTTTCTGCCACCCAAGCAGGGTTCTGCCCCGGAGGAGGCTGCAGCCCCAC  2100

Qy        CCAGCAGTTGCCCCATGCCTCCTTCCCTGAGGATCTTGCAAAGAGGCCCCC  2409
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Db  2101  CCAGCAGTTGCCCCATGCCTCCTTCCCTGAGGATCTTGCAAAGAGGCCCCC  2160

Qy        TTAGTACCCTCAAGCCCCTTCTTGGGACAGCCCCTGCCCCTGCCAAAAGCA  2469
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db  2161  TTAGTACCCTCAAGCCCCTTCTTGGGACAGCCCCTGCCCCTGCCAAAAGCA  2220

Qy        AGCCCCCCATTGGACTCTAAGATGGGCCTGGAGACATCTCTTTCCTGGAGGCCAAAA  2529
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2221  AGCCCCCCATTGGACTCTAAGATGGGCCTGGAGACATCTCTTTCCTGGAGGCCAAAA  2280

Qy        CCCGGCCCCTGCGAGTTCCCCAGGTGATGCGCTCCCATCCCTGAGCTGCTGCGGGGGCCCA  2589
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2530  CCCGGCCCCTGCGAGTTCCCCAGGTGATGCGCTCCCATCCCTGAGCTGCTGCGGGGGCCCA
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Db  2281 CCCGGCCCCTGCCAGTTCCCCAGGCGGTCAGCCTCCCAGGGCGAGCTCTTCCCAGTGAGCTCC 2340

Qy  2590 CTCAGGGTGGGCTTCCTCCTCCCAGTGGGCAGATCGCTGGGCACACAGACCTTCCCTGCGATGGCGGAGGGC 2649
         |||||||||||||||||||||||||||||||||||||||||||||||
Db  2341 CTCAGGGTGGGCTTCCTCCTCCCAGTGGGCACACAGACCTGGGCACACAGACCTGCGATGGCGGAGGGC 2400

Qy  2650 TGGACCCAGGAGCTGAGGATCGTGTCCGACTTCACACCACCTTGCACGCGGCTCAGGAA 2709
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Db  2401 TGGACCCAGGAGCTGAGGATCGTGTCCGACTTCACACCACCTTGCACGCGGCTCAGGAA 2460

Qy  2710 CAGGTGACCACCATCGCGCAAGTTCTCCCTCGGGTGGTTCGGCAGGCGGTGGCTGGC 2769
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Qy  2770 TATGGCACCTTTGCCTTTGGTGGAGATGCAGGGGCATGCTGGGCGGCCCATGTGG 2829
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Db  2521 TATGGCACCTTTGCCTTTGGTGGAGATGCAGGGGCATGCTGGGCGGCCCATGTGG 2580

Qy  2830 GCCAGGATAGCCTGGGCTGTGTCCAGTGCGGGCTGGAGCGGAGCAGGAGGCCAGGGCT 2889
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Qy  2890 GAGTCCCAGTGCGGAGGAGCAGGAGGCCAGGCTGAGAGCCACTGCCCCAGGTCAGT 2949
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Qy  2950 GCAAGGCCTGTGCCTGAGCTCGGCAGGGCTCCCACCAGGAGCTCTCCAGAGCCCACCCCA 3009
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Qy  3070 GCGGCCGACACAATATCCCTGGACATTTCCGAGGTGGACCCCGGCTCACCTCAACCTCTCA 3129
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Db  2821 GCGGCCGACACAATATCCCTGGACATTTCCGAGGTGGACCCCGGCTCACCTCAACCTCTCA 2880

Qy  3130 GACCTGTAGATATCAAGTACCTCCATTCCCATTCGAGTTTATGATCTTCAGGAAAGTCCCCAAG 3189
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Qy  3190 TCCGCTCAGCCAGAGCCGCCTGCCAGGCGCGCCCCGTGGGCAGGAGCTGCGGTGGCCGAGTTCCCGGAG 3249
         |||||||||||||||||||||||||||||||||||||||||||||||
Db  2941 TCCGCTCAGCCAGAGCCGCCTGCCAGGCGCGCCCCGTGGGCAGGAGCTGCGGTGGCCGAGTTCCCGGAG 3000

Qy  3250 CCCACGTGGGCCTGCGTGAACTGGGGCCCACGCAGGCCTCCGTGAGATCACAGAGGAG 3309
         |||||||||||||||||||||||||||||||||||||||||||||
Db  3001 CCCACGTGGGCCTGCGTGAACTGGGGCCCACGCAGGCCTCCGTGAGATCACAGAGGAG 3060

Qy  3310 TCAGGAGGATGTGGACGCGCGGAAGGTGCTGCTGCAGGAAGCGCAAGTGCCAAGTGGTCC 3369
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Db  3061 TCAGGAGGATGTGGACGCGCGGAAGGTGCTGCTGCAGGAAGCGCAAGTGCCAAGTGGTCC 3120

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Qy  3430 GAGCTGGGGCTGCGTGAGAAGAGTGAAGGCCTCGTGGAGCACATCTCCCGGATCCTGAAG 3489
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Qy  3490 GGCAGGCCGGAAGGTCTGGAGAAGAGGGGGCCCCCCAGGAAGAGAGCCAGGCCTTGCTTCC 3549
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Qy  3550 TTCCGGCTTCTCAGGTCTCAGGGCTGAGAGCTGGACGGACCGACATTCCTAAGGGAGCTCTCA 3609
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Qy  3610 GATGAGACTGTGTCCTGGGCGTGTCCAGTCAGTGACACTGGACACTGGACACTGGCCTGCCAGGTGTGCAGCCA 3669
         |||||||||||||||||||||||||||||||||||||||||||||
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Qy  3670 GCTGCCCAGGCCACCTGGGCAAAGACAGGAGCAGCGCCCCCTGAGAGCAGCGCGTGTCCTC 3729
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Db  3421 GCTGCCCAGGCCACCTGGGCAAAGACAGGAGCAGCGCCCCCTGAGAGCAGCGCGTGTCCTC 3480

Qy  3730 ATCTCTGCCACCCTCAAGACTTCCAGCTTCTGGTGTGGTGTGGTGTGGCTCAGGAGTC 3789
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Db  3481 ATCTCTGCCACCCTCAAGACTTCCAGCTTCTGACATCCTGGTGTGGTGTGGCTCAGGAGAC 3540

Qy  3790 CTGGGTGTGTACACCTGCAGCGTGAGCAATGCGCTGGGACAGTGCCATGGGGCGTC 3849
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Qy  3850 CTCCCGAAGGCAGAGCGCCCCTCATCTTCGGCCATGCCCGATATCGCCGATATCGCCCG 3909
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Qy  3910 GATGGGGTGCTGCTGGTCTGTGTGCTTCGGGAATCCTGGAAGCCCGTGACCTACGGCCCTGACCTACATTGTG 3969
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Db  3661 GATGGGGTGCTGCTGGTCTGTGTGCTTCGGGAATCCTGGAAGCCCGTGACCTACATTGTG 3720

Qy  3970 CAGTGCAGCCTAGAAGCGGCAGCTGAGCAATCACTGGCCTCCGACATCTTGACTGCTGC 4029
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Db  3721 CAGTGCAGCCTAGAAGCGGCAGCTGAGCAATCACTGGCCTCCGACATCTTGACTGCTGC 3780

Qy  4030 TACCTGACCAAGCTCTTCCCGGGGTGCGACCTACCTTCCGCACGCGGCGATGTGTCAGC 4089
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Qy  4090 AAGGCACGAATGGGTCCCTACAGCAGCCCTCGGAGCAAGTCCTCCTGGAGGGGCCCAGC 4149
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Db  3841 AAGGCAGGAATGGGTCCCTACAGCAGCCCTCGGAGCAAGTCCTCCTGGAGGGGCCCAGC 3900

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Db  3901 CACCTGCCCTCTGAGGAGAGAGCCAAGGGCGGTCAGCCGAACCCCTGCCAGCACAAAG 3960

Qy  4210 ACCTTCGCATTCCAGACACAGATCCCTGGCCGCGGGGGGCCCAAGATCATCCCCAAGGACAAG 4269
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Qy  4270 GAGAAGGCCAGCGGGGGGCCGGAATACAGGAGCCCTCAAGGACTCGGCCCCAG 4329
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Db  4021 GAGAAGGCCAGCGGGGGGCCGGAATACAGGAGCCCTCAAGGACTCGGCCCCAG 4080

Qy  4330 ACAGCAGTGCTGCGGCAATGCTGAGTCGTGCACCGTACCCAGTGAGTGCGACAAATGCTGG 4389
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Db  4081 ACAGCAGTGCTGCGGCAATGCTGAGTCGTGCACCGTACCCAGTGAGTGCGACAATGCTGG 4140

Qy  4390 CTGCACCGCAGCCTACTTCAGCGCTGCTCATCTTGGAGCTGTGTCTCATCTTGGAGCTGTCTCTGGG 4449
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Qy  4450 CCCGAGTTGCTCCCTGCCTGGGAGGCCACCCAGTGAGAGGAGGGCACCTG 4509
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Db  4201 CCCGAGTTGCTCCCTGCCTGGGAGGCCACCCAGTGAGAGGAGGAC 4260

Qy  4510 TACCTGTGCAGATGTGAGTGAGAGTGAAGCATGAGACATGAACAGCACATCCTGCACCTG 4569
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Db  4261 TACCTGTGCAGATGTGAGTGAGAGTGAAGCATGAGACATGAACAGCACATCCTGCACCTG 4320

Qy  4570 GACCTGAGGTCCGAGAACATGATCATCACCAGGAGAGGCTCAGAGACTAC 4629
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Db  4321 GACCTGAGGTCCGAGAACATGATCATCACCAGGAGAGGTCAGAGACTAC 4380

Qy  4630 GGCAATGCACAGCTTCAGCAGGCCGACATTCCTAAGGGAGCTCTCAAGGACAGTTCAAGGACTAC 4689
         |||||||||||||||||||||||||||||||||||||||||||||
Db  4381 GGCAATGCACAGCTTCAGCAGGCCGACATTCCTAAGGGAGCTCTCAAGGACAGTTCAAGGACTAC 4440

Qy  4690 CTAGAGACCATGGCTCCACAGAGCTCCTGGAGGGGCCTGTTCCACAGAGATC 4749
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ORIGIN

     Query Match       79.6%;   Score 4146.6;   DB 6;   Length 4175;
     Best Local Similarity  99.9%;   Pred. No. 0;
     Matches 4149;  Conservative 0;  Mismatches 0;  Indels 4;  Gaps 0;

Qy  1055  TGCAGTTCAGCCAGTACGGCTCCCCTGAGTTCGTCTCCCCAGATCATCAGCAGAACC  1114
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Db     5  TGCAGTTCAGCCAGTACGGCTCCCCTGAGTTCGTCTCCCCAGATCATCAGCAGAACC    64

Qy  1115  CTGTGAGGGAAGCCTCCGACATTTGGGCCATGGTGTCATCTCCACCTCAGCCTGACCT  1174
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Db    65  CTGTGAGGGAAGCCTCCGACATTTGGGCCATGGTGTCATCTCCTACCTCAGCCTGACCT   124

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Qy  1235  GCGTGTCATGGAGCAGCCCCATGGCTGCCCACCTCAGGCAGGACGCCCTAGTGCGGCCCAGTGCGCCTCTCCCACC  1294
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Db   185  GCGTGTCATGGAGCAGCCCCATGGCTGCCCACCTCAGGCAGGACGCCCTAGTGCGGCCCAGTGCGCCTCTCCCACC   244

Qy  1295  AGGCTACGGTGCAGAGAGCCCTCAGGCCCGGCCCCAGTAGTGCGGCCCAAGCAGCAGTCA  1354
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Db   245  AGGCTACGGTGCAGAGAGCCCTCAGGCCCGGCCCCAGTAGTGCGGCCCAAGCAGCAGTCA   304

Qy  1355  CCTGGTTCCTGAAATCCATGCCCTGCGGAGGAGCCCACTTCATCAACACCAAGCAGCTCA  1414
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Db   305  CCTGGTTCCTGAAATCCATGCCCTGCGGAGGAGCCCACTTCATCAACACCAAGCAGCTCA   364

Qy  1415  AGTTCCTCCTGGCCCGAAGTCGGTCGCAGCGTTCCCTGATGAGCTACAAGTCCATCCTGG  1474
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Db   365  AGTTCCTCCTGGCCCGAAGTCGGTCGCAGCGTTCCCTGATGAGCTACAAGTCCATCCTGG   424

Qy  1475  TGATGCGGTCCATCCCTGAGCTGCTGCGGGGGCCCCCCGACAGCCCCTCCCTGGGGTAG  1534
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Qy  1535  CCCGGCACCTTCTGCAGGACACTGGTGGCTCCTCCCAGTTCCTCCTCCTCCTGACAACG  1594
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Db   485  CCCGGCACCTTCTGCAGGACACTGGTGGCTCCTCCCAGTTCCTCCTCCTCCTGACAACG   544

Qy  1595  AGCTCGCCCCATTGCCCGGGCTAAGTCACTGGCTAAGTCACCACTCACCAC  1654
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Qy  1655  TGCTGCACCCCGGGGCTTCTCGGGGGCCCTGCCTGGCCAGCCCTGCCTGAGGAAGCCGAGGCCA  1714
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Qy  4810  GGTGCACGCGACCTGCAGAGGACTGCGCAAGGGACTGTCCGGCTGAGCCGTGCTAC  4869
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Qy  4930  GGCCGGCCCTGCGCGTCAGTGCCGTCAGTGCCCGTGCTAACAGAGAGGAGGCCCCGGCC  4989
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Qy  5110  TCGCCCCCGGCCACACCCTTGGTCTCCCCCGCTGGGGTGTGGGTCTGCTGCGAGACGGCGCCAATAAAA  5169
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RESULT 8
AX039409

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LOCUS       AX039409               4175 bp    DNA     linear   PAT 18-NOV-2000
DEFINITION  Sequence 2 from Patent WO0063381.
ACCESSION   AX039409
VERSION     AX039409.1  GI:11229476
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Zeng,W., Stanton.L. and Kong,H.
  TITLE     Mammalian protein with putative function in signal transduction
  JOURNAL   Patent: WO 0063381-A 2 26-OCT-2000;
            SCIOS INC. (US)
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Qy 1895 GGCACCTGCTGAAGGCGGCTACATTGCGGGGGGCGCTGCCAGGCCTGCGCGAGCCACTGA 1954
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Db  845 GGCACCTGCTGAAGGCGGGTACATTGCGGGGGGCGCTGCCAGGCCTGCGCGAGCCACTGA  904

Qy 1955 TGGAGCACCGCGTGCTGGAGGAGGAGGCCGCCAGGGAGGAGCAGGCCACCCTCCTGGCCA 2014
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  905 TGGAGCACCGCGTGCTGGAGGAGGAGGCCGCCAGGGAGGAGCAGGCCACCCTCCTGGCCA  964

Qy 2015 AAGCCCCTCATTCGAGACTGCCCTCGGCGTGCCTGCCTGGCACCCACTTGCCCCTG 2074
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Db  965 AAGCCCCTCATTCGAGACTGCCCTCGGCGTGCCTGCCTGGCACCCACTTGCCCCTG 1024

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RESULT 9
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DEFINITION  Homo sapiens mRNA for KIAA1639 protein, partial cds.
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VERSION     AB046859.1  GI:10047354
KEYWORDS    .
SOURCE      Homo sapiens (human)
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REFERENCE   1  (sites)
  AUTHORS   Nagase,T., Kikuno,R., Nakayama,M., Hirosawa,M. and Ohara,O.
  TITLE     Prediction of the coding sequences of unidentified human genes.
            XVII. The complete sequences of 100 new cDNA clones from brain
            which code for large proteins in vitro
  JOURNAL   DNA Res. 7 (4), 273-281 (2000)
  MEDLINE   20450683
   PUBMED   10997877
REFERENCE   2  (bases 1 to 4041)
  AUTHORS   Ohara,O., Nagase,T. and Kikuno,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-AUG-2000) Osamu Ohara, Kazusa DNA Research Institute,
            Department of Human Gene Research; 1532-3, Yana, Kisarazu, Chiba
            292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp,
            URL:http://www.kazusa.or.jp/huge, Tel:81-438-52-3913,
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Db   601  CTCCGCTCTGCATCTCCCCAGGGGTGCCGGGCCACCCGAGGGCTGCGTGCCCCGGC   660

Qy  1799  ACAGCGTCATCCGCAGCCTGTTCTACCACCAGGCCGGGTGAGAGCCCTGAGAGCACGGGGCCC  1858
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Db  1021  CAGCCCCTCCGGGGGGCCCCTATCAGGACATGGGCCACCCTAGGGGTCCAAGCAGC  1080
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DEFINITION  Sequence 46 from Patent WO01096547.
ACCESSION   AX642969
VERSION     AX642969.1  GI:28550118
KEYWORDS    .
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REFERENCE   1
AUTHORS     Yue,H., Lal,P., Bandman,O., Borowsky,M., Au-Young,J., Lu,Y.,
            Gandhi,A.R., Tribouley,C.M., Walia,N., Yao,M.G., Lu,D.A.,
            Greenwald,S.R., Ramkumar,J., Griffin,J.A., Kearney,L., Burford,N.,
            Nguyen,D.B., Tang,Y.T., Baughn,M.R., He,A., Thornton,M.,
            Hafalia,A., Patterson,C., Gururajan,R., Lo,T.P., Khan,F.,
            Recipon,S.A., Azinzai,Y., Policky,J.L., Ding,L., Grether,M.,
            Elliott,V.S., Thangavelu,K., Batra,S. and Ison,C.H.
TITLE       Human kinases
JOURNAL     Patent: WO 01096547-A 46 20-DEC-2001;
            Incyte Genomics, Inc. (US)
FEATURES    Location/Qualifiers
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ORIGIN

Query Match             61.4%;  Score 3197.8;  DB 6;  Length 3225;
Best Local Similarity   99.9%;  Pred. No. 0;
Matches  3210;          Conservative  0;  Mismatches  2;  Indels  1;  Gaps  1;
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Qy   1979  AGGCGCCCAGGGAGGAGGAGGAGCAGCGCCACCCCTCTGGCCAAAGCCCCTCATTCGAGACTGCCC  2038
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Db     13  AGGCGCCCAGGGAGGAGGAGGAGCAGCGCCACCCCTCTGGCCAAAGCCCCTCATTCGAGACTGCCC    72

Qy   2039  TCCGGGCTGCCTGCCTGGCACCCACTTGGCCCCTGGCCCCAGCGCCACTCCCTGGAACATG  2098
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Qy  4198 CCCAGCACAAAGACCTTCGCAATTCCAGACACAGATCCAGAGGGGCCGCTTCAGCGTGGTG 4257
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Qy  4258 CGGCAATGCTGGGAGAAGGCCAGCGGGGGCGGGCGGGCCGCCAAGATCATCCCCTACCAC 4317
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Qy  4318 CCCAAGGACAAAGACAGCAGTGCTCGCGGAATACGAGGCCCTCAAGGGCCTGCGCCACCCG 4377
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Qy  4498 GAGGTGAAGGACTACCTGTGGCAGATGTTGAGTGCCACCCAGTACCTGCACAACCAGCAC 4557
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Qy  4558 ATCCTGCACCTGGACCTGGAGGTCCGAGAACATGATCATCCGAATACACAACCTGCTCAAG 4617
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Qy  4618 GTCGTTGGACCTGGGCAATGCACAGAGCCTCAGCCAGGAGAGTGCTGCCCTCAGACAAG 4677
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Qy  4678 TTCAAGGACTACCTAGAGACCATGGCTCCAGAGCTTCCTGAGGGCCAGGGGCTGTTCCA 4737
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Qy  4738 CAGACAGACATCTGGGCCATCGGTGTGACAGCCTTCATCATGCTGAGCGGCGAGTACCCG 4797
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DEFINITION  Human DNA sequence from clone RP11-245P10 on chromosome 1, complete
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ACCESSION   AL670729
VERSION     AL670729.19  GI:22316158
KEYWORDS    HTG.
SOURCE      Homo sapiens (human)
ORGANISM   Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 62164)
AUTHORS     Van Hellmond,Z.
TITLE       Direct Submission
JOURNAL     Submitted (15-AUG-2002) Wellcome Trust Sanger Institute, Hinxton,
            Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
            humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
            On Aug 19, 2002 this sequence version replaced gi:21727388.
COMMENT     -------------- Genome Center
            Center: Wellcome Trust Sanger Institute
            Center code: SC
            Web site: http://www.sanger.ac.uk
            Contact: humquery@sanger.ac.uk
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            During sequence assembly data is compared from overlapping clones.
            Where differences are found these are annotated as variations
            together with a note of the overlapping clone name. Note that the
            variation annotation may not be found in the sequence submission
            corresponding to the overlapping clone, as we submit sequences with
            only a small overlap as described above.
            This sequence was finished as follows unless otherwise noted: all
            regions were either double-stranded or sequenced with an alternate
            chemistry or covered by high quality data (i.e., phred quality >=
            30); an attempt was made to resolve all sequencing problems, such
            as compressions and repeats; all regions were covered by at least
            one plasmid subclone or more than one M13 subclone; and the
            assembly was confirmed by restriction digest. The following
            abbreviations are used to associate primary accession numbers given
            in the feature table with their source databases: Em:, EMBL; Sw:,
            SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP
            database can be found at
            http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
            was generated from part of bacterial clone contigs of human
            chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping
            Group.  Further information can be found at
            http://www.sanger.ac.uk/HGP/Chr1
            RP11-245P10 is from the library RPCI-11.1 constructed by the group
            of Pieter de Jong. For further details see
            http://www.chori.org/bacpac/home.htm
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FEATURES             Location/Qualifiers

Tue Apr 27 10:11:33 2004                    us-10-697-263-1.rge

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ORIGIN

Query Match      39.7%;   Score 2067.2; DB 9;  Length 62164;
Best Local Similarity  99.4%;  Pred. No. 6.7e-305;
Matches 2075;  Conservative 0;  Mismatches 13;  Indels 0;  Gaps 0;
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Qy    1417  TTCCTCCTGGCCGGAGTCGCTGGCAGCGTCCTGATGAGCTACAAGTCCATCCTGGTG  1476
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Db   24359  TGCCTGCTGCCCCCCATGCGGTTCCCGGCGTTCCCGATGAGCTACAAGTCCATCCTGTG  24418

Qy    1477  ATGCGGTTCCATCCTGAGCTGCTGCGGGGCCCACCCGACACAGCCCCTCCCTCGCGTAGCC  1536
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Db   24419  ATGCGGTTCCATCCTGAGCTGCTGCGCGGGGCCCACCCGACACAGCCCCTCCCTCGGCGTAGCC  24478

Qy    1537  CGGCACCTCTGCAGGGACACTGGTGCTCCTCCAGTTCCTCCTCCTCTGACAACGAG  1596
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Db   24479  CGGCACCTCTGCAGGGACACTGGTGCTCCTCCAGTTCCTCCTCCTCTGACAACGAG  24538

Qy    1597  CTCGCCCCATTTGCCCGGGGCTAAGTCACTGCCACCCTCCCGGTGACACACTCACCACTG  1656
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Db   24539  CTCGCCCCATTTGCCCGGGGCTAAGTCACTGCCACCCTCCCGGTGACACACTCACCACTG  24598

Qy    1657  CTGCACCCCGGGGCTTCCTGCGGCCTGCCTGAGGAAGCCGAGGCCAGT  1716
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Db   24599  CTGCACCCCGGGGCTTCCTGCGGCCTGCCTGAGGAAGCCGAGGCCAGT  24658

Qy    1717  GAGGGGCATGCTGGTGGGCAGGGGCCACCAGTCATCTCCCGGGACGTGCCGGGCCACCGGCC  1776
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Qy    1777  GCCCAGGGCTGCGTGCCCCGGGAGCACGGGGCCCTGGCCCCGGGGAGCAGGGGCCGGGGT  1836
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Qy    1957  GAGCACCGGCGTGCTGAGAGGAGGAGGCGGCCAGGAGGAGGGCGCCGCAGGGAGGAGGCGG  2016
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Qy    2017  GCCCCCTCATTCGGAACTGACTGCCCTCCGGCACCCCCAGTTGGCCCCTGGC  2076
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Db   24959  GCCCCCTATTCGGAACTGACTGCCCTCCGGCACCCCCAGTTGGCCCCTGGC  25018

Qy    2077  CACAGCCACTCCCTGGAACATGACTTCCAGCCCCTCCGGCACACCCCGGCCCCTCCGGAGGCCTGC  2136
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Db   25019  CACAGCCACTCCCTGGAACATGACTTCCAGCCCCTCCGGCACACCCCGGCCCCTCCGGAGGCCTGC  25078

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Db   25139  CACCCTCAGGGCTCCAAGCAGCTTCCATCCACTGTGGCCACCCCAGGACTGCTCAGCCA  25198

Qy    2257  GAGAGGCCATCCCCGGACAGCCCTTGGGACGACAGCCCCTTTCTGCCACCCCAAGCAG  2316
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Db   25259  GGTTCTGCCCCCAGGAGGGGCTGCAGCCCCCACCCAGCAGTTGCCCATGCCCTCCTGGC  25318

Qy    2377  TCCTTCCCTCCAGGATCTTGCAAAGAGGAGGCCCCCTTAGTACCCTCAAGCCCCTTCTTGGGA  2436
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Db   25319  TCCTTCCCTCCAGGATCTTGCAAAGAGAGGCCCCCTTAGTACCCTCAAGCCCCTTCTTGGGA  25378

Qy    2437  CAGCCCCAGGCACCCCCTGCCCCTGCCCAAAGCAGCCCCATTGGACTCTAAGATGGGG  2496
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Qy    2497  CCTGGAGACATCTCTTCCTTCCTGGGAGCCAAAACCCGGCCCCTGCAGTTCCCCAGGGTCA  2556
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Db   25559  ACAGAGCCTGCCCCTCCCTGATGCGGAGGGCTGGACCCAGGAGGCTGAGGATCTGTCC  25618

Qy    2677  GACTCCACACCTTGCAGCGGGCTCAGGAACAGTGACATGCGACCATGCGCAAGTTCTCCCTG  2736
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Qy    2737  GGTGGTCGCGGGGGCTACGGCAGGGTGGTGGCTCATGGCACCTTTGCCTTTGGTGGAGAT  2796
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Qy    2917  GCCAGGGCTGAGACCCAGGAGGAGCCCACTGCCCCAGGTCAGTCAGTGCCTGGCAGG  2976
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Db   25919  GCTCCACCAGGAGCTCTCCAGAGCCCACCCATGGGAGGACATCGGGAGGACATCGGGGACACCTCCCTG  25978

Qy    3037  GTGCAGATCCGGACCTGTCAGGTGATGCGAGGCGGCCGACACAATATCCCTGGACATT  3096
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Qy    3097  TCCGAGTTGACCCCGCCTACCTCAACCTCTCAGACCTGTACGATATCAAGTACTCCCA  3156
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RESULT 12
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LOCUS        AC023889            174612 bp    DNA     linear   HTG 07-JUL-2000
DEFINITION   Homo sapiens chromosome 1 clone RP11-661B12, WORKING DRAFT
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ACCESSION    AC023889
VERSION      AC023889.3  GI:8969253
KEYWORDS     HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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AUTHORS      Waterston.R.H.
TITLE        The Sequence of Homo sapiens clone
JOURNAL      Unpublished
REFERENCE    2  (bases 1 to 174612)
AUTHORS      Waterston.R.H.
TITLE        Direct Submission
JOURNAL      Submitted (18-FEB-2000) Genome Sequencing Center, Washington
             University School of Medicine, 4444 Forest Park Parkway, St. Louis,
             MO 63108, USA
COMMENT      On Jul 7, 2000 this sequence version replaced gi:8748947.

             --------------- Genome Center -----------------
             Center: Washington University Genome Sequencing Center
             Center code: WUGSC
             Web site:http://genome.wustl.edu/gsc/index.shtml
             ----------- Project Information ---------------
             Center project name: H_NH0661B12
             ----------- Summary Statistics ---------------
             Sequencing vector: M13; 100%
             Sequencing vector: plasmid; 0%
             Chemistry: Dye-primer ET; 100% of reads
             Chemistry: Dye-terminator Big Dye; 0% of reads
             Assembly program: Phrap; version 0.990319
             Consensus quality: 163945 bases at least Q40
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             Consensus quality: 169687 bases at least Q20
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             Quality coverage: 5.67 in Q20 bases; agarose-fp
             Quality coverage: 5.55 in Q20 bases; sum-of-contigs
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             * NOTE: This is a 'working draft' sequence. It currently
             * consists of 13 contigs. The true order of the pieces
             * is not known and their order in this sequence record is
             * arbitrary. Gaps between the contigs are represented as
             * runs of N, but the exact sizes of the gaps are unknown.
             * This record will be updated with the finished sequence
             * as soon as it is available and the accession number will
             * be preserved.
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             *     9374     9473: gap of unknown length
             *     9474    13303: contig of 3830 bp in length
             *    13304    13403: gap of unknown length
             *    13404    18270: contig of 4867 bp in length
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             *    45743    45842: gap of unknown length
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             *    62988    63087: gap of unknown length
             *    63088    87584: contig of 24497 bp in length
             *    87585    87684: gap of unknown length
             *    87685   114765: contig of 27081 bp in length
             *   114766   114865: gap of unknown length
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ORIGIN

Query Match       29.1%;   Score 1517;  DB 2;  Length 174612;
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Matches 1641;  Conservative  0;  Mismatches  35;  Indels  13;  Gaps   9;

Qy    1816 CTGTTCTACCACCAGGCGGTGAGGCCCTGAGCACGGGCCCTGCCCCGGGAGCAGG 1875
                ||||||||||||||||| ||||||||||||||||||||| ||||||||||
Db   25403 CTTTTCTACCACCAGCGTGATGAAAACCCT--GCAGGGGCGCTCGGCCTCCGGCAACAAG 25346
Qy    1876 CGGCACCCGGCCCGCGGCGGCACCTCGCTGAAGGGGCCGCTACATTGCGGGGCCGCTGCCA 1935
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Db   25345 CGAAACCCGG-GCACAGTCGGCACCTGCTGAAGGGCCGGGTACATTGCGGGG--GCTGCCA 25289
Qy    1936 GGCCTGCGGCGAGCCACTGATGAGCACCGCGTGCTGCTGAGGAGGAGGCCGCAGGGAGGAG 1995
                |||||||||||||||||||||||||| ||| ||||||||||||||||||||||||||
Db   25288 GGCCTGCGGCGAGCCACTGATGAGGAGACAGCGTGCTGGAGGAGGAGGCCGCAGGGAGGAG 25229
Qy    1996 CAGGGCACCCTCCTGGCCAAAGCCCCCTCATTCGAGACTGCCCTCGGGCTGCCTGCCTCT 2055
                ||||||||||||||||||||||| ||||| |||||||| |||||||||||||||||||
Db   25228 CAGGCGCACCCTCCTCGGCCAAAGCCCCCTCATTCGAGACTGCCCTCGGGCTGCCTGCCTCT 25169
Qy    2056 GGCACCCACTTGGCCCCTGGCCACAGCCACTCCCTGGAACATGACTCTCCGAGCACCCCC 2115
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   25168 GG-ACCCACTTGGCCCCTGGCCACAGCCACTCCCTGGAACATGACTCTCCAAGCACCCCC 25110
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Qy   2116 CGCCCTCCTCGGAGGCCTGCGGTGAGGCACAGCGACTGCCTTCAGCCCCTCGGGGGG 2175
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Db  25109 CG-CCTCCTCGGAGGCCTGCGGTGAGGCACAGCGACTGCCTTCAGCCCCTCC--GGCC 25053

Qy   2176 GCCCCTATCAGGGACATGGGGCACCCCAGGGCTCCAAGCAGCTTCATCCACTGGTGGC 2235
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Db  25052 CCCCTATCAGGGACATGGGGCA-CCTCAGGGCTCCAAGCAGCTTCATCCACTGGTGGC 24994

Qy   2236 CACCCAGGCACTGCTCAGCCAGAGAGCCATCCCGGACAGCCCTTGGGGCCAGCCAGCC 2295
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Db  24993 CACCCAGGCACTGCTCAGCCAGAGAGCCATCCCGGACAGCCCTTGGGGAAGCCAGCC 24934

Qy   2296 CCTTTCTGCCACCCAGCAGGGTTCTGCCCCCAGGAGGGCTGCAGCCCCACCCAGCA 2355
          ||||||||||||||||||||||||||| |||| ||||||||
Db  24933 CCTTTCTGCCACCCAGCAGGGTTCTGCCCCCAGGAGGGCTGCAG--CCCACCCAGCA 24876

Qy   2356 GTTGCCCCATGCCCTCCTTGCTCCTTCCCTCCAGGATCTTGCAAAGAGGCCCCCTTAGTA 2415
          |||||||||||||||||||||||||||||||||||||||
Db  24875 GTTGTTCCATGCCCTCCTGGTCCTTCCCTCCAGGATCTTGCAAAGAGGACCCCCTTAGTA 24816

Db  24815 CCCTCAAG-CCCTTCTTGGGACAGCCCCAGGCACCCCCTGCCAAAGCAAGCCCC 24757

Qy   2416 CCCTCAAGCCCCTTCTTGGGACAGCCCCAGGCACCCCCTGCCAAAGCAAGCCCC 2475

Qy   2476 CCATTGGACTCTAAGATGGGGCTGGACACATCTCTTCTTCCTTGGGAGGCCAAAACCCGGC 2535
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Qy   2536 CCCTGCAGTTCCCCAGGGTCAGCCTCCCCAGGCAGCTCCTCCCAAGTGAGCTCCCTCAGG 2595
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Db  24637 CCCTGCAGTTCCCCAGGGTCAGCCTCCCCAGGCAGCTCTTCCCAAGTGAGCTCCCTCAGG 24696

Qy   2596 GTGGGCTCCTCCCAGTGGGCACAGAGCCTGGCCCCTCCCTCCTGGATGCGGAGGGCTGACC 2655
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Db  24636 GTGGGCTCCTCCCAGTGGGCACAGAGCCTGGCCCCTCCCTCCTGGATGCGGAGGGCTGACC 24577

Qy   2656 CAGGAGGCTGAGGATCGTCGGACTCCACACCCACTTGCAGGGGCCTTCAGGAACACAGTG 2715
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Db  24517 CAGGAGGCTGAGGATCGTCGGACTCCACACCCACCTTGCAGGGCGCCTTCAGGAACACAGTG 24576

Qy   2716 ACCATGCGCAAGTCTCCCTGGGTGGTCGCGGGGCTACGCAGCGTGGCTGGCTATCGGC 2775
          |||||||||||||||||||||||||||||||||||||||
Db  24457 ACCATGCGCAAGTTCTCCCTGGGTGGTCGTGCGGGGCTACGCAGCGTGGCTGGCTATCGGC 24516

Qy   2776 ACCTTTGCCTTTGGTGGAGATGCAGGGGGCATGCTGGGGCAGGGGCCCATGTGGGCCAGG 2835
          |||||||||||||||||||||||||||||||||||||||||
Db  24397 ACCTTTGCCTTTGGTGGGGGCATGCTGGGGCAGGGGCCCATGTGGGCCAGG 24456

Qy   2836 ATAGCCTGGGCTGTGTCCCAGTCGGAGGAGGAGCAGGAGGAGCCAGGGCTGAGTCC 2895
          |||||||||||||||||||||||||||||||||||||||||||||
Db  24396 ATAGCCTGGGCTGTGTCCCAGTCGGAGGAGGAGCAGGAGGAGCCAGGGCTGAGTCC 24337

Qy   2896 CAGTCGGAGGAGCAGGAGGAGCAGGGCTGAGAGCCCACTGCCCCCAGGTCAGTGCAAGG 2955
          |||||||||||||||||||||||||||||||||||||||||
Db  24277 CAGTCGGAGGAGCAGGAGGAGCAGGGCTGAGAGCCCACTGCCCCCAGGTCAGTGCAAGG 24336

Qy   2956 CCTGTGCCTGAGGTCGGCAGGGCTCCCACCCGGCTCTCCAGAGCCCACCCATGGGGAG 3015
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Db  24217 CCTGTGCCTGAGGTCGGCAGGGCTCCCACCCGGCTCTCCAGAGCCCACCCATGGGGAG 24276

Qy   3016 GACATCGGGCAGGTCTCCCTGGTCGAGATCCGGACCTGTCAGGTGATCGGGAGGCGGCGC 3075
          |||||||||||||||||||||||||||||||||||||||||||
Db  24157 GACATCGGGCAGGTCTCCCTGGTCGAGATCCGGACCTGTCAGGTGATCGGGAGGCGGCGC 24216

Qy   3076 GACACAATATCCCTGACATTCCGAGGTGACCCCGCCTACCCGGCTGACCTCTCAAACCTCTCAGACCTTG 3135
          ||||||||||||||||||||||||||||||||||||||||
Db  24097 GACACAATATCCCTGACATTCCGAGGTGACCCCGCCTACCCGGCTGACCTCTCAAACCTCTCAGACCTTG 24156

Qy   3136 TACGATATCAAGTACCTCCCATTCGAGTTTATGATCTTCAGGAAAGTCCCCAAGTCCGCT 3195
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Db  24037 TACGATATCAAGTACCTCCCATTCGAGTTTATGATCTTCAGGAAAGTCCCCAAGTCCGCT 24096

Qy   3196 CAGCCAGCAGCCGCCGCCCTCCCCCCATGGCTGAGGAGAGCTGCGCGAGTTCCCGGAGCCCACG 3255
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Db  24036 CAGCCAGCAGCCGCCGCCCTCCCCCCATGGCTGAGGAGAGCTGCGCGAGTTCCCGGAGCCCACG 23977
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Qy   3256 TGGCCCTGGCCAGGTGAACTGGGGCCCCAGCAGCAGCCTGAGATCACAGAGGAGTCAGAG 3315
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Db  23976 TGGCCCTGGCCAGGTGAACTGGGGCCCCAGCAGCAGCCTGAGATCACAGAGGAGTCAGAG 23917

Qy   3316 GATGTGGACGCGGCTGCTGGCAGAGGCTGCCCTGGGCAGGAGGCGCAAGTGGTCCTGCGG 3375
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Db  23857 GATGTGGACGCGGCTGCTGGCAGAGGCTGCCCTGGGCAGGAGGCGCAAGTGGTCCTGCGG 23916

Qy   3376 TCACGCAGCCCTTCCTCCACTTCCCTGGGAGGCACCTGCGCGCTGGATGAGCCTGCAGAGCTG 3435
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Db  23856 TCACGCAGCCCTTCCTCCACTTCCCTGGGAGGCACCTGCGCGCTGGACGAGCCTGCAGAGCTG 23797

Qy   3436 GGGCTGCGTGAGAGAGTGAAGGCCTCCGTGGAGCACATCTTCCGGATCCTGAAGGGGCAGG 3495
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Db  23796 GGGCTGCGTGAGAGAGTGAAGGCCTCCGTGGAGCACATCTTCCGGATCCTGAAGGGGCAGG 23737

Qy   3496 CCGGAAGGT 3504
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Db  23736 CCGGAAGGT 23728
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RESULT 13
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AC026657/c
LOCUS       AC026657              164766 bp    DNA     linear   HTG 01-SEP-2000
DEFINITION  Homo sapiens chromosome 1 clone RP11-245P10, WORKING DRAFT
            SEQUENCE, 31 unordered pieces.
ACCESSION   AC026657
VERSION     AC026657.4  GI:9958202
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 164766)
  AUTHORS   Waterston,R.H.
  TITLE     The sequence of Homo sapiens clone
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 164766)
  AUTHORS   Waterston,R.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-MAR-2000) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
COMMENT     On Sep 1, 2000 this sequence version replaced gi:7637349.

            ------------ Genome Center -----------
            Center: Washington University Genome Sequencing Center
            Center code: WUGSC
            Web site:http://genome.wustl.edu/gsc/index.shtml
            ----------- Project Information ------------
            Center project name: H_NH0245P10
            ----------- Summary Statistics -----------
            Sequencing vector: M13; 100%
            Sequencing vector: plasmid; 0%
            Chemistry: Dye-primer ET; 100% of reads
            Chemistry: Dye-terminator Big Dye; 0% of reads
            Assembly program: Phrap; version 0.990319
            Consensus quality: 139884 bases at least Q40
            Consensus quality: 147686 bases at least Q30
            Consensus quality: 151469 bases at least Q20
            Insert size: 169000; agarose-fp
            Insert size: 161074; sum-of-contigs
            Quality coverage: 3.60 in Q20 bases; agarose-fp
            Quality coverage: 3.92 in Q20 bases; sum-of-contigs

            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 31 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
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* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*            1..1124:   contig of 1124 bp in length
*         1124..1124:   gap of unknown length
*         1125..3032:   contig of 1808 bp in length
*         3032..3032:   gap of unknown length
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*         4494..5860:   contig of 1267 bp in length
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*         5861..7670:   contig of 1710 bp in length
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*         7771..9669:   contig of 1899 bp in length
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*         9770..11715:  contig of 1946 bp in length
*        11715..11815:  gap of unknown length
*        11816..14243:  contig of 2428 bp in length
*        14243..14343:  gap of unknown length
*        14344..16887:  contig of 2544 bp in length
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*        16988..19247:  contig of 2260 bp in length
*        19247..19347:  gap of unknown length
*        19348..21375:  contig of 2028 bp in length
*        21375..21475:  gap of unknown length
*        21476..25025:  contig of 3550 bp in length
*        25025..25125:  gap of unknown length
*        25126..28051:  contig of 2926 bp in length
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*        32155..35716:  contig of 3562 bp in length
*        35716..35816:  gap of unknown length
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*        40992..44027:  contig of 3036 bp in length
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*        44128..48899:  contig of 4772 bp in length
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*        54356..58994:  contig of 4639 bp in length
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ORIGIN

Query Match           20.8%;   Score 1081.2;   DB 2;   Length 164766;
Best Local Similarity 99.4%;   Pred. No. 4.1e-155;
Matches 1127;   Conservative  0;   Mismatches  3;   Indels  4;   Gaps  4;

Qy     2369 CTCCTGGCTCCTTCCCTCCAGGATCTTGCAAAGAGGCCCCTTAGTACCCTCAAGCCCCT 2428
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Db    70865 CTCCTGGCTCCTTCCCTCCAGGATCTTGCAAAGAGGCCCCTTAGTACCCTCAAGCCCCCT 70806

Qy     2429 TCTTGGGACAGCCCCAGGCACCCCCTGCCCAAAGCAAGCCCCCATTGGACTCTA 2488
            ||||||||||||      |||||| ||||||||||||||||||||||||||||||
Db    70805 TCTTGGGACAGCAGCCCCAGG-ACCCCCTGCCCCCAAAGCAAGCCCCCATTGGACTCTA 70747
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DEFINITION    Mouse DNA sequence from clone RP23-441I8 on chromosome 11, complete
              sequence.
ACCESSION     AL662809
VERSION       AL662809.14    GI:28881816
KEYWORDS      HTG.
SOURCE        Mus musculus (house mouse)
  ORGANISM    Mus musculus
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE     1  (bases 1 to 103129)
  AUTHORS     Pearce,A.
  TITLE       Direct Submission
  JOURNAL     Submitted (06-MAR-2003) Wellcome Trust Sanger Institute, Hinxton,
              Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
              humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
              On Mar 7, 2003 this sequence version replaced gi:21655347.
COMMENT       -------------- Genome Center
              Center: Wellcome Trust Sanger Institute
              Center code: SC
              Web site: http://www.sanger.ac.uk
              Contact: humquery@sanger.ac.uk
              --------------
              During sequence assembly data is compared from overlapping clones.
              Where differences are found these are annotated as variations
              together with a note of the overlapping clone name. Note that the
              variation annotation may not be found in the sequence submission
              corresponding to the overlapping clone, as we submit sequences with
              only a small overlap as described above.
              The following abbreviations are used to associate primary accession
              numbers given in the feature table with their source databases:
              Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information
              on the WORMPEP database can be found at
              http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
              was finished as follows unless otherwise noted: all regions were
              either double-stranded or sequenced with an alternate chemistry or
              covered by high quality data (i.e., phred quality >= 30); an
              attempt was made to resolve all sequencing problems, such as
              compressions and repeats; all regions were covered by at least one
              plasmid subclone or more than one M13 subclone; and the assembly
              was confirmed by restriction digest, except on the rare occasion of
              the clone being a YAC.
              RP23-441I8 is from the RPCI-23 Mouse BAC Library
              constructed by the group of Pieter de Jong.
              For further details see http://www.chori.org/bacpac/home.htm
              VECTOR: pBACe3.6
              Sequence from the Mouse Genome Sequencing Consortium whole genome
              shotgun may have been used to confirm this sequence. Sequence data
              from the whole genome shotgun alone has only been used where it has
              a phred quality of at least 30.
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ORIGIN

Query Match      16.0%;     Score 831.8;  DB 10;  Length 103129;
Best Local Similarity   67.6%;     Pred. No. 3.7e-117;
Matches 1453;    Conservative     0;   Mismatches 537;   Indels 159;   Gaps   14;

Qy    1398  CAACACCAAGCAGCTCAAGTTCCTCCTGGCCCGAGTCGCTGGCAGCGTTCCCTGATGAG  1457
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Db    85696  CATGACCAGTCATGCCCAATGGATGTCCCTGTCCTCATTTCCAGCGTCCTCGTGATGAG  85637

Qy    1458  CTACAAGTCCATCCTGGTGATCGCTCCATCCTGAGCTGCTGGGGCCCACCCGACACAG  1517
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Qy    1518  CCCCTCCCTGGCGTAGCCCGGCACCTCTGCAGGAGCACTGGTGGCTCCTCCAGTTCCTC  1577
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Qy    2489  AGATGGGGCCTGAGAGACATCTCTTCCTGGGAGGCCAAAACCCGGCCCTGCAGTTCCC  2548
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Db    70746  AGATGGGGCCTGAGAGACATCTCTCTCCTCTGGGA-GCCAAAACCCGGCCCTGCAGTTCCC  70688

Qy    2549  CAGGGTCAGCGTCCCCAGGCGGAGCTCTTCCCAAGTGAGCTCCCTCAGGGTGGGCTCCTCCC  2608
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Qy    2609  AGGTGGGCACAGAGCCTGGCCCCTCCCTGGATGCGGAGGGGCTGGACCCAGAGGGCTGAGG  2668
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Db    70628  AGGTGGGCACAGAGCCTGGCCCCTCCCTGGATGCGGAGGGGCTGGACCCAGAGGGCTGAGG  70569

Qy    2669  ATCTGTCCGACTCCACACCACCTTGCAGCGGCCTCAGGAACAGTGACCATGCGCAAGT  2728
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Db    70558  ATCTGTCCGACTCCACACCACCTTGCAGCGGCCTCAGGAACAGTGACCATGCGCAAGT  70509

Qy    2729  TCTCCCTGGGTGGTCGCGGGGGCAGGGCTACGGCAGGCGTGGCTATGGCACCTTTGCCTTTG  2788
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Qy    2789  GTGGAGATGCAGGGGGCATGCTGGGGCAGGGGCCCATGTGGGCCAGGATAGCCTGGGCTG  2848
            ||||||||||||||||||||| ||||||||||||||| |  |||||||||||||||||||
Db    70448  GTGGAGATGCAGGGGGCATGCTGGGGCAGGGGCCCATG-CCATGTGGGCCAGGATAGCCTGGGCTG  70390

Qy    2849  TGTCCCAGTCGGAGGAGGAGGAGCAGGAGGAGGAGCCAGGGCTGAGTCCCAGTCCCAGGAGGAGC  2908
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Db    70389  TGTCCCAGTCGGAGGAGGAGGAGCAGGAGGAGGAGCCAGGGCTGAGTCCCAGTCCCAGGAGGAGC  70330

Qy    2909  AGCAGGAGGCCCAGGGCTGAGACCTGAGAGCCCACTGCCCCCAGGTCAGTGCAAGGCCTGTGCCTGAGG  2968
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Qy    2969  TCGGCAGGGCTCCACCAGGAGCTCTCCAGAGCCACCCATGGGAGGACATCGGGCAGG  3028
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Qy    3029  TCTCCCTGGTGCAGATCCGGGACCTGTGATGCGGAGGCGGCCGACACCAAATATCCC  3088
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Db    70209  TCTCCCTGGTGCAGATCCGGGACCTGTGATGCGGAGGCGGCCGACACCAAATATCCC  70150

Qy    3089  TGGACATTTCCGAGGTGACCCCGCCTACCTCAACCTTCTCAGACCTGTACGATATCAAGT  3148
            |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    70149  TGGACATTTCCGAGGTGACCCCGCCTACCTCAACCTTCTCAGACCTGTACGATATCAAGT  70090

Qy    3149  ACCTGCCATTCGAGTTTATGATCTTCAGGAAAGTCCCCAGCTTCCCGCTCAGCCAGAGCCGC  3208
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Db    70089  ACCTGCCATTCGAGTTTATGATCTTCAGGAAAGTCCCCAGCTTCCCGCTCAGCCAGAGCCGC  70030

Qy    3209  CCTCCCCATGGCCGAGTGGAGCTGGCCGAGTTCCCGGAGCCCACGTGGCCCTGGCCAG  3268
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Db    70029  CCTCCCCATGGCCGAGTGGAGCTGGCCGAGTTCCCGGAGCCCACGTGGCCCTGGCCAG  69970

Qy    3269  GTGAACTGGGCCCCCAGCGGCCTGGAGATCACAGAGGAGTCAGAGGATGTGGACCGCGC  3328
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Db    69969  GTGAACTGGGCCCCCAGCGGCCTGGAGATCACAGAGGAGTCAGAGGATGTGGACCGCGC  69910

Qy    3329  TGCTGGCCAGAGGCTGCCGTGGGCAGGAGGCGCAAGTGGTCCTTCGCCGTCACGCAGCCTCT  3388
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Qy    3389  TCCACTTCCTGGGAGGACACCTGCCGCTGGATGAGCGCTGCAGAGCTGGGGGCTGGGTGCGTGAGA  3448
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Db    69849  TCCACTTCCTGGGAGGACACCTGCCGCTGGATGAGCGCTGCAGAGCTGGGGGCTGGGTGCGTGAGA  69790

Qy    3449  GAGTGAAGGCCTTCCGTGGAGCACATCTCCCGGATCCTGAAGGGCAGGCCGGAAG  3502
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RESULT 14
AL662809/c
LOCUS       AL662809       103129 bp    DNA     linear     ROD 06-MAR-2003

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

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REFERENCE   1  (bases 1 to 258622)
  AUTHORS   DOE Joint Genome Institute.
  TITLE     Sequencing of Mouse
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 258622)
  AUTHORS   DOE Joint Genome Institute.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-JAN-2000) Production Sequencing Facility, DOE Joint
            Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
COMMENT     On Mar 29, 2000 this sequence version replaced gi:6686431.
            ------Genome Center
              Center: Joint Genome Institute
              Center Code: JGI
              Web site: http://www.jgi.doe.gov
            ------Summary Statistics
              Consensus quality: 140189 bases at least Q40
              Consensus quality: 191513 bases at least Q30
              Consensus quality: 208421 bases at least Q20
              Estimated insert size: 258622; sum-of-contigs estimation
              Estimated insert size: 216000; pulse field gel estimation
              Quality coverage: 4.19x in Q20 bases; pulse field gel estimation
              Quality coverage: 3.50x in Q20 bases; sum-of-contigs estimation
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 97 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *         1     1069: contig of 1069 bp in length
            *      1070     2085: gap of unknown length
            *      2086     3153: contig of 1068 bp in length
            *      3154     4722: gap of unknown length
            *      4723     5728: contig of 1006 bp in length
            *      5729     6764: gap of unknown length
            *      6765     7830: contig of 1066 bp in length
            *      7831     8859: gap of unknown length
            *      8860     9865: contig of 1006 bp in length
            *      9866    10869: gap of unknown length
            *     10870    11962: contig of 1093 bp in length
            *     11963    13013: gap of unknown length
            *     13014    14338: contig of 1325 bp in length
            *     14339    15557: gap of unknown length
            *     15558    16667: contig of 1110 bp in length
            *     16668    17748: gap of unknown length
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            *     19090    20675: gap of unknown length
            *     20676    22435: contig of 1761 bp in length
            *     22436    23683: gap of unknown length
            *     23684    25215: contig of 1532 bp in length
            *     25216    26431: gap of unknown length
            *     26432    27491: contig of 1060 bp in length
            *     27492    28737: contig of 1246 bp in length
            *     28738    29742: gap of unknown length
            *     29743    30947: contig of 1205 bp in length
            *     30948    31992: gap of unknown length
            *     31993    33108: contig of 1116 bp in length
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            *     34436    35651: gap of unknown length
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            *     37356    38598: contig of 1243 bp in length
            *     38599    39644: gap of unknown length
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            *     41276    42381: contig of 1106 bp in length
            *     42382    43462: gap of unknown length
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            *     44823    45961: gap of unknown length
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            *     51834    52901: contig of 1068 bp in length
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            *     54596    56094: contig of 1499 bp in length
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*  75620   76851:  gap of unknown length
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*  78212   80704:  gap of unknown length
*  80705   81729:  contig of 1360 bp in length
*  81730   84042:  gap of unknown length
*  84043   85320:  contig of 2493 bp in length
*  85321   87117:  gap of unknown length
*  87118   88340:  contig of 1025 bp in length
*  88341   89484:  gap of unknown length
*  89485   90573:  contig of 2313 bp in length
*  90574   93019:  gap of unknown length
*  93020   94631:  contig of 1278 bp in length
*  94632   96750:  gap of unknown length
*  96751   98951:  contig of 1797 bp in length
*  98952  100658:  gap of unknown length
* 100659  102977:  contig of 1223 bp in length
* 102978  106226:  gap of unknown length
* 106227  107977:  contig of 1144 bp in length
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* 110244  113543:  contig of 1089 bp in length
* 113544  118028:  gap of unknown length
* 118029  120548:  contig of 2446 bp in length
                   contig of 1612 bp in length
                   contig of 2119 bp in length
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Best Local Similarity  67.6%;   Pred. No. 3e-117;
Matches 1453;  Conservative 0;  Mismatches 537;  Indels 159;  Gaps 14;
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Qy   1458  CTACAAGTCCATCCTGTGATGAGCCGGCACCTGTCAGCCTGCTGCGGGGCCCGACCAG  1517
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Qy   1638  GGTGACACACTCACCACTGCTGCACCCCCGGGGCTTCCTGCGCGGCCCTCGGCCAGCCTGCC  1697
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Qy   1698  TGAGGAAGCCGGAGGCCCAGTGAGCGCTCCACCGAGGCCCCAGCTTCCGCCTGCATCTCCGA  1757
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Qy  1818  GTTCTACCACCAGCAGGGGTTGAGAGCACAGGGGCCCTGGCCCTCGGCCCGGGGAGCAGGCG  1877
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Qy  1938  CCTGCGGCCGAGCCACTGATGAGCACCGGGGCTGCTGGGAGGAGGCGCCCAGGGAGGAGCA  1997
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Qy     2877 GGAGGCCAGGGCTGAGTCCCAGTCGGAGGAGCAGCAGGCCAGGGCTGAGAGCCCACT 2936
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Db   248807 --------------CTCAGAAGAGCAGGATGAAGCTGCGACTGAGAGCCCCTCA 248769

Qy     2937 GCCCCAGGTCAGTGCAGGCCTGTGCTGGCAAGGCCTGTCGGCAGGGTCCCACCAGGAGCTCCC 2996
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Qy     2997 AGAGCCCACCCCATGGGAGGACATCGGGCAGTCTCCCTGGTGCAGATCCGGACCTGTC 3056
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Db   248708 AAGCCTCACCCCTTGGGAGGAAGTTGAGCAGGTTTCCCTGGTGCAGATCCGGATCTGTC 248649

Qy     3057 AGGTGATGCGGAGGCGGCCGACACAATATCCCTGGACATTCCGAGTTGACCCCGCCTA 3116
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Db   248648 TGGTGATGCGGAAGCAGCTGACACTATCTCCTTGGACATTTCTGAGGTCGATCCTGCCTA 248589

Qy     3117 CCTCAACCTCTGTACGATCGTGATATCAAGTACCTCCATTCGAGTTATGATCTTCAG 3176
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Qy     3228 GGAGCTGGCCGAGTTCC---CGGAGCCCACGTGGCCCTGGCCAGGTGAACTGGGCCCCCA 3284
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Qy     3285 CGCAGCCTGAGATCACA--------GAGGAGTCAGGAGATGTGGACGCGCTGCTGGC 3335
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Qy     3456 GGCCTCCGTGGAGCACATCTCCCGGATCCTGAAAGGGCAGGCCGGAAGGT 3504
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Search completed: April 26, 2004, 12:45:37
Job time : 13046 secs

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                GenCore version 5.1.6
          Copyright (c) 1993 - 2004  Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:     April 26, 2004, 12:45:44 ; Search time 1365 Seconds
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Title:      US-10-697-263-1
Perfect score: 5207
Sequence:   1 cagcacgaggaactccttct........aaaaaaaaaaaaaaaaa 5207

Scoring table: IDENTITY.NUC
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Searched:   2907579 seqs, 2254313464 residues

Total number of hits satisfying chosen parameters:     5815158

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

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| 1 | 5207 | 100.0 | 5207 | 9 | US-09-858-664A-1 | Sequence 1, Appli |
| 2 | 5207 | 100.0 | 5207 | 13 | US-10-697-263-1 | Sequence 1, Appli |
| 3 | 5207 | 100.0 | 5207 | 13 | US-10-697-263-3 | Sequence 3, Appli |
| 4 | 5173.6 | 99.4 | 5454 | 13 | US-10-415-011-44 | Sequence 44, Appli |
| 5 | 4940.4 | 94.9 | 8106 | 14 | US-10-077-130-1 | Sequence 1, Appli |
| 6 | 4940.4 | 94.9 | 24120 | 14 | US-10-077-130-4 | Sequence 4, Appli |
| 7 | 4915.8 | 94.4 | 5007 | 15 | US-10-307-019-3 | Sequence 3, Appli |
| 8 | 4915.8 | 94.4 | 7928 | 15 | US-10-307-019-5 | Sequence 5, Appli |
| 9 | 4885.2 | 93.8 | 4936 | 13 | US-10-182-243-14 | Sequence 14, Appl |
| 10 | 4841 | 93.0 | 7893 | 14 | US-10-077-130-3 | Sequence 3, Appli |
| 11 | 4841 | 93.0 | 23907 | 14 | US-10-077-130-6 | Sequence 6, Appli |
| 12 | 4146.6 | 79.6 | 4175 | 15 | US-10-307-019-2 | Sequence 2, Appli |
| 13 | 3197.8 | 61.4 | 3225 | 17 | US-10-111-034-46 | Sequence 46, Appl |
| 14 | 1251.4 | 24.0 | 1253 | 13 | US-10-425-114-26278 | Sequence 26278, A |
| 15 | 358.4 | 6.9 | 382 | 11 | US-09-864-408A-8947 | Sequence 8947, Ap |
| 16 | 327.6 | 6.3 | 7789 | 13 | US-10-333-314-38 | Sequence 38, Appl |
| 17 | 327.6 | 6.3 | 9698 | 16 | US-10-210-130-37 | Sequence 37, Appl |
| 18 | 327.6 | 6.3 | 9807 | 16 | US-10-379-381-1 | Sequence 1, Appli |
| 19 | 308.4 | 5.9 | 9930 | 16 | US-10-210-110-33 | Sequence 33, Appl |
| 20 | 308.4 | 5.9 | 10122 | 16 | US-10-210-130-35 | Sequence 35, Appl |
| 21 | 224.4 | 4.3 | 1627 | 13 | US-10-425-114-26265 | Sequence 26265, A |
| 22 | 223.4 | 4.3 | 225 | 13 | US-09-864-408A-2403 | Sequence 2403, Ap |
| 23 | 205.2 | 3.9 | 860 | 16 | US-10-210-130-39 | Sequence 39, Appl |
| 24 | 173.4 | 3.3 | 2132 | 16 | US-10-262-445-118 | Sequence 118, App |
| 25 | 173.4 | 3.3 | 2224 | 15 | US-10-059-585-11 | Sequence 11, Appl |
| 26 | 157.2 | 3.0 | 1971 | 10 | US-09-849-138-3 | Sequence 3, Appli |
| 27 | 157.2 | 3.0 | 2558 | 10 | US-09-849-138-5 | Sequence 5, Appli |
| 28 | 153.8 | 3.0 | 1788 | 9 | US-09-797-039-9 | Sequence 9, Appli |
| 29 | 153.8 | 3.0 | 1788 | 15 | US-10-170-789-9 | Sequence 9, Appli |
| 30 | 153.8 | 3.0 | 1791 | 13 | US-09-797-039-7 | Sequence 26, Appl |
| 31 | 153.8 | 3.0 | 2046 | 9 | US-09-797-039-7 | Sequence 7, Appli |
| 32 | 153.8 | 3.0 | 2046 | 13 | US-10-423-543-24 | Sequence 24, Appl |
| 33 | 153.8 | 3.0 | 2046 | 15 | US-10-170-789-7 | Sequence 7, Appli |
| 34 | 153.8 | 3.0 | 3199 | 13 | US-10-112-944-49 | Sequence 49, Appl |
| 35 | 153.6 | 2.9 | 8906 | 13 | US-10-182-936A-85 | Sequence 85, Appl |
| 36 | 153.6 | 2.9 | 8906 | 16 | US-10-374-979-85 | Sequence 85, Appl |
| 37 | 153.6 | 2.9 | 8906 | 16 | US-10-331-496A-87 | Sequence 87, Appl |
| 38 | 152.2 | 2.9 | 1839 | 10 | US-09-849-138-7 | Sequence 7, Appli |
| 39 | 152 | 2.9 | 3731 | 9 | US-09-925-299-114 | Sequence 114, App |
| 40 | 152 | 2.9 | 3731 | 10 | US-09-925-299-114 | Sequence 114, App |
| 41 | 148.6 | 2.9 | 1467 | 13 | US-10-125-114-16427 | Sequence 16427, A |
| 42 | 148.6 | 2.9 | 3164 | 15 | US-10-210-120-25 | Sequence 25, Appl |
| 43 | 148.6 | 2.9 | 4564 | 10 | US-09-814-353-21660 | Sequence 21660, A |
| 44 | 148.6 | 2.9 | 5926 | 9 | US-09-969-708-302 | Sequence 302, App |
| 45 | 148.6 | 2.9 | 5926 | 9 | US-09-954-456-522 | Sequence 522, App |

ALIGNMENTS

```
RESULT 1
US-09-858-664A-1
; Sequence 1, Application US/09858664A
; Patent No. US20020072491A1
; GENERAL INFORMATION:
;   APPLICANT: WEI, Ming-Hui, et al.
;   TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
;   TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
;   TITLE OF INVENTION: THEREOF
;   FILE REFERENCE: CL000927-CIP
;   CURRENT APPLICATION NUMBER: US/09/858,664A
;   CURRENT FILING DATE: 2001-05-17
;   PRIOR APPLICATION NUMBER: 09/711,134
;   PRIOR FILING DATE: 2000-11-11
;   NUMBER OF SEQ ID NOS: 33
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 5207
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-858-664A-1

Query Match             100.0%;  Score 5207;     DB 9;  Length 5207;
Best Local Similarity   100.0%;  Pred. No. 0;
Matches 5207;    Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy          1 CAGCACGAGGAACTCCTTCTCGATCACCTGGCCAGTGAGGTCAGAGTGGAGGAGGCAGTG 60
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Db          1 CAGCACGAGGAACTCCTTCTCGATCACCTGGCCAGTGAGGTCAGAGTGGAGGAGGCAGTG 60

Qy         61 GTTCCATTGAAGGAGTACTCCTAACTGTCAGAAGCCTGGGCGGTCAGGATGGGGTGCTGT 120
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Db         61 GTTCCATTGAAGGAGTACTCCTAACTGTCAGAAGCCTGGGCGGTCAGGATGGGGTGCTGT 120

Qy        121 CGCTTGGGCTGCGCGGGGGTGTTCAGTTGCCCACAGTGTATCTCACCAACCAT 180
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Db        121 CGCTTGGGCTGCGCGGGGGTGTTCAGTTGCCCACAGTGTATCTCACCAACCAT 180
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Right column block:

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Qy  1261 GCCACCCTCAGCGACGAGAACGGCCAAGACTTCATCAAGGCTACGCTGCAGAGAGCCCCTCAG 1320
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Db  1261 GCCCACCTCACGGACGAGAACGGCCAAGACTTCATCAAGGCTACGCTGCAGAGAGCCCCTCAG 1320

Qy  1321 GCCCGGCCAGTGCGGCCAGTGCCTCCTCCCACCCCTGGTTCCTGAAATCCATGCTGCTGCG 1380
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Db  1321 GCCCGGCCTAGTGCGGCCAGTGCCTCCTCCCACCCCTGGTTCCTGAAATCCATGCTGCTGCG 1380

Qy  1381 GAGGAGGCCCACTTCATCAACACAGCAGTCCTTCCTCCTGGCCCGAAGTCGCTGG 1440
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Db  1381 GAGGAGCCCACTTCATCAACACAGCAGTCAAGTTCCTCCTGCCCGAAGTCGCTGG 1440

Qy  1441 CAGCGTTCCTGATGAGCTACAAGTCCATCCTGGTGATGGCGCTCCATCCCTGAGCGTGCTG 1500
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Db  1441 CAGCGTTCCTGATGAGCTACAAGTCCATCCTGGTGATGGCGCTCCATCCCTGAGCGTGCTG 1500

Qy  1501 CGGGGGCCACCCGACAGCCCCTCCTCGGCGTAGCCCGGCTAGCCGGGGACACTGGT 1560
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Db  1501 CGGGGGCCACCCGACAGCCCCTCCTCGGCGTAGCCCGGCGCACCTCGCAGGGACACTGGT 1560

Qy  1561 GGCTCCTCCAGTTCCTCCTCCTCCTGACAACGAGCTCGCCCATTGCCCGGGCTTCCTGCGG 1620
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Db  1561 GGCTCCTCCAGTTCCTCCTCCTCCTGACAACGAGCTCGCCCATTGCCCGGGCTTCCTGCGG 1620

Qy  1621 TCACTGCACCCTCCCGGTGACACACTCACCACTCGTGCACCCCCGGCGTTCCTGCGG 1680
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Db  1681 CCCTCGGCAGCCTGCCTGAGGAGGTGCCGGAAGCCAGTGAGCGTCCACCGAGCCCCAGCT 1740

Qy  1741 CGGCTCATCCCGCAGCCGTGTTCTCACCAGGCGGGTGAGAGCCCTGAGCGCGGGCCCTG 1800
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Db  1741 CCGCCTGCATCTCCCGGAGGGTGCCGGGGGTGAGAGCGCGGGTGAGAGCCCTGAGCGGGGCCCTG 1800

Qy  1801 AGGGTCATCCGCAGCCGTGTTCTCACCAGGCGGGTGAGAGGCGCGGGCTCGGCTACATT 1860
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Db  1861 GCCCCGGGAGCAGGCGGCGCCCGGCCACCGTGCTGCGAGCCACTGATGAGGGCACTGGAGGAGGAG 1920

Qy  1921 GCGGGGGCGCTGCCAGGCGCAGGCGCACCCTCTGGGGCCAAAGCCCCTCTCATTCGAGACTGCCCTC 1980
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1921 GCGGGGGCGCTGCCAGGCGCAGGCGCACCCTCTGGGGCCAAAGCCCCTCTCATTCGAGACTGCCCTC 1980

Qy  1981 GCGCCAGGGAGGAGCAGGCCACCCCTCCTGGCCCACAGCCACTCCTGGAACATGAC 2040
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Db  1981 GCGCCAGGGAGGAGCAGGCCACCCCTCCTGGCCCACAGCCACTCCTGGAACATGAC 2040

Qy  2041 CGGCTGCCTGCCTCTGCGCCACCCGCCCGCCCCCGGGAGGCGCTGCGGCGTGAGGCGACTGCCTTCA 2100
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Db  2041 CGGCTGCCTGCCTCTGCGCCACCCGCCCGCCCCCGGGAGGCGCTGCGGCGTGAGGCGACTGCCTTCA 2100

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Qy  2161 GCCCCTCCGGGGGCCCCTATCAGGGACATGGGGCACCCCAGAGGCTCCAAGCAGCTT 2220
                |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2161 GCCCCTCCGGGGGCGGCCCCTATCAGGGACACTGCTCAGCCAGCCACCCGGACAGCCCT 2220

Qy  2221 CCATCCACTGGTGCCACCCCGGGCCATCCCGGACAGCCCT 2280
                |||||||||||||||||||||||||||||||||||||||
Db  2221 CCATCCACTGGTGCCACCCCTTTCTGCCACATTGCCCGGCCATCCCGGACAGCCCT 2280

Qy  2281 TGGGGGCAGCCAGCCCCTTTCTGCCCACCCCCAGGAGGGGCTGC 2340
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Db  2281 TGGGGGCAGCCAGCCCCTTTCTGCCCACCCCCAGGAGGGGCTGC 2340

Qy  2341 AGCCCCCACCAGCAGTTGCCCGAGTCAGTGCCCCTCTCCTGGCTCTTCCCTCCCTCCGGATCTTGCAA 2400
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Left column block:

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Qy  181 CCAAGCATGGTAGGCTGTGGCTGGCACCCAGGGTTGTGTGGCTGGGGAGGTGGTCTCCCAC 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 CCAAGCATGGTAGGCTGTGGCTGGCACCCAGGGTTGTGTGGCTGGGGAGGTGGTCTCCCAC 240

Qy  241 AGTTCCCTCCTGCCTCCCAGGGCCCCCATCCATCCATCCATCCGAGGATGTGCAG 300
                |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 AGTTCCCTCCCTGCCTCCCCAGGGCCCCATCCATCCATCCGAGGATGTGCAG 300

Qy  301 GCACAGACAGGCGGAACGGCCGAACGCCCATTCGAGGCTATCATTGAGGCGACCCCAGCCCTCG 360
                |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 GCACAGACAGGCGGAACGGCCGAACGCCCATTCGAGGCTATCATTGAGGCGACCCCAGCCCTCG 360

Qy  361 GTGACCTGGTACAAGGACAGCAGCGGTGCAGCTGGTGCGACAGCAGCCCGGCTTAGCCAGCAGCAA 420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 GTGACCTGGTACAAGGACAGCAGCGGTCCAGCTGGTGCGACAGCAGCCCGGCTTAGCCAGCAGCAA 420

Qy  421 GAAGGCACCACCATACTCCCTGGTGCTGAGGCATGTGGCCTGAAGGATGCCGGCGTTTAC 480
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Qy  481 ACCTTGCCTGGCCCAAAAACACTGGTGCCCAGGTGCTCTGCAAGGCAGAGCTGCTCCTCTT 540
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  481 ACCTTGCCTGGCCCAAAAACACTGGTGCCCAGGTGCTCTGCAAGGCAGAGCTGCTGGTGCTT 540

Qy  541 GGGGGGGACAATGAGCCCGACTCAGAGAAGCAAAGCCACCGGAGGAAGCACGTGCACTCCTTC 600
                |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  541 GGGGGGACAATGAGCCCGACTCAGAGAAGCAAAGCCACCGGAGGAAGCACGTGCACTCCTTC 600

Qy  601 TATGAGGTCAAGGAGGAGATTGGAAGGGGCGTGTTTGGCTTCGTAAAAAGAGTGCAGCAC 660
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Db  601 TATGAGGTCAAGGAGGAGATTGGAAGGGGCGTGTTTGGCTTCGTAAAAAGAGTGCAGCAC 660

Qy  661 AAAGGAAACAAGAGATCTGTGCGCGCTCCAAGTTCATCCCCTACGGAGCAGAACTCGGGGCC 720
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  661 AAAGGAAACAAGAGATCTGTGCGCGCTCCAAGTTCATCCCCTACGGAGCAGAACTCGGGGCC 720

Qy  721 CAGGCATACAGGGAGGCGAGACATCCTGATGTGCATCTTGGCATCGCCGCTGAGCCCACCCGGTCACGGGGCTG 780
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Db  721 CAGGCATACAGGGAGGCGAGACATCCTGATGTGCATCTTGGCATCGCCGCTGAGCCCACCCGGTCACGGGGCTG 780

Qy  781 CTGGACCAGTTTGAGACCCGCAAGACCCTCATCCTGCGAGCTCGTGCTCATCCGAG 840
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Db  781 CTGGACCAGTTTGAGACCCGCAAGACCCTCATCCTGCGAGCTCGTGCTCATCCGAG 840

Qy  841 GAGCTGCTGACGAAGGGGGGCTGTACGACGCGCTGTACAGGAAGGGCGTGGTGACCGAGGTCAAGGTCTAC 900
                |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  841 GAGCTGCTGACGAAGGGGGGCTGTACGACGCGCTGTACAGGAAGGGCGTGGTGACCGAGGTCAAGGTCTAC 900

Qy  901 ATCCAGCAGCTGGTGTGGAGGGGCTGCACTACCTGCACACCTGCGACAGCAGCCATGGCGGTTCTCCACCTGGAC 960
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Qy  961 ATAAAGCCCTCCAACATCCTGATGTGCATCTTGGCATCGCCGCTGGAAGACATTAAAATCTGCGAC 1020
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Db  961 ATAAAGCCCTCCAACATCCTGATGTGCATCTTGGCATCGCCGCTGGAAGACATTAAAATCTGCGAC 1020

Qy 1021 TTTGGCTTTGCCCAGAACATCACCCCCAGAGACTTCAGCCAGTACGGCTTCCCCT 1080
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Qy 1081 GAGTTCGTCTCCCCGAGATCATCAGCAGCAGAACCCTGTGAGCGAAGCCTTCCGACATTGG 1140
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Db 1081 GAGTTCGTCTCCCCGAGATCATCAGCAGCAGAACCCTGTGAGCGAAGCCTTCCGACATTGG 1140

Qy 1141 GCCATGGTGTCATCTCCTACCTCAGCCTGACCTGCTCATCCCATTGCGGCGGAGT 1200
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Db 1141 GCCATGGTGTCATCTCCTACCTCAGCCTGACCTGCTCATCCCATTGCGGCGGAGT 1200

Qy 1201 GACCGTGCCACCCTGAACGTCCTGGAGCGGCGGCGCGTGTCATGGAGCAGCCCCATGGCT 1260
                ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1201 GACCGTGCCACCCCTGAACGTCCTGGAGCGGCGGCGCGTGTCATGGAGCAGCCCCATGGCT 1260
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Qy  2401  GAGGCCCCCTTAGTACCCTGGGCAGCCCCGTCTCAAGCCCTGGCAGCCCCGCACCCCTGCCCCT     2460
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Db  2401  GAGGCCCCCTTAGTACCCTCTTCAAGCCCCGTCTCAAGCCCTGGGACAGCCCCGCACCCCTGCCCCT    2460

Qy  2461  GCCAAAGCAAGCCCCCATTGGACTCTAAGATGGGGCTGGGGCTGGACACATCTCTCTTCCCTCCTGGG   2520
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Db  2461  GCCAAAGCAAGCCCCCATTGGACTCTAAGATGGGGCTGGGGCTGGACACATCTCTCTTCCCTCCTGGG   2520

Qy  2521  AGCCAAAACCCGGCCCCCGACTCAGTTCCCAGGTCAGCCTCCAGCGGTCTTCCAGAGTCTTCCCAA    2580
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Db  2521  AGCCAAAACCCGGCCCCCGACTCAGTTCCCAGGTCAGCCTCCAGCGGTCTTCCAGAGTCTTCCCAA    2580

Qy  2581  GTGAGCTCCCTCAGGGTGGGCTCCTCCCAGGTGGCACAGAGCCTGGCCCCTCCCCTCCTCTCAAGG   2640
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Db  2581  GTGAGCTCCCTCAGGGTGGGCTCCTCCCAGGTGGCACAGAGCCTGGCCCCTCCCCTCCTCTCAAGG   2640

Qy  2641  GCGGAGGGCTGGACCCAGGAGGCTGAGGATCTGTCCGGACTCCACACCCACCCCACCACCCACCCAC   2700
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Qy  2701  CCTCAGGAACAGGTGACCATGCGCAAGTCTCCCTGGGTGGTCGCGGGCAGGGGCTACGCAGGC     2760
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Db  2701  CCTCAGGAACAGGTGACCATGCGCAAGTCTCCCTGGGTGGTCGCGGGCAGGGGCTACGCAGGC     2760

Qy  2761  GTGGCTGGCTATGGCACTTTGCCTTTGCTTTGGTGGAGATGCAGGGGCATGCTGGGGCAGGGG      2820
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Db  2761  GTGGCTGGCTATGGCACCTTTGCCTTTGCTTTGGTGGAGATGCAGGGGCATGCTGGGGCAGGGG     2820

Qy  2821  CCCATGTGGGCCAGGAGACATCGGGCAGGCCTGGCGTGTGTCCCAGTGTGTCCCAGTGCTGGCAGCAG   2880
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2821  CCCACCCATGTGGGCCAGGAGACATCGGGCAGGCCTGGCGTGTGTCCCAGTGCTGGCAGCAG       2880

Qy  2881  GCCAGGGCTGAGTCCCAGTCGGGAGGACATCGGGGACGCGGCCAGGCCAGGGGCTGAGCCCACTGCCC  2940
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Db  2881  GCCAGGGCTGAGTCCCAGTCGGGAGGACATCGGGGACGCGGCCAGGCCAGGGGCTGAGCCCACTGCCC  2940

Qy  2941  CAGGTCAGTGCAAGGCCTGTGCCTGAGGTCGGCAGCGGCTCCCACCAGGAGCTCTCCAGAG      3000
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Db  2941  CAGGTCAGTGCAAGGCCTGTGCCTGAGGTCGGCAGCGGCTCCCACCAGGAGCTCTCCAGAG      3000

Qy  3001  CCCACCCCATGGGAGGAGGACATCGGGCAGGGCCTCTCCGGTCAGATCCGGGGACCTGTCAGGT     3060
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Db  3001  CCCACCCCATGGGAGGAGGACATCGGGCAGGGCCTCTCCGGTCAGATCCGGGGACCTGTCAGGT     3060

Qy  3061  GATGCGGAGGCGGCGGCCAGGGCCGGACAACAATATCCCTGGACATTTCCGAGGTGGACCCCGCCTACTC   3120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3061  GATGCGGAGGCGGCGGCCAGGGCCGGACAACAATATCCCTGGACATTTCCGAGGTGGACCCCGCCTACTC   3120

Qy  3121  AACCTCAGACCTGTACGATATCAAGTACACCTCAAGTACTTCGAGTTTATGATCTTTCAGGAAA     3180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3121  AACCTCAGACCTGTACGATATCAAGTACACCTCCATTCCGAGTTTATGATCTTTCAGGAAA      3180

Qy  3181  GTCCCCAAGTCGCGCTCACCGCAGCCTCTCCATCTGGGCCCCCACGCGCAGCGCCTGGGAGATC     3240
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Db  3181  GTCCCCAAGTCGCGCTCACCGCAGCCTCTCCATCTGGGCCCCCACGCGCAGCGCCTGGGAGATC     3240

Qy  3241  TTCCCGGAGCCAGCGTGGGCGGGCCCTGGCAGGTGAACTGGGCCCCCACGCGCAGCCTGGGAGATC   3300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3241  TTCCCGGAGCCAGCGTGGGCGGGCCCTGGCAGGTGAACTGGGCCCCCACGCGCAGCCTGGGAGATC   3300

Qy  3301  ACAGAGGAGTCAGAGGATGTGGACCGCGTCTCGCTCAGCGCAGCCTCTCCACTTCCCTGGGAGGCAGAAGCGC  3360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3301  ACAGAGGAGTCAGAGGATGTGGACCGCGTCTCGCTCAGCGCAGCCTCTCCACTTCCCTGGGAGGCAGAAGCGC  3360

Qy  3361  AAGTGGTCCTGCGGCTCACCGCAGCCTCTCGCAGGCTCCCTGGGAGGCCACTGCCCCTGGAT     3420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3361  AAGTGGTCCTGCGGCTCACCGCAGCCTCTCGCAGGCTCCCTGGGAGGCCACTGCCCCTGGAT     3420

Qy  3421  GAGCCTGCAGAGCTCTGGGGCTGCGTGAGAGTGAAGGCCTCCGTGTGAGCACATCTCCGG      3480
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Db  3421  GAGCCTGCAGAGCTCTGGGGCTGCGTGAGAGTGAAGGCCTCCGTGTGAGCACATCTCCGG      3480
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Db  3481  ATCCTGAAGGGCAGGCCGGAAGGTCTGGACAAGGAGGGGCCCCAGGGAAGAAGCCAGGC       3540

Qy  3541  CTTGCTTCCTTCCGGCTCTCAGTGTCGAAGCTCTGAAGCTCTGGGACGACCGGCCGCGACATTCCTAAGG  3600
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Db  3601  GAGCTCTCAGATGAGACTGTGTCCTGGGCCAGTCAGTGACACTGCCTGCCAGTGTCA          3660

Qy  3661  GCCCAGCCAGCTGCCCAGGACAAAGACGGAGCCCCCTGGGGAGCAGCAGCAGC             3720
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Qy  3721  CGTGTCCTCATCTCTGCCACCCTCAAGAACTTCCAGCTTCTGACCATCCTGTGGTGGTG       3780
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Db  3721  CGTGTCCTCATCTCTGCCACCCTCAAGAACTTCCAGCTTCTGACCATCCTGTGGTGGTG       3780

Qy  3781  GCTGAGGACCTGGGTGTGTACACCTGCAGCAGCCAATGGCTGAGCAGTGACCACC           3840
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Qy  3841  ACGGGGCGTCCTCCGAAGGCAGCAGAGCGCCCCTCATCTTCGCCATGCCGATATCGGGGAG     3900
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Qy  3901  GTGTACGGGGATGGGGTGCTGCTGGTCTGGAAGCCCGTGGAATCCTACGGCCCTGTGACC       3960
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Db  3901  GTGTACGGGGATGGGGTGCTGCTGGTCTGGAAGCCCGTGGAATCCTACGGCCCTGTGACC       3960

Qy  3961  TACATTGTGCAGTGAGCTCCTAGAAGGGCGCAGCTGACCACACTGGCCTCCGCACACTCTTT    4020
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3961  TACATTGTGCAGTGAGCTCCTAGAAGGGCGCAGCTGACCACACTGGCCTCCGCACACTCTTT    4020

Qy  4021  GACTGCTGCTACCTGACCAGCAAGCTCTCCCGGGGTGGCACCTTCAGCCTTACACCTTCCGCACGGCA   4080
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Db  4021  GACTGCTGCTACCTGACCAGCAAGCTCTCCCGGGGTGGCACCTTCAGCCTTACACCTTCCGCACGGCA   4080

Qy  4081  TGTGTCAGCAAGGCAGGAATGGGTGTCAGCAGCCCTCCTGGGAGCAAGTCCTCCTGGGA        4140
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Db  4081  TGTGTCAGCAAGGCAGGAATGGGTCCTACAGCAGCCCTCCTGGGAGCAAGTCCTCCTGGGA      4140

Qy  4141  GGGCCCAGCCACCTGGCCTCTGAGGAGAGGCCAGGCCCAGGGGCCGTCAGCCCAACCCCTGCCC     4200
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          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4201  AGCACAAAGACCTTCGGCATTCGATCTCCATTCGAGTTTATGATCTTCAGACAGATCCAGAAA       4260

Qy  4261  GTCCCCAAGTCGCGCTCAGCCGAGCTGCGCGCCGCCCTCAAGGCGCTGGCCAAGATCATCCCCGGCGG     4320
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4261  GTCCCCAAGTCGCGCTCAGCCGAGCTGCGCGCCGCCCTCAAGGCGCTGGCCAAGATCATCCCCGGCGG    4320

Qy  4321  TTCCCGGAGAGGCTGGGCGGGCCCTGGCAGGCTGAAATCCTCAAGGGCCTCAAGGGCCTGTCTCATCTTGGAGCTG  4380
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4321  TTCCCGGAGAGGCTGGGCGGGCCCTGGCAGGCTGAAATCCTCAAGGGCCTCAAGGGCCTGTCTCATCTTGGAGCTG  4380

Qy  4381  ACAGAGGAGTCAGAGGATGTGGACCGCGTCGCTCAGCGCGCCCCAGCCTCGTGCTCTTCTACTCAGAAGCGC  4440
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4381  ACAGAGGAGTCAGAGGATGTGGACCGCGTCGCTCAGCGCGCCCCAGCCTCGTGCTCTTCTACTCAGAATCTGAG  4440

Qy  4441  AAGTGGTCCTGCGGCTCACCTTCCCACTTCGCCGCTGGAT           4500
          ||||||||||||||||||||||||||||||||||||||||||||
Db  4441  TGCTCTGGGCCCGAGCTGCTCCCCCTGCCTGGCCGAGAGGGGCCTCCTACTCAGAATCTGAG        4500

Qy  4501  GTGAAGGACTACCTGTGGCAGATGTTGAGCAGATGTTGAGCAGTTGGAGTTGGAGTTGGAGTG       4560
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4501  GTGAAGGACTACCTGTGGCAGATGTTGAGCAGTTGGAGTTGGAGTTACCACCAGCAACAACATC     4560
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Best Local Similarity  100.0%;  Pred No. 0;
Matches 5207;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy      1 CAGCACGAGGAACTCCTTCTGATCACCGAATACAACCTGCTCAAGGTC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 CAGCACGAGGAACTCCTTCTGATCACCGAATACAACCTGCTCAAGGTG 60

Qy     61 GTTCCATTGAAGGAGTACTCCTAACTGTCAGAAGCCTGGGCGGTCAGGATGGGGTGCTGT 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GTTCCATTGAAGGAGTACTCCTAACTGTCAGAAGCCTGGGCGGTCAGGATGGGGTGCTGT 120

Qy    121 CGCTTGGCTGCGGGGGTGTTCAGTTGCCACCAGTGTATCTCAGGGTCTCACCAACCAT 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 CGCTTGGCTGCGGGGGTGTTCAGTTGCCCACAGTGTATCTCAGGGTCTCACCAACCAT 180

Qy    181 CCAAGCATGGTAGGCTGTGGCTGGCACCCAGGTTGTGTGCTGGCTGGCAGTGGTGTCCAC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CCAAGCATGGTAGGCTGTGGCTGGCACCCAGGGTTGTGTGGCTGGCAGTGGTGTCTCCAC 240

Qy    241 AGTTCCCTCCCTGCCCTCCCAGGGCCCCATCCATGCAGTAACCATCGAGGATGTGCAG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 AGTTCCCTCCCTGCCCTCCCAGGGCCCCATCCATGCAGTAACCATCGAGGATGTGCAG 300

Qy    301 GCACAGACAGGGGAACGGCCCAATTGAGGCTATCATTGAGGGACCCCACAGCCCTCG 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 GCACAGACAGGGGAACGGCCCAATTCGAGGCTATCATTGAGGGACCCCACAGCCCTCG 360

Qy    361 GTGACCTGGTACAAGACACAGCGTCCAGCTGGTGACAGGACACCCGGCTTAGCCAGCAGCAA 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GTGACCTGGTACAAGACACAGCGTCCAGCTGGTGACAGGACACCCGGCTTAGCCAGCAGCAA 420

Qy    421 GAAGGCACCACATACTCCCTGGTGTCTGAGGCATGTGGCCTCGAAGGATGCCGGCGTTTAC 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 GAAGGCACCACATACTCCCTGGTGTCTGAGGCATGTGGCCTCGAAGGATGCCGGCGTTTAC 480

Qy    481 ACCTGCTGGCCAAAACACTGGTGGCCAGGTGCTGCTCTCGCAAGGCAGAGCTGCTGGTGCTT 540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 ACCTGCTGGCCAAAACACTGGTGGCCAGGTGCTGCTCTCGCAAGGCAGAGCTGCTGGTGCTT 540

Qy    541 GGGGGGGACAATGAGCCGGACTCAGAGAAGCAAAGCCACCGGAGGAAGCAAGCTGCACTCCTTC 600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GGGGGGGACAATGAGCCGGACTCAGAGAAGCAAAGCCACCGGAGGAAGCAAGCTGCACTCCTTC 600

Qy    601 TATGAGGTCAAGGAGGAGATTGGAAGGGCGTGTTTGGCTTCGTAAAAGAGTGCAGCAC 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 TATGAGGTCAAGGAGGAGATTGGAAGGGGTGTTTGGCTTCGTAAAAGAGTGCAGCAC 660

Qy    661 AAAGGAAACAAGATCTGTGCGCTGCCAAGTTCATCCCCTACGGACGAGAACTCGGGCC 720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 AAAGGAAACAAGATCTGTGCGCTGCCAAGTTCATCCCCTACGGACGAGAACTCGGGCC 720

Qy    721 CAGGCATACAGGGAGCGAGACATCCTGGCCCGCTGAGCCACCGTCACGGGGCTG 780
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 CAGGCATACAGGGAGCGAGACATCCTGGCCCGCTGAGCCACCGTCACGGGGCTG 780

Qy    781 CTGGACCAGTTGAGACCCGCAAGACCCTACCTCATCCTGAGCTGTGCTCATCCGAG 840
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 CTGGACCAGTTTGAGACCCGCAAGACCCTACCTCATCCTGAGCTGTGCTCATCCGAG 840

Qy    841 GAGCTGCTGGACCGCCTGTACAGGAAGGGCGTGTGTGACGAGGCCGAGGTCAAGGTCTAC 900
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 GAGCTGCTGGACCGCCTGTACAGGAAGGGCGTGGTGACGAGGCCGAGGTCAAGGTCTAC 900

Qy    901 ATCCAGCAGCTGGTGGAGGGCTGCACTACCTGCACAGCATGCGGTTCTCCACCTGAC 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 ATCCAGCAGCTGGTGGAGGGCTGCACTACCTGCACAGCATGCGGTTCTCCACCTGAC 960

Qy    961 ATAAAGCCCCTCAACATCCTGATGGTGCATCCTGCCCCGGGAAGACATTAAAATCTGGAC 1020
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 ATAAAGCCCCTCAACATCCTGATGGTGCATCCTGCCCCGGGAAGACATTAAAATCTGGAC 1020

Qy   1021 TTTGGCTTTGCCCAGAACATCACCCCAGCAGAGCTGCAGTTCAGCCAGTACCGGCTCCCCT 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   4561 CTGCACCTGGACCTGGAGGTCCGAGAACATGATCATCACCGAATACAACCTGCTCAAGGTC 4620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4561 CTGCACCTGGACCTGGAGGTCCGAGAACATGATCATCACCGAATACAACCTGCTCAAGGTC 4620

Qy   4621 GTTGGACCTGGGCAATGCACAGAGCCTCAGCCAGGAGAGGTGCTGCCCTCAGACAAGTTC 4680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4621 GTTGGACCTGGGCAATGCACAGAGCCTCAGCCAGGAGAGGTGCTGCCCTCAGACAAGTTC 4680

Qy   4681 AAGGACTACCTAGAGACCATGGCTCCAGAGCTTCCTGAGGGCAGGGGCTGTTCCACAG 4740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4681 AAGGACTACCTAGAGACCATGGCTCCAGAGCTTCCTGAGGGCAGGGGCTGTTCCACAG 4740

Qy   4741 ACAGACATCTGGGCCATCGGTGTGACACGCCTTCATCATGCTGAGGGTCTCACCAACCAT 4800
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4741 ACAGACATCTGGGCCATCGGTGTGACACGCCTTCATCATGCTGAGGGTCTCACCAACCAT 4800

Qy   4801 AGCAGCGAGGGTGCACGGACCTGCAGAGGACTCGCAAGGGCCAAGGGCCGAGTACCCGGTG 4860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4801 AGCAGCGAGGGTGCACGGACCTGCAGAGGACTCGCAAGGGCCAAGGGCCGAGTACCCGGTG 4860

Qy   4861 CGCTGCTACGCGCGGGCTGTCCGGGGCCTTCGCCGGGGCCGCCGGTCCCGTCAGTGCGCC 4920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4861 CGCTGCTACGCGCGGGCTGTCCGGGGCCTTCGCCGGGGCCGCCGGTCCCGTCAGTGCGCC 4920

Qy   4921 CAGCCCTGGGGCGTGCCCCGGCCCGCCCTGCGGCGTCCGTCCTGCCAGTGCCTGGCTAACAGAGGAG 4980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4921 CAGCCCTGGGGCGTGCCCCGGCCCGCCCTGCGGCGTCCGTCCTGCCAGTGCCTAACAGAGGAG 4980

Qy   4981 GGCCCGGCCTGTTCGCGGCCCGTGGGCCCGGGCCCGCCGGCGGGCGGCGTCTTC 5040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4981 GGCCCGGCCTGTTCGCGGCCCGTGGGCCCGGGCCCGCCGGCGGGCGGCGTCTTC 5040

Qy   5041 GTGCGCAATCGCGGAGAAGAGAGACGCGGCGCTGCTGTACAAGAGGCACAACTGGCCCAGGTG 5100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5041 GTGCGCAATCGCGGAGAAGAGAGACGCGGCGCTGCTGTACAAGAGGCACAACTGGCCCAGGTG 5100

Qy   5101 CGCTGAGGGTGCGCCCCGGCCACACCCTTGGTCTCCCCGGCTGGGGGTCGCAGCGCGGC 5160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5101 CGCTGAGGGTGCGCCCCGGCCACACCCTTGGTCTCCCCGGCTGGGGGTCGCAGCGCGGC 5160

Qy   5161 CAATAAAAACGCACAGCCCGGCGCGGCGCGAGAAAAAAAAAAAAAAAAA 5207
          ||||||||||||||||||||||||||||||||||||||||||||
Db   5161 CAATAAAAACGCACAGCCCGGCGCGGCGCGAGAAAAAAAAAAAAAAAAAAAA 5207
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RESULT 2
US-10-697-263-1
; Sequence 1, Application US/10697263
; Publication No. US20040063142A1
; GENERAL INFORMATION:
;  APPLICANT: WEI, Ming-Hui, et al
;  TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
;  TITLE OF INVENTION:  ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: CL000927-CIP-DIV2
;  CURRENT APPLICATION NUMBER: US/10/697,263
;  CURRENT FILING DATE:  2003-10-31
;  PRIOR APPLICATION NUMBER: 10/274,978
;  PRIOR FILING DATE: 2002-10-22
;  PRIOR APPLICATION NUMBER: 09/858,664
;  PRIOR FILING DATE: 2001-05-17
;  PRIOR APPLICATION NUMBER: 09/711,134
;  PRIOR FILING DATE: 2000-11-14
;  NUMBER OF SEQ ID NOS: 34
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;  LENGTH: 5207
;  TYPE: DNA
;  ORGANISM: Homo sapiens
US-10-697-263-1

Query Match        100.0%;  Score 5207;  DB 13;  Length 5207;

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Qy   2161 GCCCCCTCCGGGGGGCCCTATCAGGACTCGAGTTCAGCAGCAGCACCCTCAGGGCTTCCAAGCAGCTT 2220
               |||||||||||||||||| |||||||||||||||||||||||||||||  |||||||||||||||||
Db   2161 GCCCCCTCCGGGGGGGCCCTATCAGGACATGGGGCCCTCAGGGCTCCAAGCAGCTT 2220

Qy   2221 CCATCCACTGGTGCCACCCAGGCACTGCTCAGCCGACACTGCTCATCCCCATTTGCCGGCGAGAGT 2280
               |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Db   2221 CCATCCACTGGTGCCACCCAGCACTGCTCAGCCAGAGAGCCATCCCCGGACAGCCCT 2280

Qy   2281 TGGGGGCAGCCAGCCCCTTTCTGCCACCCAAGCAGGTTCTGCCCCCCCAGGAGGGCTGC 2340
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281 TGGGGGCAGCCAGCCCCTTTCTGCCACCCAAGCAGGTTCTGCCCCCCAGGAGGGCTGC 2340

Qy   2341 AGCCCCACCCAGCAGTTGCCCATGGCCCTCCTCGGCTCTCCTCCCTCCCTGCCCT 2400
               |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341 AGCCCCACCCAGCAGTTGCCCATGGCCCTCCTCGGCTCCTCCCTCCCTGCCCT 2400

Qy   2401 GAGGCCCCTTAGTACCCTCAGCCCCTTCTTGGACAGCCCCAGGCACCCCTGCCCCT 2460
               |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2401 GAGGCCCCTTAGTACCCTCAGCCCCTTCTTGGACAGCCCCAGGCACCCCTGCCCCT 2460

Qy   2461 GCCAAAGCAAGCCCCCATTGGACTCTAAGATGGGGCCTGAGACATCTCTCTTCCTTCTGGG 2520
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2461 GCCAAAGCAAGCCCCCATTGGACTCTAAGATGGGGCCTGAGACATCTCTCTTCCTTCTGGG 2520

Qy   2521 AGGCCAAAACCCGGCCCCTGCAGTTCCCCAGGGTCAGCTCCCCAGAGCGAGCTCTTCCCAA 2580
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2521 AGGCCAAAACCCGGCCCCTGCAGTTCCCCAGGGTCAGCTCCCCAGAGCGAGCTCTTCCCAA 2580

Qy   2581 GTGAGCTCCTCAGGGTGGGCTCCTCCTCCCCAGGAGCCTGGCACAGAGCCTGGCCCCCTGGAT 2640
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2581 GTGAGCTCCTCAGGGTGGGCTCCTCCTCCCCAGGTGGGCACAGAGCCTGGCCCCCTGGAT 2640

Qy   2641 GCGGAGGGCTGGACCCAGGAGGCTGAGGAGCTCGAGGATCGTGTCGACTCCACACCCACCTTGCAGCGG 2700
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2641 GCGGAGGGCTGGACCCAGGAGGCTGAGGAGCTCGAGGATCGTGTCGACTCCACACCCACCTTGCAGCGG 2700

Qy   2701 CCTCAGGAACAGGTGACCATGCGCAAGTTCTCCCTTGGTGGAGATGCAGGGGGCATGCTGGGCCAGGGC 2760
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2701 CCTCAGGAACAGGTGACCATGCGCAAGTTCTCCCTTGGTGGAGATGCAGGGGGCATGCTGGGCCAGGGC 2760

Qy   2761 GTGGCTGGCTATGGCAACCTTTGCCTTTGGTGGAGATGCAGGGGGCATGCTGGGCCAGGGG 2820
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2761 GTGGCTGGCTATGGCAACCTTTGCCTTTGGTGGAGATGCAGGGGGCATGCTGGGCCAGGGG 2820

Qy   2821 CCCATGTGGGCCAGGATAGCCTGGGCTGTGTCCCAGTCGACATCGGGGACCTGTGTCAGGT 2880
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2821 CCCATGTGGGCCAGGATAGCCTGGGCTGTGTCCCAGTCGACATCGGGGACCTGTGTCAGGT 2880

Qy   2881 GCCAGGGCTGAGTCCCAGTCGGAGGAGCAGCAGGAGGCTGAGAGCCCACTGCCC 2940
               ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2881 GCCAGGGCTGAGTCCCAGTCGGAGGAGCAGCAGGAGGCTGAGAGCCCACTGCCC 2940

Qy   2941 CAGGTCAGTGCAAGGCCTGTGCCTGAAGGGCGGCTCACATT 3000
               ||||||||||||||||||||||||||||||||||||||||
Db   2941 CAGGTCAGTGCAAGGCCTGTGCCTGAAGGGCGGCTCACATT 3000

Qy   3001 CCCACCCCATGGGAGGACATCGGGGACCTGTCCTGGTGCGATCGGGGACCTGTCAGGT 3060
               ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3001 CCCACCCCATGGGAGGACATCGGGGACCTGTCCTGGTGCGATCGGGGACCTGTCAGGT 3060

Qy   3061 GATGCGGAGGCGGCCGACACAATATCCTGGACATTCCGAGGTGGACCCGCCTACCTC 3120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3061 GATGCGGAGGCGGCCGACACAATATCCTGGACATTCCGAGGTGGACCCGCCTACCTC 3120

Qy   3121 AACCTTCAGACCTGTACGATATCAAGTACCTCCCATTCGAGTTTATGATCTTCAGGAA 3180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3121 AACCTTCAGACCTGTACGATATCAAGTACCTCCCATTCGAGTTTATGATCTTCAGGAA 3180

Qy   3181 GTCCCAAGTCCGCTCAGCCAGAGCCGCCTCCCCCCATGGCTGAGGAGGAGCTGGCCGAG 3240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3181 GTCCCAAGTCCGCTCAGCCAGAGCCGCCTCCCCCCATGGCTGAGGAGGAGCTGGCCGAG 3240
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Db   1021 TTTGGCTTTGCCCAGAACATCACCCCAGCAGAGCTCGAGTTCAGCCAGTACGGCTCCCCT 1080

Qy   1081 GAGTTCGTCTCCCCCGAGATCATCCAGAGACCCTGTGAGCGAAGCCTCCGACATTTGG 1140
               ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 GAGTTCGTCTCCCCCGAGATCATCCAGAGACACCCTGTGAGCGAAGCCTCCGACATTTGG 1140

Qy   1141 GCCATGGGTGTCATCTCCTACCTGACCTGCTCATCCCCATTTGCCGGCCGAGAGT 1200
               ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 GCCATGGGTGTCATCTCCTACCTGACCTGCTCATCCCCATTTGCCGGGCGAGAGT 1200

Qy   1201 GACCCTGCCACCCTCCTGAAGTCCTGGAGGGGCGCGTCATGGAGCAGCCCCATGGCT 1260
               ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 GACCCTGCCACCCTCCTGAAGTCCTGGAGGGGCGCGTGTCATGGAGCAGCCCCATGGCT 1260

Qy   1261 GCCCACCTCAGGCGAAGACGCCAAAGACTTCATCAAGGCTACGCTGCAGAGAGCCCTCAG 1320
               ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 GCCCACCTCAGGCGAAGACGCCAAAGACTTCATCAAGGCTACGCTGCAGAGAGCCCCTCAG 1320

Qy   1321 GCCCGGCCAGTGCGGCCCAGTGCCTCTCCCACCCCTGGTTCCTGAAATCCATGCCTGCG 1380
               ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 GCCCGGCCAGTGCGGCCCAGTGCCTCTCCCACCCCTGGTTCCTGAAATCCATGCCTGCG 1380

Qy   1381 GAGGAGGCCCACTTCATCAACAACCAAGCAGTCAAGTTCCTCCTGCCCGAAGTCGCTGG 1440
               ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 GAGGAGGCCCACTTCATCAACAACCAAGCAGTCAAGTTCCTCCTGCCCGAAGTCGCTGG 1440

Qy   1441 CAGCGTTCCCTGATGAGCTACAAGTCCATCCTGGTGATGCGCTCCATCCTGAGCTGCTG 1500
               ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 CAGCGTTCCCTGATGAGCTACAAGTCCATCATCGTGATGCGCTCCATCCTGAGCTGCTG 1500

Qy   1501 CGGGGCCCACCCGACAGCCCCTCCCTCGGCCTAGCCCGGCACCTGTCGCAGGGACACTGGT 1560
               ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 CGGGGCCCACCCGACAGCCCCTCCCTGGCGTAGCCCGGCACCTGTCGCAGGGACACTGGT 1560

Qy   1561 GGCTCCTCCAGTTCCTCTCTCTGACAACGAGCTCGCCCATTTGCCGGGGCTTCCTGCGG 1620
               ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 GGCTCCTCCAGTTCCTCTCTCTGACAACGAGCTCGCCCATTTGCCGGGGCTTCCTGCGG 1620

Qy   1621 TCACTGCCACCCTCCCCGGTGACACACTCACCACTGCGCACCCCGGGCGTTCCTGCGCG 1680
               ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 TCACTGCCACCCTCCCCGGTGACACACTCACCACTGCGCACCCCGGGCGTTCCTGCGCG 1680

Qy   1681 CCCTCGGCCAGCTGCCTGAGGAAGCCAGCCAGTAGAGCTCACCGAGGCTCACATT 1740
               ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 CCCTCGGCCAGCTGCCTGAGGAAGCCAGCCAGTGAGAGCTCACCGAGGCCCCAGCT 1740

Qy   1741 CCGGCTGCATCTCCGAGGGTGCCGGGCACCCGGCGTGCGTTCCCCGGCAC 1800
               ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 CCGGCTGCATCTCCGAGGGTGCCGGGCACCCGGCGTGCGTGCCCCGGGCAC 1800

Qy   1801 AGGGTCATCCGAGCCTGTTCTTCACCAGCAGGCGGTGAGAGCCCTGAGCACGGGGCCCTG 1860
               ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 AGGGTCATCCGAGCCTGTTCTTCACCAGCAGGCGGTGAGAGCCCTGAGCACGGGGCCCTG 1860

Qy   1861 GCCCCGGGAGCAGGCGGCACCCGGCGCCCGGCGGCCACTGCTGAAGGGCGGCTACATT 1920
               ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 GCCCCGGGGAGCAGGCGGCACCCGGCGCCCGGCGGCCACTGCTGAAGGGCGGCTACATT 1920

Qy   1921 GCGGGGGCCTGCCAGGCCTGCCGAGCCACTGATGGAGCACCGGCGTGCTGGAGGAGGAG 1980
               ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 GCGGGGGCCTGCCAGGCCTGCCGAGCCACTGATGGAGCACCGGCGTGCTGGAGGAGGAG 1980

Qy   1981 GCCGCCAGGGAGAGGAGCAGGCGCACCCTCTGGCCCAAAGCCCCCCTCATTCGAGACTGCCCTC 2040
               ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 GCCGCCAGGGAGAGGAGCAGGCGCACCCTCTGGCCCAAAGCCCCCCTCATTCGAGACTGCCCTC 2040

Qy   2041 CGGCTGCCTCCTCGGCACCCACCCAGCGCACTCCCTGGAACATGAC 2100
               ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041 CGGCTGCCTCCTCGGCACCCACCCACTTGGCCCACCACTCCCGGAACATGAC 2100

Qy   2101 TCTCCGACACCCCCGCCCCTCCTCGGAGGCCTGCCGGTGAGGCACAGCCGACTGCCTTCA 2160
               ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101 TCTCCGAGCACCCCCGCCCCTCCTCGGAGCCTGCCGGTGAGGCACAGCCGACTGCCTTCA 2160
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Qy  3241  TTCCCGGAGCCCACGTGCCCTGGCCCAGGTGAACTGGGCCCCACGCGCAGCCTGCGAGATC  3300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3241  TTCCCGGAGCCCACGTGCCCTGGCCCAGGTGAACTGGGCCCCACGCGCAGCCTGCGAGATC  3300

Qy  3301  ACAGAGGAGTCAGAGATGTGGACGCGGCTGGCAGAGGCGTGCCGTGGGCAGGAAGCGC     3360
          |||||||||||||||||  |||||| |||||||||||||||| |||||||||||||||
Db  3301  ACAGAGGAGTCAGAGATGTGGACGCGGCTGGCAGAGGCGTGCCGTGGGCAGGAAGCGC     3360

Qy  3361  AAGTGGTCCTCGCCGTCACGCAGCGCCTCTTCCACTTCCCTGGGAGGCACCTGCCGCTGGAT  3420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3361  AAGTGGTCCTCGCCGTCACGCAGCGCCTCTTCCACTTCCCTGGGAGGCACCTGCCGCTGGAT  3420

Qy  3421  GAGCCTGAGAGTGGGCGTCGGTGAGAGTGAAGGCCTCGTGGAGCACATCCCCGG        3480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3421  GAGCCTGCGAGCTGGGGCGTGCGTGAGAGTGAAGGCCTCGTGGAGCACATTCCCGG        3480

Qy  3481  ATCCTGAAGGGCAGGCCGGAAGGTCTGGAGAAGGAGGGGGCCCCCAGGAAGAGCCAGGC   3540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3481  ATCCTGAAGGGCAGGCCGGAAGGTCTGGACCCGGAGGGGGCCGACATTCCTAAGG       3540

Qy  3541  CTTGCTTCCTTCCGGGCTCTCAGGTCTGAAGAGCTGGGCCAGTCACTGCCAGGTGTCA     3600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3541  CTTGCTTCCTTCCGGGCTCTCAGGTCTGAAGAGCTGGGCCAGTCACTGCCAGGTGTCA     3600

Qy  3601  GAGCTCTCAGATGAGACTGTGTCCTGGGCCAGTCAGTGACACTGGCCTGCCAGGTCA      3660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3601  GAGCTCTCAGATGAGACTGTGTCCTGGGCCAGTCAGTGACACTGGCCTGCCAGGTGTCA     3660

Qy  3661  GCCCAGCCAGCTGCCCAGGCCACCTGAGCAAAGACGGAGCCCCCTGGAGCAGCAGCAGC    3720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3661  GCCCAGCCAGCTGCCCAGGCCACCTGAGCAAAGACGGAGCCCCCTGGAGCAGCAGCAGC    3720

Qy  3721  CGTGTCCTCATCTGCCACCCTCAAGAACTTCAGCTTCTGACCATCCTGGTCGTGGTG     3780
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3721  CGTGTCCTCATCTGCCACCCTCAAGAACTTCAGCTTCTGACCATCCTGGTGGTGGTG     3780

Qy  3781  GCTGAGGACCTGGGTGTGTACACCTGCACACTCGGGGACAGTGACCAGTGACCACC       3840
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3781  GCTGAGGACCTGGGTGTGTACACCTGCACACTCGGGGACAGTGACCAGTGACCACC       3840

Qy  3841  ACGGGCGTCCTCGGAAGGCAGAGCGCCCCTCATCTTCGGCCATGCCGGATATGGGGAG     3900
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3841  ACGGGCGTCCTCGGAAGGCAGAGCGCCCCTCATCTTCGGCCATGCCGGATATGGGGAG     3900

Qy  3901  GTGTACGGGGATGGGGTGCTGCTGGTCTGGAAGCCCGTGAATCCTACGGCCCCTGTGACC    3960
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3901  GTGTACGGGGATGGGGTGCTGCTGGTCTGGAAGCCCGTGAATCCTACGGCCCCTGTGACC    3960

Qy  3961  TACATTGTGCAGTGACGTCAGCCTAGAAGGCGGCAGCTGGACCACACTGGCCTCCGACATCTTT  4020
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3961  TACATTGTGCAGTGACGTCAGCCTAGAAGGCGGCAGCTGGACCACACTGGCCTCCGACATCTTT  4020

Qy  4021  GACTGTGCTACCTGACCAGCAGCAAGCTCTCCCGGGTGGCACCTCCGCCACCGCA    4080
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4021  GACTGTGCTACCTGACCAGCAGCAAGCTCTCCCGGGTGGCACCTCCGCCACCGCA    4080

Qy  4081  TGTGTCAGCAAGGCAGGAATGGGTGCTGCTGGTCCCCTACGACCAAGTCCTTCCTGGGA    4140
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4081  TGTGTCAGCAAGGCAGGAATGGGTGCTGCTGGTCCCCTACGACCAAGTCCTTCCTGGGA    4140

Qy  4141  GGGCCCAGCCACCTGGCCTTCGGAGGAGGAGCCTCTGGGGGCGGTCAGCCCCAACCCCTGCCC  4200
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4141  GGGCCCAGCCACCTGGCCTTCGGAGGAGGAGCCTCTGGGGGCGGTCAGCCCCAACCCCTGCCC  4200

Qy  4201  AGCACAAAGACCTTCGCATTCCGACACAGATCCAGACAACAGATCCAGAGGGGCCGCTTCAGCGTGGTGCGG  4260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4201  AGCACAAAGACCTTCGCATTCCGACACAGATCCAGACAACAGATCCAGAGGGGCCGCTTCAGCGTGGTGCGG  4260

Qy  4261  CAATGCTGGGACGAAGGCCAGCGGCGGCGGGGCCGCCAAGATCATCCCCTACCACCCCC  4320
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4261  CAATGCTGGGACGAAGGCCAGCGGCGGCGGGGCCGCCAAGATCATCCCCTACCACCCCC  4320

Qy  4321  AAGGACAAGACAGCAGTGCTGCGCGAATACGAGGCCCTCAAGGGCCTGCCACCCCGCAC  4380
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db  4321  AAGGACAAGACAGCAGTGCTGCGCGAATACGAGGCCCTGCGGCCACCTCGTCATCTTCATCTTGGAGCTG  4380

Qy  4381  CTGGCCCAGCTGCACGCAGCCTACCTCAGCCCCGCCACCTACCTGCTCATCTTGGAGCTG  4440
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4381  CTGGCCCAGCTGCACGCAGCCTACCTCAGCCCCGCCACCTACCTGCTCATCTTGGAGCTG  4440

Qy  4441  TGCTCTGGGCCCGAGCTGTCTCCCCTGCCTGGCCGAGAGGGCCTCCTACTCAGAATCTGAG  4500
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4441  TGCTCTGGGCCCGAGCTGTCTCCCCTGCCTGGCCGAGAGGGCCTCCTACTCAGAATCTGAG  4500

Qy  4501  GTGAAGGACTACCTGTGGCAGATGTTGAGTGCCACCCAGTACCTGCACAACCAGCACATC  4560
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4501  GTGAAGGACTACCTGTGGCAGATGTTGAGTGCCACCCAGTACCTGCACAACCAGCACATC  4560

Qy  4561  CTGCACCTGGACCTGAGGTCCGAGAACATGATCATCACCGAATACAACCTGCTCAAGGTC  4620
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4561  CTGCACCTGGACCTGAGGTCCGAGAACATGATCATCACCGAATACAACCTGCTCAAGGTC  4620

Qy  4621  GTGGACCTGGCAATGCACAGAGCCTCAGCCAGGAAGGTGCTGCCCCTCAGACAAGTTC  4680
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4621  GTGGACCTGGCAATGCACAGAGCCTCAGCCAGGAAGGTGCTGCCCCTCAGACAAGTTC  4680

Qy  4681  AAGGACTACCTAGAGACCATGGCATCGGTGTGACAGCCTTCATCATGCTGAGCTACCCGGTG  4740
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4681  AAGGACTACCTAGAGACCATGGCATCGGTGTGACAGCCTTCATCATGCTGAGCTACCCGGTG  4740

Qy  4741  ACAGACATCTGGGCATCGTGTGACAGCTTCATCATGCTGCAGAGGAGACTGCGCAAGGGAGC  4800
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4741  ACAGACATCTGGCCATCGTGTGACAGCTTCATCATGCTGCAGAGGAGACTGCGCAAGGGAGC  4800

Qy  4801  AGCAGGGAGGGTGCACGCGACCTGCAGAGGAGACTGCGCAAGGGGCTGGTCGTCCGGCTGAGC  4860
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4801  AGCAGGCGAGGGTGCACGCGACCTGCAGAGGAGACTGCGCAAGGGGCTGGTCGTCCGGCTGAGC  4860

Qy  4861  CGCTGCTACGCGGGGCGTGTCCGGGGGCGCCCGGGGCCTTCCTGCGCCAGCACTCTGTGCGCC  4920
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4861  CGCTGCTACGCGGGGCGTGTCCGGGGGCGCCCGGGGCCTTCCTGCGCCAGCACTCTGTGCGCC  4920

Qy  4921  CAGCCCTGGGGCCCGGCCGCGTCCAGCTGCGCCTGCGCGTCCAGTGCTAACAGAGAGAG  4980
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4921  CAGCCCTGGGGCCCGGCCGCGTCCAGCTGCGCCTGCGCGTCCAGTGCTAACAGAGAGAG  4980

Qy  4981  GGCCCCGGCCTGTTCGCGGGCGTGACCTTCCCTACCGCGCGGCGTGCGCGTCTTC       5040
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4981  GGCCCCGGCCTGTTCGCGGGCGTGACCTTCCCTACCGCGCGGCGTGCGCGTCTTC       5040

Qy  5041  GTGCGCAATCGCGAGAAGAGACGCGCGCTGCGTGCTGTACAAGAGGCACAACCTGGCCCAGTG  5100
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5041  GTGCGCAATCGCGAGAAGAGACGCGCGCTGCGTGTGCTGTACAAGAGGCACAACCTGGCCCAGTG  5100

Qy  5101  CGCTGAGGGGTCGCCCCGGCCACACCCTTGGTCTCCCCGCGTGGGGTCGCTCGCAGACGCGGC  5160
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5101  CGCTGAGGGGTCGCCCCGGCCACACCCTTGGTCTCCCCGCGTGGGGTCGCTCGCAGACGCGGC  5160

Qy  5161  CAATAAAACGCACAGCCCGGGCGAGAAAAAAAAAAAAAAAAA  5207
          ||||||||||||||||||||||||||||||||
Db  5161  CAATAAAACGCACAGCCCGGGCGAGAAAAAAAAAAAAAAAAA  5207
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Query Match      100.0%;   Score 5207;   DB 13;   Length 5207;
Best Local Similarity   100.0%;   Pred. No. 0;
Matches 5207;   Conservative    0;   Mismatches    0;   Indels    0;   Gaps    0;

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Qy     1 CAGCACGAGGAACTCCTTCTGATCACCTGGCCAGCTGGAGGTCAGAGTGGGAGAGGCAGTG  60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 CAGCACGAGGAACTCCTTCTGATCACCTGGCCAGCTGGAGGTCAGAGTGGGAGAGGCAGTG  60

Qy    61 GTTCCATTGAAGGAGTACTCCTAACTGTCAGAAGCCTGGGCGGTCAGGATGGGGTGCTGT 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 GTTCCATTGAAGGAGTACTCCTAACTGTCAGAAGCCTGGGCGGTCAGGATGGGGTGCTGT 120

Qy   121 CGCTTGGGCTGCGGGGGGTGTTCAGTTGCCCACAGTGTATCTCAGGGTCTCACCAACCAT 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 CGCTTGGGCTGCGGGGGGTGTTCAGTTGCCCACAGTGTATCTCAGGGTCTCACCAACCAT 180

Qy   181 CCAAGCATGGTAGGCTGTGGCTGGCACCCAGGGTTGGCTGGGGAGGTGGTCTCCAC 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 CCAAGCATGGTAGGCTGTGGCTGGCACCCAGGGTTGTGGCTGGGGAGGTGGTCTCCAC 240

Qy   241 AGTTCCCTCCCTGCCCTCCAGGGCCCCATCATGCAGGTAACCATGAGGATGTGCAG 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 AGTTCCCTCCCTGCCCTCCAGGGCCCCATCATGCAGGTAACCATGAGGATGTGCAG 300

Qy   301 GCACAGACAGGCCGGAACGGCCCAATTGGAGGCTATCATTGAGGGCGACCCACAGCCCTCG 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 GCACAGACAGGCCGGAACGGCCCAATTGGAGGCTATCATTGAGGGCGACCCACAGCCCTCG 360

Qy   361 GTGACCTGTACAAGGACAGCGTCCAGCTGGTGGACAGCACCCGGCTTAGCCAGCAGCAA 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 GTGACCTGTACAAGGACAGCGTCCAGCTGGTGGACAGCACCCGGCTTAGCCAGCAGCAA 420

Qy   421 GAAGGCACCACATACTCCCTGGTGCTGAGGCATGTGGCCTTCGAAGGATGCCGGCGTTTAC 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 GAAGGCACCACATACTCCCTGGTGCTGAGGCATGTGGCCTTCGAAGGATGCCGGCGTTTAC 480

Qy   481 ACCTGCCCGGCCCAAAACACTGGTGGCCAGGTGCTCTGCAAGGCAGAGAGTCGCACTCCTTC 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 ACCTGCCCGGCCCAAAACACTGGTGGCCAGGTGCTCTGCAAGGCAGAGAGTCGCACTCCTTC 540

Qy   541 GGGGGGACAATGAGCCGGACTCAGAGAACAAAGCACCGGAAGAAGTCGCACTCCTTC 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 GGGGGGACAATGAGCCGGACTCAGAGAACAAAGCACCGGAAGAAGTCGCACTCCTTC 600

Qy   601 TATGAGGTCAAGGAGGAGATTGGAAGGGCCGTGTTGGCTTCGTAAAAAGAGTGCAGCAC 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 TATGAGGTCAAGGAGGAGATTGGAAGGGCCGTGTTGGCTTCGTAAAAAGAGTGCAGCAC 660

Qy   661 AAAGGAAACAAGATCTTGTGCCGTGCAAGTTCATCCCCTACGGAGCAGAACTCGGGGC 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 AAAGGAAACAAGATCTTGTGCCGTGCAAGTTCATCCCCTACGGAGCAGAACTCGGGGC 720

Qy   721 CAGGCATACAGGGAGCGAGACATCCTTGGCCTGCCAGGTCACCCGCTGGTCACGGGGCTG 780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 CAGGCATACAGGGAGCGAGACATCCTTGGCCTGCCAGGTCACCCGCTGGTCACGGGGCTG 780

Qy   781 CTGACCAGTTTGAGACCCGCAAGACCCTCATCCTGGAGCTGTGTCATCCGAG 840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 CTGACCAGTTTGAGACCCGCAAGACCCTCATCCTGGAGCTGTGTCATCCGAG 840
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Qy   841 GAGTGCTGGACCGCCTGTACAGGAAGGGCGTGGTGACGGAGGCCGAGGTCAAGGTCTAC  900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 GAGTGCTGGACCGCCTGTACAGGAAGGGCGTGGTGACGGAGGCCGAGGTCAAGGTCTAC  900

Qy   901 ATCCAGCAGCTGGTGAGGGGCTGCACTACCTGCACAGCCATGGCCGTTCTCCACCTGGAC  960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 ATCCAGCAGCTGGTGAGGGGCTGCACTACCTGCACAGCCATGGCCGTTCTCCACCTGGAC  960

Qy   961 ATAAAGCCCTCTAACATCCTGATGGTGCATCCTGCCCGGGAAGACATTAAAATCTGCGAC 1020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 ATAAAGCCCTCTAACATCCTGATGGTGCATCCTGCCCGGGAAGACATTAAAATCTGCGAC 1020

Qy  1021 TTTGGCTTTGCCCAGAACATCACCCCAGCAGAGCTGCAGTCAGTTCAGCCAGTACGGCTCCCCT 1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021 TTTGGCTTTGCCCAGAACATCACCCCAGCAGAGCTGCAGTCAGTTCAGCCAGTACGGCTCCCCT 1080

Qy  1081 GAGTTCGTCTCCCCGAGATCATCCAGCAGCAGACCCGTGTGAGCGAAGCCTCCGACATTTGG 1140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1081 GAGTTCGTCTCCCCGAGATCATCCAGCAGCAGACCCGTGTGAGCGAAGCCTCCGACATTTGG 1140

Qy  1141 GCCATGGGTGTCATCTCCTAACTCAGCCTGACCTGCTCATCCCCATTTGCCGGCGGGAGAGT 1200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1141 GCCATGGGTGTCATCTCCTAACTCAGCCTGACCTGCTCATCCCCATTTGCCGGCGGGAGAGT 1200

Qy  1201 GACCGTGCCACCCTCCTGAAGTCTCTGGAGGGCCGCGTGTCATGAGCAGCCCCATGGCT 1260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1201 GACCGTGCCACCCTCCTGAAGTCTCTGGAGGGCCGCGTGTCATGAGCAGCCCCATGGCT 1260

Qy  1261 GCCCACCTCAGCGAAGACGCCAAAGACTTCATCAAGGCTACGCTGCAGAGAGCCCCTCAG 1320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1261 GCCCACCTCAGCGAAGACGCCAAAGACTTCATCAAGGCTACGCTGCAGAGAGCCCCTCAG 1320

Qy  1321 GCCGGCCTAGTGCGGCCCAGTGCCTCTCCCACCCCTGGTTCCTGAAATCCATGCCTGCG 1380
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1321 GCCGGCCTAGTGCGGCCCAGTGCCTCTCCCACCCCTGGTTCCTGAAATCCATGCCTGCG 1380

Qy  1381 GAGGAGGCCCACTTCATCAACAACCAAGCAGTCAAGTTCCTCCTGCTGGCTCCATCCCTGAGCTCCTG 1440
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1381 GAGGAGGCCCACTTCATCAACAACCAAGCAGTCAAGTTCCTCCTGCTGGCTCCATCCCTGAGCTCCTG 1440

Qy  1441 CAGCGTTCCCTGATGAGCTACAAGTCCATCCTGGTATGCGTCCATCCCTCGAGCTGCTG 1500
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1441 CAGCGTTCCCTGATGAGCTACAAGTCCATCCTGGTATGCGTCCATCCCTCGAGCTGCTG 1500

Qy  1501 CGGGGCCACCCGACAGCCCCCTCCTGGCGGTAGCCGGCACCTCTGCAGGGACACTGGT 1560
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1501 CGGGGCCACCCGACAGCCCCCTCCTGGCGGTAGCCGGCACCTCTGCAGGGACACTGGT 1560

Qy  1561 GGCTCCTCCAGTTCCTCCTCCCGGTGACACTCCACCACTGCTTGCGCCCCATTTGCCCGGGCTAAG 1620
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1561 GGCTCCTCCAGTTCCTCCTCCCGGTGACACTCCACCACTGCTTGCGCCCCATTTGCCCGGGCTAAG 1620

Qy  1621 TCACTGCCACCCTCCCGGTGACACCTCATCCTCACCACTACCACTCCACTGCTCGCCCGG 1680
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1621 TCACTGCCACCCTCCCGGTGACACCTCATCCTCACCACTACCACTCCACTGCTCGCCCGG 1680

Qy  1681 CCCTCGGCCAGCCTGCCTCAGGAAGCCGAGGCCAGTGAGCGCTTCACCGAGGCCCCAGCT 1740
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1681 CCCTCGGCCAGCCTGCCTCAGGAAGCCGAGGCCAGTGAGCGCTTCACCGAGGCCCCAGCT 1740

Qy  1741 CCGCCTGCATCTCCCAGCGGTGCCGGGCCCACCAGGGTGCTGGTGCCCCGGCAC 1800
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1741 CCGCCTGCATCTCCCAGCGGTGCCGGGCCCACCAGGGTGCTGGTGCCCCGGCAC 1800

Qy  1801 AGCGTCATCCGGCCGGAGCCCCTGTTCTACCACCAGGCGGTGAGACGCCCTGAGCACGGGCCTG 1860
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1801 AGCGTCATCCGGCCGGAGCCCCTGTTCTCACCACCAGGCGGTGAGACGCCCTGAGCACGGGCCTG 1860

Qy  1861 GCCCCGGGAGCAGGCGGCGCAACCCGCCCCGGCGCGGCGGCACCTGCTGAAGGGCGGCTACATT 1920
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1861 GCCCCGGGAGCAGGCGGCGGCGGCGCCCGGCCCGCCGGGCGGCGGGCCGGCGGCTACATT 1920

Qy  1921 GCGGGGGGCGCTGCCGCGAGCCGTGCGCGATGGAGACCGGCGTGTGGAGGAGGAG 1980
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Db        CCCACCCCATGGAGGAGGACATCGGGCAGGTCTTCCCTGGTCGAGATCCGGACACCCGCCGCCTCACCTC   3060
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3061  GATGCGGAGGCGGGCCGACACAATATCCTGGACATTCCGAGGTGCCACCCTC                     3120
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3061  GATGCGGAGGCGGGCCGACACACATATCCTGGACATTCCGAGGTGCCACCCTC                    3120

Qy  3121  AACCTCTCAGACCTGTACGATATCAAGTACCTCCCATTCGAGTTTATGATCTTCAGGAAA             3180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3121  AACCTCTCAGACCTGTACGATATCAAGTACCTCCCATTCGAGTTTATGATCTTCAGGAAA             3180

Qy  3181  GTCCCCAAGTCGCTCAGCCAGAGCCGCCTTCCCCCCATGCTGAGGAGGAGCTGGCCGAG              3240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3181  GTCCCCAAGTCGCTCAGCCAGAGCCGCCTTCCCCCCATGCTGAGGAGGAGCTGGCCGAG             3240

Qy  3241  TTCCGGAGCCCACGTGGCCCTGGCCAGGTGAACTGGGCCCCACGCAGGCCTGGAGATC               3300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3241  TTCCGGAGCCCACGTGGCCCTGGCCAGGTGAACTGGGCCCCACGCAGGCCTGGAGATC               3300

Qy  3301  ACAGAGAGTCAGAGGATGTGGACCGCGTCGCTGGCAGAGGCTGCCGTGGGCAGGAAGGC             3360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3301  ACAGAGAGTCAGAGGATGTGGACCGCGTCGCTGGCAGAGGCTGCCGTGGGCAGGAAGCGC            3360

Qy  3361  AAGTGGTTCTCCCGTCACGGAGCTCGCGTGAGAGTGAAGGCTTCCGTGGAGGCACACATCTCCCGG      3420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3361  AAGTGGTTCTCCCGTCACGGAGCTCGCGTGAGAGTGAAGGCTTCCGTGGAGGCACACATCTCCCGGAT    3420

Qy  3421  GAGCCTGGAGAGCTGGGGGCTGCGTCAGGTCTGAGAGTCTGAGAGTGAAGAGAGCCAGGC            3480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3421  GAGCCTGCAGAGCTGGGGGCTGCGTCAGGTCTGAGAGTCTGAGAGTGAAGAGAGCCAGGC           3480

Qy  3481  ATCCTGAAAGGCAGGCCGGAAGGTCTGGAGGAAGGTCGGAGAAGGAAGAGAGCCAGGC             3540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3481  ATCCTGAAAGGCAGGCCGGAAGGTCTGGAGGAAGGTCGGAGAAGGAAGAGAGCCAGGC             3540

Qy  3541  CTTGCTTCCCTTCCGGCTCTCAGGTCTGAGAGTCTGAGAGGCTGGCTCAGTGACACTGGCCCAGGTGTCA 3600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3541  CTTGCTTCCCTTCCGGCTCTCAGGTCTGAGAGTCTGAGAGGCTGGCTCAGTGACACTGGCCCAGGTGTCA 3600

Qy  3601  GAGCTCTCAGATGAGACTGTGGTCCTGGGCCAGTCAGTCAGTGACACTGGCCCAGGTGTCA            3660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3601  GAGCTCTCAGATGAGACTGTGGTCCTGGGCCAGTCAGTCAGTGACACTGGCCCAGGTGTCA            3660

Qy  3661  GCCCAGCCAGCTGCCCAGGTGGCACCCTGGAGCAAAGACGGAGCCCCCCCTGGAGAGCAGAGC         3720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3661  GCCCAGCCAGCTGCCCAGGTGGCACCCTGGAGCAAAGACGGAGCCCCCCCTGGAGAGCAGAGC         3720

Qy  3721  CGTGTCCTCATCTCTGCCACCCTCACAAGAACTTCCAGCTTCTGGACATCCTGGTGGTGGTG          3780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3721  CGTGTCCTCATCTCTGCCACCCTCACAAGAACTTCCAGCTTCTGGACATCCTGGTGGTGGTG          3780

Qy  3781  GCTGAGGACCTGGGTGTGTACACCTGCAGCGTGACCAATGCGCTGGGGACAGTGACCACC            3840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3781  GCTGAGGACCTGGGTGTGTACACCTGCAGCGTGACCAATGCGCTGGGGACAGTGACCACC            3840

Qy  3841  ACGGGGTCTCCGAAGGCAGAGCGCCCCTCATCTTCGCCATGTGGAATCGGGGAG                  3900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3841  ACGGGGTCTCCGAAGGCAGAGCGCCCCTCATCTTCGCCATGTGGAATCGGGGAG                  3900

Qy  3901  GTGTACGCGGATGGGGTGCTGCTGGTCTGAAGGCGCAGCTGACCACCACTGGCCCCGTGACC          3960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3901  GTGTACGCGGATGGGGTGCTGCTGGTCTGAAGGCGCAGCTGACCACCACTGGCCCCGTGACC          3960

Qy  3961  TACATTGTGCTACCTGACCAGCAGAGAAGGCGGCTGACCTTCCGGACCTTCCGACATCTTT           4020
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3961  TACATTGTGCTACCTGACCAGCAGAGAAGGCGGCTGACCTTCCGGACCTTCCGACATCTTT           4020

Qy  4021  GACTGCTGCTACCTGACCAGCAGGCTCTCCCGGGTGCACCTTCCGGACACGGCA                  4080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4021  GACTGCTGCTACCTGACCAGCAGGCTCTCCCGGGTGCACCTTCCGGACACGGCA                  4080

Qy  4081  TGTGTCAGAAGGCAGGAATGGGTCCCTACAGCAGCCCCTCGGAGCAAGTCTCCTGGA              4140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4081  TGTGTCAGCAAGGCAGGAATGGGTCCCTACAGCAGCCCCTCCGGAGCAAGTCTCCTGGGA           4140
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Db        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1921  GCGGGGGCGGCCTGCCAGGCCTGCGCGGAGCAGCCACCGCGTGCTGAGGAGGAG                   1980
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        GCGGGGGCGGCCTGCCAGGCCTGCGCGGAGCAGCCACCGCGTGCTGAGGAGGAG

Qy  1981  GCCGCGCCAGGGAGGAGCAGGAGCTGGCCACCCTCTGGCCAAAGCCCCTCCATTCGAGACTGACTGCCCTC 2040
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1981  GCCGCCAGGGAGGAGCAGGAGCTGGCCACCCTCTGGCCAAAGCCCCTCCATTCGAGACTGCCCACCTC    2040

Qy  2041  CGGCTGCCTGCCTCTGGCACCCATTGGCCCCTGGCCCACAGCCACTCCCTGAACATGAC             2100
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2041  CGGCTGCCTGCCTCTGGCACCCATTGGCCCCTGGCCCACAGCCACTCCCTGAACATGAC             2100

Qy  2101  TCTCCGAGCACCCCCGCCCCTCCGGAGGCCTGCGGTGAGGCACAGCGACTGCCTTCA              2160
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2101  TCTCCGAGCACCCCCGCCCCTCCGGAGGCCTGCGGTGAGGCACAGCGACTGCCTTCA              2160

Qy  2161  GCCCCTCCGGGGGCCCCATCAGGGACATGGGCACCCTCAGGGCTCCAAGCAGCTT                 2220
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Db  2161  GCCCCTCCGGGGGCCCCATCAGGGACATGGGCACCCTCAGGGCTCCAAGCAGCTT                 2220

Qy  2221  CCATCCACTGGTGGCCACCAGGCACTGCTCAGCCAGGACCATCCCCGGACAGCCCT                2280
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2221  CCATCCACTGGTGGCCACCAGGCACTGCTCAGCCAGGACCATCCCCGGACAGCCCT                2280

Qy  2281  TGGGGGCAGCCAGCCCCTTTCTGCCACCCAAGCAGGGTTCTGCCCCCAGGAGGGCTGC             2340
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Db  2281  TGGGGGCAGCCAGCCCCTTTCTGCCACCCAAGCAGGGTTCTGCCCCCAGGAGGGCTGC             2340

Qy  2341  AGCCCCACCAGCAGTGCCCCATTGGACTCTAAGATGGGCCTGAGACATCTCTTGCAAA             2400
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2341  AGCCCCACCAGCAGTGCCCCATTGGACTCTAAGATGGGCCTGAGACATCTCTTGCAAA             2400

Qy  2401  GAGGGCCCCTTAGTACCCTCAAGCCCTTCTTGGGACAGCCCCAGGACACCCCTGCCCT             2460
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2401  GAGGGCCCCTTAGTACCCTCAAGCCCTTCTTGGGACAGCCCCAGGACACCCCTGCCCT             2460

Qy  2461  GCCAAAGCAAGCACCCCCCATTGGACTCTAAGATGGGCACCCTGAGACATCTCTTCCTTCCTGGG        2520
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Db  2461  GCCAAAGCAAGCACCCCCCATTGGACTCTAAGATGGGCACCCTGAGACATCTCTTCCTTCCTGGG        2520

Qy  2521  AGGCCAAAACCCGGCCCCTGCAGTTCCCCAGGTCAGCCTCCCAGGGAGCTCTTCCAA              2580
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2521  AGGCCAAAACCCGGCCCCTGCAGTTCCCCAGGTCAGCCTCCCAGGGAGCTCTTCCAA              2580

Qy  2581  GTGAGCTCCCTCAGGGTGGCTCCTCCGGTGGGCACAGACCTGGCCCCTCCTGGAT                2640
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2581  GTGAGCTCCCTCAGGGTGGCTCCTCCGGTGGGCACAGACCTGGCCCCTCCTGGAT                2640

Qy  2641  GCGGAGGGCTGGACCCAGGAGGCTGACCGTGTCCGACTCTCCACACCCACCTTGCAGCGCG          2700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2641  GCGGAGGGCTGGACCCAGGAGGCTGACCGTGTCCGACTCTCCACACCCACCTTGCAGCGCG          2700

Qy  2701  CCTCAGGAACAGGGTGACCATGCGCAAGTTCTCCCTGGGTGGTCGCGGGGGCTACGGCAGGC         2760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2701  CCTCAGGAACAGGGTGACCATGCGCAAGTTCTCCCTGGGTGGTCGCGGGGGCTACGGCAGGC         2760

Qy  2761  GTGGCTGGCTATGGCACCTTTGCCTTTGCCTTTGGTGGAGATGCAGGGGCCATGGGGGCAGGGG       2820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2761  GTGGCTGGCTATGGCACCTTTGCCTTTGGTGGAGATGCAGGGGCCATGGGGGCAGGGG            2820

Qy  2821  CCCATGTGGGCCAGGATAGCCTGGCTGGGGCAGGAGCAGGGGGCTGAGGAGGAG                 2880
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Db  2821  CCCATGTGGGCCAGGATAGCCTGGCTGGGGCAGGAGCAGGGGGCTGAGGAGGAG                 2880

Qy  2881  GCCAGGGCTGAGTCCCAGTCGGAGCAGGAGCAGGAGGCCAGGGCTCACTGCCC                  2940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2881  GCCAGGGCTGAGTCCCAGTCGGAGCAGGAGCAGGAGGCCAGGGCTCACTGCCC                  2940

Qy  2941  CAGGTCAGTGCAAGGCGTCGGCAGGCCTGCCGTGAGGTCGGCAGGGCTCTCCAGAG               3000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2941  CAGGTCAGTGCAAGGCGTCGGCAGGCCTGCCGTGAGGTCGGCAGGGCTCTCCAGAG               3000

Qy  3001  CCCACCCCATGGAGGAGGACATCGGGCAGGTCTTCCCTGGTCGAGATCCGGACACCCGTCAGGT        3060
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RESULT 4
US-10-415-011-44
; Sequence 44, Application US/10415011
; Publication No. US20040053394A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE CORPORATION
; APPLICANT: GURURAJAN, Rajagopal
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: CHAWLA, Narinder K.
; APPLICANT: ELLIOTT, Vicki S.
; APPLICANT: XU, Yuming
; APPLICANT: ARVIZU, Chandra S.
; APPLICANT: YAO, Monique G.
; APPLICANT: RAMKUMAR, Jayalaxmi
; APPLICANT: DING, Li
; APPLICANT: TANG, Y. Tom
; APPLICANT: HAFALIA, April J.A.
; APPLICANT: NGUYEN, Danniel B.
; APPLICANT: GANDHI, Ameena R.
; APPLICANT: LU, Yan
; APPLICANT: YUE, Henry
; APPLICANT: BURFORD, Neil
; APPLICANT: BANDMAN, Olga
; APPLICANT: TRIBOULEY, Catherine M.
; APPLICANT: LAL, Preeti G.
; APPLICANT: RECIPON, Shirley A.
; APPLICANT: LU, Dyung Aina M.
; APPLICANT: BOROWSKY, Mark L.
; APPLICANT: THORNTON, Michael B.
; APPLICANT: SWARNAKER Anita
; APPLICANT: THANGAVELU, Kavitha
; APPLICANT: KHAN, Farrah A.
; APPLICANT: ISON, Craig H.
; TITLE OF INVENTION: HUMAN KINASES
; FILE REFERENCE: PI-0262 USN
; CURRENT APPLICATION NUMBER: US/10/415,011
; CURRENT FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: PCT/US01/47728
; PRIOR APPLICATION NUMBER: 2001-10-20
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: US 60/242,410
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: US 60/244,068
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/245,708
; PRIOR FILING DATE: 2000-11-03
; PRIOR APPLICATION NUMBER: US 60/247,672
; PRIOR FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: US 60/249,565
; PRIOR FILING DATE: 2000-11-16
; PRIOR APPLICATION NUMBER: US 60/252,730
; PRIOR FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: US 60/250,807
; PRIOR FILING DATE: 2000-12-01
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PERL Program
; SEQ ID NO 44
; LENGTH: 5454
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040053394A1 7638121CB1
US-10-415-011-44

Query Match      99.4%;   Score 5173.6;   DB 13;   Length 5454;
Best Local Similarity   99.8%;   Pred. No. 0;   Indels   0;   Gaps   0;
Matches 5179;   Conservative   0;   Mismatches   9;   Indels   9;

Qy        3 GCACGAGGAACTCCTTCTGATCACCTGGCCAGCTGAGGTCAGAGTGGGAGAGGCAGTGGT   62
Db      267 GCCCACCACCAACTCCTTCTGATCACCTGGCCAGCTGAGGTCAGAGTGGGAGAGGCAGTGGT   326

Qy     4141 GGGCCAGCCACCTGGCCTCTGAGGAGGAGCCAGGGCGGTCAGCCCAACCCCTGCCC   4200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     4141 GGGCCAGCCACCTGGCCTCTGAGGAGGAGCCAGGGCGGTCAGCCCAACCCCTGCCC   4200

Qy     4201 AGCACAAAGACCTTCGCATTCCGCATCCAGACACAGATCCAGAGGGGCCTTCAGCGTGGTGCGG   4260
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     4201 AGCACAAAGACCTTCGCATTCCGCATCCAGACACAGATCCAGAGGGGCCGCTTCAGCGTGGTGCGG   4260

Qy     4261 CAATGCTGGGAGAAGGCCAGCGGGGGCGTGGCCGCCAAGATCATCCCCTACCACCCC   4320
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Db     4261 CAATGCTGGGAGAAGGCCAGCGGGGGCCGGCGGCCGCCAAGATCATCCCCTACCACCCC   4320

Qy     4321 AAGGACAAGACAGCAGTGCTGCGCGAATACGAGGGCCTCAAGGGCCTCACCCGCAC   4380
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     4321 AAGGACAAGACAGCAGTGCTGCGCGAATACGAGGGGCCCTCAAGGGCCTCGCCCACCCGCAC   4380

Qy     4381 CTGGCCCAGTGCACGGCAGCCTACCTGGTGCTCAGCATCTTCGGAGCTG   4440
            |||||||||||||||||||||||||||||||||||||||||||||||||
Db     4381 CTGGCCCAGTGCACGGCAGCCTACCTGGTGCTCAGCATCTTCGGAGCTG   4440

Qy     4441 TGCTCTGGGCCCGAGCTGCTCCCCTGCCGAGGGGCCTTCCTACTCAGAATCTGAG   4500
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     4441 TGCTCTGGGCCCGAGCTGCTCCCCTGCCGAGGGGCCTTCCTACTCAGAATCTGAG   4500

Qy     4501 GTGAAGGACTACCTGTGGCAGATGTTGAGTGCCACCCAGTACCTGCACAACCAGCACATC   4560
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Db     4501 GTGAAGGACTACCTGTGGCAGATGTTGAGTGCCACCCAGTACCTGCACAACCAGCACATC   4560

Qy     4561 CTGCACCTGGACCTGAGGTCCGAGAACATGATCATCACCGAATACAACCTGCTCAAGGTC   4620
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Db     4561 CTGCACCTGGACCTGAGGTCCGAGAACATGATCATCACCGAATACAACCTGCTCAAGGTC   4620

Qy     4621 GTGGACCTGGCAATGCACAGAGCCTCAGCCAGGAAGTGCTGCCCTCAGACAAGTTC   4680
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     4621 GTGGACCTGGCAATGCACAGAGCCTCAGCCAGGAGAGGTGCTGCCCTCAGACAAGTTC   4680

Qy     4681 AAGGACTACCTAGAGACCATGGCCTCCAGAGTCCTCGAGAGGTCCTGGAGGGGCTGTTCCACAG   4740
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     4681 AAGGACTACCTAGAGACCATGGCCTCCAGAGCTCCGAGAGCTCCTGGAGGGGCTGTTCCACAG   4740

Qy     4741 ACAGACATCTGGGCCATCGGTGAGACAGCCTTCATCATGCTGGCCAAGGGCGTACCCGGTG   4800
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     4741 ACAGACATCTGGGCCATCGGTGAGACAGCCTTCATCATGCTGGCCAAGGGCGTACCCGGTG   4800

Qy     4801 AGCAGCGAGGGTGCACGGCGACCTGCGCAGAGGACTGCGCAAGGGGCTGGTCCGGCTGAGC   4860
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     4801 AGCAGCGAGGGGTCACGGCGACCTGCGCAGAGGACTGCGCAAGGGGCTGGTCCGGCTGAGC   4860

Qy     4861 CGCTGCTACGGCGGGGGCTGTCGGGGGCGGCCGTGGCCTTCCTGCGCCACTCGTGTCGCGCC   4920
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     4861 CGCTGCTACGGCGGGGGCTGTCGGGGGCGGCCGTGGCCTTCCTGCGCCAGCACTCGTGTCGCGCC   4920

Qy     4921 CAGCCCTGGGGGCCTGTTCCGGGGCCCCCGGCCCCGTCCCTACCGGCGGCGGCGGGGTCTTC   4980
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     4921 CAGCCCTGGGGGCCGGCCCCGTCCCTACCGGCGCGGCGGCGGGGTCTTC   4980

Qy     4981 GGGCCGGCCTGTTCGGGGCCCCGGCCCCGTCCCTACCGGCGGCGCGGGTCTTC   5040
            |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     4981 GGGCCGGCCTGTTCGCGGCCCCGGCCCCGTCCCTACCGGCGCGGCGCGGCGTCTTC   5040

Qy     5041 GTGCGCAATCGCCGAGAAGACGCGCGGCCGCTGCTGTACAAGAGGCACAACCTGGCCCAGTG   5100
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     5041 GTGCGCAATCGCCGAGAAGACGCGCGGCCGCTGCTGTACAAGAGGCACAACCTGGCCCAGTG   5100

Qy     5101 CGCTGAGGGTCGCCCCCACCACCCTTGGTCTCCCCGCTGGGGTCGCTGCAGACGCGC   5160
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Db     5101 CGCTGAGGGTCGCCCCCACCACCCTTGGTCTCCCCGCTGGGGTCGCTGCAGACGCGC   5160

Qy     5161 CAATAAAAACGCACAGCCCCGGCCGAGAAAAAAAAAAAAAAAAAAAAA   5207
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Db     5161 CAATAAAAACGCACAGCCCCGGCCGAGAAAAAAAAAAAAAAAAAAAAA   5207

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Qy    63  TCCATTGAAGGAGTACTCCTAACTGTTGCAGAAGCCTGGGGTGGTCAGGATGGGTGCTGTCG  122
          ||||||||||||||||||||||||||||||||||||| ||  ||  ||  ||  |||||||
Db   327  TCCATTGAAGGAGTACTCCTAACTGTCAGAAGCCTGGGGTGCTGTCAGGATGGGTGCTGTCG  386

Qy   123  CTTGGGCTGTCGGGGGGTGTTCAGTTGGCCACCAGTGTATCTCAGGGTCTCACCAACCATCC  182
          |||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Db   387  CTTGGGCTGTCGGGGGGTGTTCAGTTGGCCACCAGTCTATCTCAGGGTCTCACCAACCATCC  446

Qy   183  AAGCATGTAGGCTGTGGCTGGCACCCAGGGTTGTGGCTGGGAGGTGGTCTCCACAG  242
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   447  AAGCATGTAGGCTGTGGCTGGCACCCAGGGTTGTGGCTGGGAGGTGGTCTCCACAG  506

Qy   243  TTCCCCTCCCTGCCTCCCAGGGCCCCATCCATGCAGGTAACCATGGAGGATGTGCAGGC  302
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   507  TTCCCCTCCCTGCCTCCCAGGGCCCCATCCATGCAGGTAACCATCGAGGATGTGCAGGC  566

Qy   303  ACAGACAGGCGAACGGCCCAATTCGAGGCTATCATTGAGGGCGACCCACAGCCCTCGGT  362
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   567  ACAGACAGGCGAACGGCCCAATTCGAGGCTATCATTGAGGGCGACCCACAGCCCTCGGT  626

Qy   363  GACCTGGTACAAGGACAGCGTTCCAGCTGGTGGACAGCACCCGGCTTAGCCAGCAGCAAGA  422
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   627  GACCTGGTACAAGGACAGCGTTCCAGCTGGTGGACAGCACCCGGCTTAGCCAGCAGCAAGA  686

Qy   423  AGGCACCACCATACTCCCTGGTGCTGAGGCATGTGGCCTCGAAGGATGCCGGCGTTTACAC  482
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   687  AGGCACCACCATACTCCCTGGTGCTGAGGCATGTGGCCTCGAAGGATGCCGGCGTTTACAC  746

Qy   483  CTGCCTGGCCAAAAACACTGGTGGCCAGGTGCTCTGCAAGGCAGAGCTGCTCGGTGCTTGG  542
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   747  CTGCCTGGCCAAAACACTGGTGGCCAGGTGCTCTGCAAGGCAGAGCTGCTCGGTGCTTGG  806

Qy   543  GGGGGACAATGAGCCGACTCAGAGAACAAAGCCACCGGAAGGGCGTGTCACTCCTTCTA  602
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   807  GGGGGACAATGAGCCGACTCAGAGAACAAAGCCACCGGAAGGGCGTGTCACTCCTTCTA  866

Qy   603  TGAGGTCAAGGAGGAGATTCGCGCTGCCAAGTTCATCCCCACGGAGCAGCAGCACAA  662
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   867  TGAGGTCAAGGAGGAGATTCGCGCTGCCAAGTTCATCCCCACGGAGCAGCAGCACAA  926

Qy   663  AGGAAACAAGATCTTGTGCGGCTGCCAAGTTCATCCCCACGGAGCAGCAGACTCGGGCCCA  722
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   927  AGGAAACAAGATCTTGTGCGGCTGCCAAGTTCATCCCCACGGAGCAGCAGACTCGGGCCCA  986

Qy   723  GGCATACAGGGACGGAGACATCCTGGCCGCGCTGAGCCACCCCGCTGGTTCACGGGGCTGCT  782
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   987  GGCATACAGGGACGGAGACATCCTGGCCGCGCTGAGCCACCCCGCTGGTTCACGGGGCTGCT  1046

Qy   783  GGACCAGTTTGAGACCCGCAAGACCCTGTACAGGAAGGCGTGGTGACGGAGGCCCAGGTCATCCGGAGGA  842
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1047  GGACCAGTTTGAGACCCGCAAGACCCTGTACAGGAAGGCGTGGTGACGGAGGCCCAGGTCATCCGGAGGA  1106

Qy   843  GCTGCTGGACCGCCCTGTACAGGAAGGGCGTGGTGACGAGGCCGAGGCCCAGGTCAAGGTCTACAT  902
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1107  GCTGCTGGACCGCCCTGTACAGGAAGGGCGTGGTGACGAGGCCGAGGCCCAGGTCAAGGTCTACAT  1166

Qy   903  CCAGCAGCTGGTGGAGGGCTGCACTACCTGCACAGCCATGGGGTTCTCCACCTGGACAT  962
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1167  CCAGCAGCTGGTGGAGGGCTGCACTACCTGCACAGCCATGGGGTTCTCCACCTGGACAT  1226

Qy   963  AAAGCCCTCTAACATCCTGATGGTGCATCCGGGGAAGACATTAAAATCTGCGACTT  1022
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1227  AAAGCCCTCTAACATCCTGATGGTGCATCCGGGGAAGACATTAAAATCTGCGACTT  1286

Qy  1023  TGGCTTTGCCCAGAACATCACCCCAGAGCTGCAGTTCAGCCAGTACGGCTTCCCCTGA  1082
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1287  TGGCTTTGCCCAGAACATCACCCCAGAGCTGCAGTTCAGCCAGTACGGCTTCCCCTGA  1346

Qy  1083  GTTCGTCTCCCCCGAGATCATCCGAGACCCTGTGAGCGAAGCCCTCGACAATTGGGC  1142
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1347  GTTCGTCTCCCCCGAGATCATCCGAGACCCTGTGAGCGAAGCCCTCGACAATTGGGC  1406

Qy  1143  CATGGGTGTCATCTCCTACCTCAGCCTGCTCATCCCCATTTGCCGGCGGAGAGTGA  1202
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Db  1407  CATGGGTGTCATCTCCTACCTCAGCCTGCTCATCCCCATTTGCCGGCGGAGAGTGA  1466

Qy  1203  CCGTGCCACCCTCCTGAACGTCTGGAGGGCCGGCTGTGTCATGAGCACCATCC  1262
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1467  CCGTGCCACCCTCCTGAACGTCTGGAGGGCGGCTGTGTCATGAGCAGCCCATGGCTGCCA  1526

Qy  1263  CCACCTCAGCGAAGACGCCAAAGACTTCATCACAGGCTACGCTGCAGAGCCCTCAGGC  1322
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Db  1527  CCACCTCAGCGAAGACGCCAAAGACTTCATCACAGGCTACGCTGCAGAGCCCTCAGGC  1586

Qy  1323  CCGGCTAGTGCGGCCCAGTGCCTCTCCCACCCCTGGTTCCTGAAATCCATGCCGGGA  1382
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Db  1587  CCGGCTAGTGCGGCCCAGTGCCTCTCCCACCCCTGGTTCCTGAAATCCATGCCGCGA  1646

Qy  1383  GGAGGCCCACTCATCAACACCAGCAGCAGTTCCTCCTGCCCGAAGTGCTGCTGCA  1442
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1647  GGAGGCCCACTTCATCAACACCAGCAGTTCCTCCTGCCCGAAGTCGCTGCTGCA  1706

Qy  1443  GCGTTCCTGATGAGCTACAAGTCCATCCTGGTGATGCGGCTCCATCCTGAGCTGCTGCG  1502
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1707  GCGTTCCTGATGAGCTACAAGTCCATCCTGGTGATGCGGCTCCATCCTGAGCTGCTGCG  1766

Qy  1503  GGGCCACCAGCCGACAGCCCCTCCGGCGTAGCCCGGCACCTGCTGCAGGGACACTGGTGG  1562
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1767  GGGCCACCAGCCGACAGCCCCTCCGGCGTAGCCCGGCACCTGCTGCAGGGAACTGGTGG  1826

Qy  1563  CTCCTCCAGTTCTCCTCCTCTGACAACGAGACTCGCCCATTGCCCGGCTAAGTC  1622
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1827  CTCCTCCAGTTCTCCTCCTCTGACACGAGACTCGGCCCATTTGCCCGGCTAAGTC  1886

Qy  1623  ACTGCCACCTCCCGGTGACACTCACCACTGCTGCCACGGCCCCGAGGCTTCCTGCGCC  1682
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Db  1887  ACTGCCACCTCCCGGTGACACTCACCACTGCTGCCACGGCCCCGAGGCTTCCTGCGCC  1946

Qy  1683  CTCGGCCAGCCTGCCTGAGGGTGCCGGCGCCAGGGTGCGTGCCCGGCCACAG  1742
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Db  1947  CTCGGCCAGCCTGCCTGAGGGTGCCGGCGCCAGGGTGCGTGCCCGGCCACAG  2006

Qy  1743  GCCTGCATTCCCAGGGTGCCGGCCACCAGGGGTGCGTGCCCCGGCACAG  1802
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db  2007  GCCTGCATCCCGAGGGTGCCGGCCACCAGGGGTGCGTGCCCCGGCACAG  2066

Qy  1803  CGTCATCCGCAGCCGTTCTACCACGGCCCTGGTTCACGGGGCCCTGGC  1862
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db  2067  CGTCATCCGCAGCCGTTCTTACCACCACGGCCCTGGTTCACGGGGCCCTGGC  2126

Qy  1863  CCCGGGAGCAGGGCGCGGGAGGCCGGCACCTGCTGTGAAGGGCGGCGTACATTGC  1922
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2127  CCCGGGAGCAGGGCGCGGGAGGCCGGCACCTGCTGCTGAAGGGCGGCGTACATTGC  2186

Qy  1923  GGGGGGCGTGCCAGGCCTGCGGGAGGCCACTGATGAGGACACCGGCGTGCTGGAGGAGGGC  1982
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2187  GGGGGGCGTGCCAGGCCTGCGGGAGGCCACTGATGAGGACACCGGCGTGCTGGAGGAGGGC  2246

Qy  1983  CGCAGGGAGGAGGAGCAGGCCACCTCCTGGCCCAAAGCCCACTGCCCTCCG  2042
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2247  CGCCAGGGAGGAGGAGCAGGCCACCCCCCTCCTGGCCCAAAGCCCACTGCCCTCCG  2306

Qy  2043  GCTGCCTGGCCTGGACAGCCGCCACTCCCTGGCACCACCATGGAACATGACTC  2102
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2307  GCTGCCTGGCCTGGACAGCCCGCCACTCCCTGGCACCACCATGGAACATGACTC  2366

Qy  2103  TCCGACACCCCCGGGGGCCCTTGCGGTGAGGCCCTCCAGGGCACAGCAGCTTCAGC  2162
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2367  TCCGACACCCCCGGGGGCCCTTGCGGTGAGGCCCTCGGTGAGGCCCACAGCAGCTTCAGC  2426

Qy  2163  CCCCTCCGGGGGCCCTATCAGGGACATGGGGCACCCCAGGGCTCCAAGGCTTCC  2222
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2427  CCCCTCCGGGGGCCCATCAGGGACATGGGGCACCCCAGGGCTCCAAGGCTTCC  2486

Qy  2223  ATCCACTGGTGGCCACCCAGGCACTGCTCAGCCCGGCGGAGAGTGA  2282
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Qy  3363 GTGGTCCTGCCGTCACGCAGCCTCTTCCACTTCCCTGGAGGCACCTGCGCTGGATGA 3422
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Db  3627 GTGGTCCTGCCGTCACGCAGCCTCTTCCACTTCCCTGGAGGCACCTGCGCTGGACGA 3686

Qy  3423 GCCTGCAGAGCTGGGCTGCGTGAGAGTGAAGGCCTCCGTGAGCACATCTCCCGGAT 3482
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3687 GCCTGCAGAGCTGGGCTGCGTGAGAGTGAAGGCCTCCGTGAGCACATCTCCCGGAT 3746

Qy  3483 CCTGAAGGGCAGGCCGGAAGTCTGGAGAAGAGAGGGCCCCCAGGAAGAAGCCAGGCCT 3542
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3747 CCTGAAGGGCAGGCCGGAAGTCTGGAGAAGAGAGGGCCCCCAGGAAGAAGCCAGGCCT 3806

Qy  3543 TGCTTCCTTCCGGCTCTCAGGTCTGAAGAGCTGGGACCGGGACCGGGACCGGGAGCGCCGACATTCCTAAGGGA 3602
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3807 TGCTTCCTTCCGGCTCTCAGGTCTGAAGAGCTGGGACCGGGACCGGCGCCGACATTCCTAAGGGA 3866

Qy  3603 GCTCTCAGATGAGACTGTGTCCTGGCCCAGTCAGTCGACACTGGCCTGCCAGGTGTCAGC 3662
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3867 GCTCTCAGATGAGACTGTGTCCTGGGCCAGTCAGTCGACTGACACTGGCCTGCCAGGTGTCAGC 3926

Qy  3663 CCAGGCAGTGCCCAGGCCACCTGAGCAAAGACGGAGCCCCTGGACAGCAGCAGCCG 3722
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3927 CCAGGCAGTGCCCAGGCCACCTGGGCGAGCAAAGACGGAGCCCCTGGACAGCAGCAGCCG 3986

Qy  3723 TGTCCTCATCCTGCCACCTCAAGAACTTCCAGCTTCTGAGCCATCCTGGTGGTGGTGGC 3782
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Db  3987 TGTCCTCATCCTGCCACCTCAAGAACTTCCAGCTTCTGAGCCATCCTGGTGGTGGTGGC 4046

Qy  3783 TGAGGACCTGGGTGTGTACACCTGCAGCGTGAGCAATGGCTGGGGACAGTGACCACCAC 3842
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Db  4047 TGAGGACCTGGGTGTGTACACCTGCAGCGTGAGCAATGGCTGGGGACAGTGACCACCAC 4106

Qy  3843 GGGCGTCCTCCGGAAGGCAGAGCGCCCCTCATCTTCGCCATGCCCGTGATATCGGGGAGGT 3902
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Db  4107 GGGCGTCCTCCGGAAGGCAGAGCGCCCCTCATCTTCGCCATGCCCGTGATATCGGGGAGGT 4166

Qy  3903 GTACGCGGATGGGGTGCTGGTGTGGCTGCTGGTGGTCTGGAAGCCCGTTACGGCCCTGTGACCTA 3962
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Db  4167 GTACGCGGATGGGGTGCTGGTGTGGCTGCTGGTGGTCTGGAATCCGGCCCTGTGACCTA 4226

Qy  3963 CATTGTGCAGTGCAGCTGACGAGGCGGCAGCTGACCACACTGGCCTCCGACATCTTTGA 4022
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4227 CATTGTGCAGTGCAGCTGACGAGGCGGCAGCTGACCACACTGGCCTCCGACATCTTTGA 4286

Qy  4023 CTGCTGCTACCTGACCAGCAAGCTCTCCCGGGGTGGCACCTTCCGCACGGCATG 4082
         |||||||||||||||||||||||||||||||||||||||||||||||||
Db  4287 CTGCTGCTACCTGACCAGCAAGCTCTCCCGGGGTGGCACCTTCCGCACGGCATG 4346

Qy  4083 TGTCAGCAAGGCAGGAAATGGGTCCCTACAGCAGCCCCTCCTGGGAGG 4142
         |||||||||||||||||||||||||||||||||||||||||||||
Db  4347 TGTCAGCAAGGCAGGAAATGGGTCCCTACAGCAGCCCCTCCTGGGAGG 4406

Qy  4143 GCCCAGCCACCTGGGCGGTCAGCCGGAGAGCCAGGGGCGCGTTCAGCGGGCA 4202
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4407 GCCCAGCCACCTGGGCGGTCAGCCGGAGAGCCAGGGGCGCGTTCAGCGGGCA 4466

Qy  4203 CACAAAGACCTTCGCATTCGAGTTTATGATCTTCAGGAAAGT 4262
         |||||||||||||||||||||||||||||||||||||
Db  4467 CACAAAGACCTTCGCATTCGAGTTTATGATCTTCAGGAAAGT 4526

Qy  4263 ATGTGGGAGAAGGCCAGCGGGCGCGGCCCAAGATCATCCCCACCCCCAA 4322
         |||||||||||||||||||||||||||||||||||||||||||||
Db  4527 ATGTGGGAGAAGGCCAGCGGGCGCGGCCCAAGATCATCCCCACCCCCAA 4586

Qy  4323 GGACAAGACAGCAGTGCTGCGCGAATACGAGGCCCTCAAGGGCCTCACC 4382
         |||||||||||||||||||||||||||||||||||||||||||||
Db  4587 GGACAAGACAGCAGTGCTGCGCGAATACGAGGCCCTCAAGGGCCTCACC 4646

Qy  4383 GGCCCAGTCACGCAGCCTACCTCAGCCCCGCACCTTGGAGCTGTG 4442
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Db  4647 GGCCCAGTCACGCAGCCTACCTCAGCCCCGCACCTTGGAGCTGTG 4706
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Db  2487 ATCCACTGGTGGCCACCCAGGCACTGCTCAGCCAGAGAGGCATCCCCGGACAGCCCTTG 2546
Qy  2283 GGGCAGCCAGCCCCTTTCTGCCACCCCAAGCAGGGTTCTGCCCCCCAGGAGGGCTGCAG 2342
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Db  2547 GGGCAGCCAGCCCCTTTCTGCCACCCCAAGCAGGGTTCTGCCCCCCAGGAGGGCTGCAG 2606

Qy  2343 CCCCACCAGCAGTTGCCCCATGCCCTCTGCTCCTTCCCTCCAGGATCTTGCAAAGA 2402
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Db  2607 CCCCACCCAGCAGTTGCCCCATGCCCTCTGCTCCTTCCCTCCAGGATTTGCAAAGA 2666

Qy  2403 GGCCCCCTTAGTACCCTCAAGCCCTCTTGGGACAGCCCAGGCACCCCCTGCCCCTGC 2462
         |||||||||||||||||||||||||||||||||||||||||||||||
Db  2667 GGCCCCCTTAGTACCCTCAAGCCCTTCAAGCCCTCTTGGGACAGCCCAGGCACCCCCTGCCCCTGC 2726

Qy  2463 CAAAGCAAGCCCCCCATTGGACTCTAAGATGGGGCCTGGAGACATCTCTCTTCCTCCTGGGAG 2522
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Db  2727 CAAAGCAAGCCCCCCATTGGACTCTAAGATGGGGCCTGGAGACATCTCTCTTCCTCCTGGGAG 2786

Qy  2523 GCCAAAACCGGCCCTGCAGTTCCCAGGGTCAGCCTCCCAGGCGAGCTCTTCCCAAGT 2582
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Db  2787 GCCAAAACCGGCCCTGCAGTTCCCAGGGTCAGCCTCCCAGGCGAGCTCTTCCCAAGT 2846

Qy  2583 GAGCTCCCTCAGGGTGGGGCTCCTCCCAGGTGGGCTGGGACAGAGCCTGGCCCTGGATGC 2642
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Qy  2643 GGAGGGGCTGGACCCAGGAGGCTGAGGATCGTCGACTCCACACCCACCTTGCAGCGGGGC 2702
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Db  2907 GGAGGGGCTGGACCCAGGAGGCTGAGGATCTGTCCGACTCCACACCCACCTTGCAGCGGGGC 2966

Qy  2703 TCAGGAACAGGTGACCATGCGCAAGTTCTCTCCCTGGGTGGTCGCGGGGGCTACGCAGGCGT 2762
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Db  2967 TCAGGAACAGGTGACCATGCGCAAGTTCTCTCCCTGGGTGGTCGCGGGGGCTACGCAGGCGT 3026

Qy  2763 GGCTGGCTATGGCACCTTTGCCTTTGCCTTTGGCTGGAGATGCAGGGGGCATGCTGGGGCAGGGGGC 2822
         ||||||||||||||||||||||||||||||||||||||||||||||
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Qy  2823 CATGTGGGCCAGGATAGCCTGGGCTGGCTGTGTGTCCCAGTCAGCAGCAGAGGAGCAGGAGGAGGC 2882
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Db  3087 CATGTGGGCCAGGATAGCCTGGGCTGGCTGTGTGTCCCAGTCAGCAGCAGAGGAGCAGGAGGAGGC 3146

Qy  2883 CAGGGGAGGCTGAGTCCCAGTCCCGACACAATATCCCGGGGAGCCCACTGCCCCA 2942
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Db  3147 CAGGGGAGGCTGAGTCCCAGTGCAGCAGCCCCAGGGCTGAGAGCCCACTGCCCCA 3206

Qy  2943 GGTCAGTGCAAGCCTGTCCGTGTCCCAGTCGGCAGAGGGCTCTCCCACCAGAGCC 3002
         |||||||||||||||||||||||||||||||||||||||||||||||
Db  3207 GGTCAGTGCAAGCCTGTCCGTGTCCGGTCGGCAGAGGGCTCCCACCAGAGCC 3266

Qy  3003 CACCCCCATGGGAGGACAATGCGGAGCCGCGCCCCTCGTGCAGATCGGGACCTGTCAGGTGA 3062
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Db  3267 CACCCCCATGGGAGGACAATGCGGGAGCCGCGCCCCTCGTGCAGATCGGGACCTGTCAGTGA 3326

Qy  3063 TGCGGAGGCCGGCCCAGACAATATCCCTGGGACATTTCCGAGGTGGACCCCGCCTACCTCAA 3122
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Db  3327 TGCGGAGGCCGGCCCAGCACAATATCCCTGGGACATTTCCGAGGTGGACCCCGCCTACCTCAA 3386

Qy  3123 CCTCTCAGACCTGTACGATATCAAGTACACTCCCATTCGAGTTTATGATCTTCAGGAAAGT 3182
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Db  3387 CCTCTCAGACCTGTACGATATCAAGTACACTCCCATTCGAGTTTATGATCTTCAGGAAAGT 3446

Qy  3183 CCCAAGTCCGCTCAGCCTCAGCCAGAGCCGCGCCCCTCCCATGGCTGAGGAGGAGCTGGCCCAGTT 3242
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Db  3447 CCCAAGTCCGCTCAGCCTCAGCCAGAGCCGCGCCCCTCCCATGCCTGAGGAGGAGCTGGCCCAGTT 3506

Qy  3243 CCCGGAGCCCACGTGGGCCCTGGCCCAGGTGAACTGGGCCCCACGCAGCCTGAGATCAC 3302
         |||||||||||||||||||||||||||||||||||||||||||||||
Db  3507 CCCGGAGCCCACGTGGGCCCTGGCCCAGGTGAACTGGGCCCCACGCAGCCTGAGATCAC 3566

Qy  3303 AGAGGAGTCAGAGGATGTGGACGCGCCGCGTGCTGCTGGCAGGCTGCCGTGGGCAGAGGGCAA 3362
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Db  3567 AGAGGAGTCAGAGGATGTGGACGCGCCGCGTGCTGCTGGCAGGCTGCCGTGGGCAGGGAGGCCAA 3626
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;    LOCATION: (1)...(71)
;    NAME/KEY: CDS
;    LOCATION: (72)...(7964)
;    NAME/KEY: 3'UTR
;    LOCATION: (7965)...(8106)
US-10-077-130-1

  Query Match           94.9%;   Score 4940.4;   DB 14;   Length 8106;
  Best Local Similarity 99.9%;   Pred. No. 0;
  Matches 4944;  Conservative 0;  Mismatches 0;  Indels 6;  Gaps 0;

Qy    258 CCCAGGGCCCCATCCATCCAGGTAACCATCGAGGATGTGCAGGCAGCAGACAGGCGGAAC  317
          ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3116 CGCACGGGCCCCATCCATCCAGGTAACCATCGAGGATGTGCAGGCAGCAGACAGGCGGAAC 3175

Qy    318 GGCCCAATTCGAGGCTATCATTGAGGGGCACCCACCACCCACCTGGTACAAGGA        377
          ||||||||||||||||||||||||||||| |||||| ||||||||||||||||||
Db   3176 GGCCCAATTCGAGGCTATCATTGAGGGGCGACCCACAGCCCACCTGGTACAAGGA       3235

Qy    378 CAGGCTCCAGCTGGTGGACAGCACCCGGCTTAGCCAGCAGCAAGAAGGCACCACCATACTC  437
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Db   3236 CAGGCTCCAGCTGGTGGACAGCACCCGGCTTAGCCAGCAGCAAGAAGGCACCACCATACTC 3295

Qy    438 CCTGGTGCTGGACAGATGTGCCTCGAAGGATGCCGGCGTTTACACCTGCCTGGCCCCAAAA  497
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Db   3296 CCTGGTGCTGGACAGATGTGCCTCGAAGGATGCCGGCGTTTACACCTGCCTGGCCCCAAAA 3355

Qy    498 CACTCGGTGGCCAGTGCGCTGCTGCAAGGCAGAGAGTGCACTCCTTCTTATGAGGTCAAGGAGAGG  557
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3356 CACTCGGTGGCCAGTGCGCTGCTGCAAGGCAGAGCTGCACTCCTTCTTATGAGGTCAATGAGCC 3415

Qy    558 GGACTCAGAGAAGCAAAGCACCGGAGGAAGCCACCGGAAGCAGAAGCAGAGGAGA        617
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3416 GGACTCAGAGAAGCAAAGCACCGGAGGAAGCCACCGGAAGCAGAAGCAGAGGAGA       3475

Qy    618 GATTGGAAGGGGGTGTTTGGCTTCGTAAAAAGAGTGCAGACAAAGGAAACAAAGATCTT    677
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3476 GATTGGAAGGGGGTGTTTGGCTTCGTAAAAAGAGTGCAGACAAAGGAAACAAAGATCTT   3535

Qy    678 GTGCGTGCCAAGTTCATCCCCCTACGAGCAGAGAACTCGGGCCCAGGCATACAGGGAGCG    737
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3536 GTGCGTGCCAAGTTCATCCCCCTACGAGCAGAGAACTCGGGCCCAGGCATACAGGGAGCG  3595

Qy    738 AGACATCCTGGCCGCGGCTGAGCCACCCGCTGGTCACGGGCTGCTGGACAGTTTGAGAC    797
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Db   3596 AGACATCCTGGCCGCGGCTGAGCCACCCGCTGGTCACGGGCTGCTGGACAGTTTGAGAC   3655

Qy    798 CCGCAAGACCCTCATCCTCATCCTGGACGTGTGCTCATCCGAGGAGCTGCTGGACCGCCT  857
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Db   3656 CCGCAAGACCCTCATCCTCATCCTGGACGTGTGCTCATCCGAGGAGCTGCTGGACCGCCT 3715

Qy    858 GTACAGGAAGGGCCGTGGCGTGGTGACGGAGGCCGAGGTCAAGGTCTCACATCCAGCAGCTGGTGA  917
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3716 GTACAGGAAGGGCCGTGGCGTGGTGACGGAGGCCGAGGTCAAGGTCTCACATCCAGCAGCTGGTGA 3775

Qy    918 GGGGCTGCACTACCTGCACCTGGACATGGCGTTCCCACCTGGACACTAAAGCCCTCTAACAT  977
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3776 GGGGCTGCACTACCTGCACCTGGACATGGCGTTCCCACCTGGACATAAAGCCCTCTAACAT 3835

Qy    978 CCTGATGGTGCATCGCCGGGAAGACATTAAAATCTGCGACTTTGGCTTTGCCCCAGAA   1037
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3836 CCTGATGGTGCATCGCCGGGAAGACATTAAAATCTGCGACTTTGGCTTTGCCCCAGAA  3895

Qy   1038 CATCACCCCAGCAGAGCTGCAGTTCAGCCAGTACGGCTCCCCGAGTTCGTCTCCCCCGA  1097
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3896 CATCACCCCAGCAGAGCTGCAGTTCAGCCAGTACGGCTCCCCGAGTTCGTCTCCCCCGA 3955

Qy   1098 GATCATCCAGCAGACCCTGTGAGCGAAGCCTCCGACATTTGGGCCATGGGTGTCATCTC  1157
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3956 GATCATCCAGCAGACCCTGTGAGCGAAGCCTCCGACATTTGGGCCATGGGTGTCATCTC 4015


Qy   4443 CTCTCGGCCCGAGCTGCTCCCCTGCCTCTGCCGAGAGGGCCTCCTACTCAGAAATCGAGGT 4502
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Db   4707 CTCTCGGCCCGAGCTGCTCCCCTGCCTCTGCCGAGAGGGCCTCCTACTCAGAAATCCGAGGT 4766

Qy   4503 GAAGGACTACCTGTGGCAGATGTTGAGTGCCACCCAGTACCTGCCACAACCAGCACATCCT 4562
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Db   4767 GAAGGACTACCTGTGGCAGATGTTGAGTGCCACCCAGTACCTGCCACAACCAGCACATCCT 4826

Qy   4563 GCAACCTGGACCTGGAGGTCCGAGAACATGATCATCACCGAATCATCACCTGCTCAAGGTCGT 4622
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Db   4827 GCAACCTGGACCTGGAGGTCCGAGAACATGATCATCACCGAATCATCACCTGCTCAAGGTCGT 4886

Qy   4623 GGACTGGGCAATGCACAGAGCCTCAGCCAGGAGAAGGTGCTGCCCCTGCCCTCAGACAACGTTCAA 4682
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Db   4887 GGACTGGGCAATGCACAGAGCCTCAGCCAGGAGAAGGTGCTGCCCCTGCCCTCAGACAACGTTCAA 4946

Qy   4683 GGACTACCTAGAGACACCATGGCTCCAGAGCTCCTGGAGGGGCAAGGGGCGTGTCCACAGAC 4742
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4947 GGACTACCTAGAGACCATGGCTCCAGAGCTCCTGGAGGGGCAAGGGGCGTGTCCACAGAC 5006

Qy   4743 AGACATCTGGGCCACATCGGTGTGACAGCCTTCATCATGTCGACGCGCCGAGTACCCGGTGAG 4802
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Db   5007 AGACATCTGGGCCACATCGGTGTGACAGCCTTCATCATGTCGACGCGCCGAGTACCCGGTGAG 5066

Qy   4803 CAGGGAGGGTGCACGGACCTGGGCGCAAGGACTGGTCCGGCTGGAGCCG 4862
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Db   5067 CAGCGAGGGTGCACGCGACCTGCGCGCAAGGGCTGTCGTCCGGCTGGAGCCG 5126

Qy   4863 CTGCTACGGCGGGGGCGCCCGTGTCCGGGGCGCCCGTGGCCTTCGTGCGGCCGCAGCACTCGTGTGCGCCCA 4922
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Db   5127 CTGCTACGGCGGGGGCGCCCGTGTCCGGGGCGCCCGTGGCCTTCGTGCGGCCGCAGCACTCGTGTGCGCCCA 5186

Qy   4923 GCCCTGGGCGCCCGGCCCGTGCGCGTTCAGCTGCCTGCAGTGCCCGTGGCTAACAGAGGAGGG 4982
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Db   5187 GCCCTGGGCGCCCGGCCCGTGCGCGTTCAGCTGCCTGCAGTGCCCGTGGCTAACAGAGGAGGG 5246

Qy   4983 CCCGCCTGTTCGGGGCCCGGGCCCCGTGACCTTCCCTACCGCGGCCGGCGTCTTCGT 5042
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5247 CCCGGCCTGTTCGGGGCCCGGGCCCCGTGACCTTCCCTACCGCGGCCGGCGTCTTCGT 5306

Qy   5043 GCGCAATCGCGACGAAGACGCGGCGCGCGTGCTGCTGTACAAGAGGCACAACCTGGCCCAGGTGCG 5102
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Db   5307 GCGCAATCGCGACGAAGACGCGGCGCGCGTGCTGCTGTACAAGAGGCACAACCTGGCCCAGGTGCG 5366

Qy   5103 CTGAGGGTGCCCCGGCCACACCCTTGGTCTCCCCGCTGGGGGGTCGCTGCGAGACGCGCCA 5162
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Db   5367 CTGAGGGTGCGCCCGGCCACACCCTTGGTCTCCCCGCTGGGGGGTCGCTGCGAGACGCGCCA 5426

Qy   5163 ATAAAAACGCACAGCCGGGCGAGAAAA 5190
          |||||||||||||||||||||||||||
Db   5427 ATAAAAACGCACAGCCGGGCGAGAAAA 5454
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Db   2487 ATCCACTGGTGGCACCCAGCACTGCTCAGCCAGAGAGGCCATCCCGACAGCCCTTG 2546

Qy   2283 GGGGCAGCCAGCCCTTTCTGCCACCCAAGCAGGGTTCTGCCCCCCAGAGGGGCTGCAG 2342
          ||||||||||||||||  ||||||||||||| ||||  ||||||||
Db   2547 GGGGCCGCCAGCCCCCTTTCTGCCACCCAAGCAGAGGGTTCTGCCCCCCAGAGGGGCTGCAG 2606

Qy   2343 CCCCACCCAGCAGTTGCCCCATGCCCTCCTGCCTCCTTCCTCCGATCTGCAAAGA 2402
          |||||||||||||||||||||||||  |||||||||  |||||||||||||||||
Db   2607 CCCCACCCAGCAGTTGCCCCATGCCCTGCTGCCTCCTTCCTCCGATCTGCAAAGA 2666

Qy   2403 GGCCCCTTAGTACCCTCAAGCCCCTTCTTGGGACAGCCCCAGGCACCCCTGCCCCTGC 2462
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Qy   2463 CAAAGCAAGCCCCCATTGGACTCTAAGATGGGGCCTGGAGACATCTCTTCCTGGGAG 2522
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Db   2727 CAAAGCAAGCCCCCATTGGACTCTAAGATGGGGCCTGGAGACATCTCTTCCTGGGAG 2786

Qy   2523 GCCAAAACCCGGCCCCCTGCAGTTCCCCAGGGTCAGCGTCTTCCCAAGT 2582
          |||||||||||||||||||||||||||||||||||||||||||||||||
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Db   2907 GGAGGGCTGAGCCCAGGAGGCTGAGGATCTGTTCCGAGCCTTCCACCCACCTTGCAGGGGC 2966

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Qy   2823 CATGTGGGCCAGGATAGCCTGGGCTGTGTCCCCAGTCGGAGGAGGAGGAGGAGGAGGC 2882
          |||||||||||||||||||||||  |||||||||||||||||||||||||||||||||
Db   3087 CATGTGGGCCAGGATAGCCTGGGCTGTGTCCCCAGTCGGAGGAGGAGGAGGAGGAGGC 3146

Qy   2883 CAGGGGCTGAGTCCCAGTCGGAGGAGCAGAGGAGGCCAGGGCCCCACTGCCCCA 2942
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3147 CAGGGGCTGAGTCCCAGTCGGAGGAGCAGGAGGCCAGGGCCCCACTGCCCCA 3206

Qy   2943 GGTCAGTGCAAGGCCGTGCCTGAGGTCGGCAGGGCTCGGCAGGGCTCTCCAGAGCC 3002
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3207 GGTCAGTGCAAGGCCGTGCCTGAGGTCGGCAGGGCTCGGCAGGGCTCTCCAGAGCC 3266

Qy   3003 CACCCCATGGAGGACATCGGGAGCATCGGGAGGTCCCTGGTGCAGATTCCGGACCCCTCAGGTGA 3062
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3267 CACCCCATGGAGGACATCGGGAGCATCGGGAGGTCCCTGGTGCAGATTCCGGACCCCTGTCAGGTGA 3326

Qy   3063 TGCGGAGGCGGCCGACACAATATCCCGGACATTTCCGAGGTGGACCCCGCCTACCTCAA 3122
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3327 TGCGGAGGCGGCCGACACAATATCCCGGACATTTCCGAGGTGGACCCCGCCTACCTCAA 3386

Qy   3123 CCTCTCAGACCTTCGATATCAAGTAACTACCTCCATTCAGAGTTTATGATCTTCAGGAAAGT 3182
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3387 CCTCTCAGACCTTCGATATCAAGTAACTACCTCCATTCAGAGTTTATGATCTTCAGGAAAGT 3446

Qy   3183 CCCCAAGTCCCGTCAGCCAGCAGCAGCCGCCCCTCCCCCCCAATGCTGAGGAGTGGCCAGTT 3242
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3447 CCCCAAGTCCCGTCAGCCAGCAGCAGCCGCCCCTCCCCCCCAATGCTGAGGAGTGGCCAGTT 3506

Qy   3243 CCCGGAGCCCACGTGCCCTCAGCCAGCAGCCGCCACGTGGGGCCCCACGCGACGCCGAGATCAC 3302
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3507 CCCGGAGCCCACGTGCCCTGGCCAGCAGCCGCCACGTGGGGCCCCACGCGACGCCGAGATCAC 3566

Qy   3303 AGAGGAGTCAGGAGATGTGGACGCGCTGCGTGCCAGAGGCTGCGTGGGCAGGAAGCGCAA 3362
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3567 AGAGGAGTCAGGAGATGTGGACGCGCTGCGTGCCAGAGGCTGCGTGGGCAGGAAGCGCAA 3626


Qy   3363 GTGGTCTCCGCGTCACGCAGCAGCCTCCTCCACTTCCCTGGGAGGCACCTGCCGCTGGGATGA 3422
          |||||||||||||||||||||||||  |||||||||||||||||||||||||  ||||||
Db   3627 GTGGTCCTCGCCGTCACGCAGCAGCCTCTTCCACTTCCCTGGGAGGCACCTGCCGCTGGACGA 3686

Qy   3423 GCCTGCAGAGCTGGGGCTGCCTGAGAGAGTGAAAGGCCTCCGTGAGCACATCTCCCGGAT 3482
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3687 GCCTGCAGAGCTGGGGCTGCGTGAGAGAGTGAAAGGCCTCCGTGAGCACATCTCCCGGAT 3746

Qy   3483 CCTGAAGGGCAGGCCGAAGGTCTGAGAGAGGAGGGGCCCCCAGGAGGAAGAAGCCAGGCCT 3542
          ||||||||||||||||||||||||||||||||||||||||||||||||  ||||||||||
Db   3747 CCTGAAGGGCAGGCCGAAGGTCTGAGAGAGGAGGGGCCCCCAGGAGGAAGAAGCCAGGCCT 3806

Qy   3543 TGCTTCCTTCCGGCTCAAGTCTGAAGAGTCGGAACTCGGACCTGGCCCGACATTCCTAAGGGA 3602
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3807 TGCTTCCTTCCGGCTCTCAGGTCTGAAGAGTCGGAACTCGGACCTGGCCCGACATTCCTAAGGGA 3866

Qy   3603 GCTCTCAGATGAGACTTGGTCTCCTGGGCCCAGTCAGTGACACTGCCTGCCCAGGTGTCAGC 3662
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3867 GCTCTCAGATGAGACTTGGTCTCCTGGGCCCAGTCAGTGACACTGCCTGCCCAGGTGTCAGC 3926

Qy   3663 CCAGCCAGCTGCCCAGGCCACCTGGACAAAGACGAGCCCCCTGGAGAGGAGCAGCAGCAGCCG 3722
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3927 CCAGCCAGCTGCCCAGGCCACCTGGACAAAGACGAGCCCCCTGGAGAGGAGCAGCAGCCG 3986

Qy   3723 TGTCCTCATCGTGTGTACACCTGCAGCGTGAGCAATGGCCTGGGACAATGCCGGGTGGTGGTGGC 3782
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3987 TGTCCTCATCGTGTGTACACCTGCAGCGTGAGCAATGGCCTGGGACAGTGACCACCACCAC 4046

Qy   3783 TGAGGACCTGGGTGTGTACACCTGCAGCGTGAGCCATGCCCGGATATCGGGAGT 3842
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4047 TGAGGACCTGGGTGTGTACACCTGCAGCGTGAGCCATGCCCGGATATCGGGAGGT 4106

Qy   3843 GGGCGTCCTCCGGAAGCGAAGGCGCCCCTCATCTTCGCCATGCCCGGATATCGGGGAGT 3902
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4107 GGGCGTCCTCCGGAAGCGAAGGCGCCCCTCATCTTCGCCATGCCCGGATATCGGGGAGGT 4166

Qy   3903 GTACGCCGGATGGGGTGCGTGCTGGTCTGGAAGCCCGTGGAAGCCCGTGACCTA 3962
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4167 GTACGCCGGATGGGGTGCGTGCTGGTCTGGAATCCCGTGGAAGCCCGTGACCTA 4226

Qy   3963 CATTGTGCAGTGCAGCTAGAAGGCGGCAGCTGACCAACCACTGGCCTCCGACATCTTTGA 4022
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4227 CATTGTGCAGTGCAGCTAGAAGGCGGCAGCTGACCAACCACTGGCCTCCGACATCTTTGA 4286

Qy   4023 CTGCTGTACCTGACCAGCAAGCTCTCCCGGGGTTGGCACCTACACCTTCGCACGGCATG 4082
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4287 CTGCTGTACCTGACCAGCAAGCTCTCCCGGGGTTGGCACCTACACCTTCCGCACGGCATG 4346

Qy   4083 TGTCAGCAAGGCAGGAATGGGTCCCTACAGGGCCAGCCCCTGGAGCAAGTCCTCTGGGAGG 4142
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4347 TGTCAGCAAGGCAGGAATGGGTCCCTACAGCAGCCCCTCGGAGCAAGTCCTCTGGGAGG 4406

Qy   4143 GCCCAGCCACCTGGCCTCTGAGGTGGAGGAGGAGCCAGGGCGGTCAGCCCAACCCCTGCCCAG 4202
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4407 GCCCAGCCACCTGGCCTCTGAGGTGGAGGAGGAGCCAGGGCGGTCAGCCCAACCCCTGCCCAG 4466

Qy   4203 CACAAAGACCTTCGATTCAGACACAGATCCAGAGGGCCGTTCAGCGGGGTGCGGCA 4262
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4467 CACAAAGACCTTCGATTCAGACACAGATCCAGAGGGGCCGTTCAGCGGGGTGCGGCA 4526

Qy   4263 ATGCTGGGAGAAGCAGCAGTGCTGCGCGGATTACGGACGCCTCAAGGAGGCCCAGTT 4322
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4527 ATGCTGGGAGAAGCAGCAGTGCTGCGCGAATACGGAGGCCTCAAGGAGGCCCAGTT 4586

Qy   4323 GGACAAGCAGCAGTGCTGCGCGGAATACGGACGCCCTCAAGGGCCTGCGCACCCGCACCT 4382
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4587 GGACAAGCAGCAGTGCTGCGCGAATACGGAGGCCTCAAGGGCCGCGCCACCCGCACCT 4646

Qy   4383 GGCCCAGTGCACGCGACGCCTACCTCGACACCGGTGCTCATCTTGGAGCTGTGTG 4442
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4647 GGCCCAGCTGCACGCGACGCCTACCTCAGCACCGGTGCTCATCTTGGAGCTGTGTG 4706
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;  FEATURE:
;  NAME/KEY: 5'UTR
;  LOCATION: (1)...(71)
;  NAME/KEY: CDS
;  LOCATION: (72)...(7964)
;  NAME/KEY: 3'UTR
;  LOCATION: (7965)...(8106)
US-10-077-130-1

Query Match        94.9%;   Score 4940.4;   DB 14;   Length 8106;
Best Local Similarity  99.9%;   Pred. No. 0;
Matches 4944;  Conservative 0;  Mismatches 0;  Indels 6;  Gaps 0;

Qy    258  CCCAGGGCCCATCCATGCAGGTAACCATCAGGATGTGAGGACGCAGCAGGCCGGAAC  317
           ||||  ||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db   3116  CGCACGGCCCCATCCATGCAGGTAACCATCGAGGATGTGCAGCAGCAGGCCGGAAC  3175

Qy    318  GGCCCAATTGAGGCTATCATTGAGGGGACCACAGCCCTCGGTGACCTGGTACAAGGA  377
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3176  GGCCCAATTGAGGCTATCATTGAGGGGACCCACAGCCCTCGGTGACCTGGTACAAGGA  3235

Qy    378  CAGGGTCCAGCTGGTGGACAGCACCCGGCTTAGCAGCAGCAAGAGGCACCACCATACTC  437
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3236  CAGCGTCCAGCTGGTGGACAGCACCCGGCTTAGCAGCAGCAAGAGGCACCACCATACTC  3295

Qy    438  CCTGGTGCTGAGGCATGTGGCCTCGAAGGATGCCGGCGTTACACCTGCCTGGCCCAAAA  497
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3296  CCTGGTGCTGAGGCATGTGGCCTCGAAGGATGCCGGCGTTACACCTGCCTGGCCCAAAA  3355

Qy    498  CACTGGTGGCCAGGTGCTCTGCAAGGCAGAGCTGCTGGTGCTTGGGGGACAATGAGCC  557
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3356  CACTGGTGGCCAGGTGCTCTGCAAGGCAGAGCTGCTGGTGCTTGGGGGGACAATGAGCC  3415

Qy    558  GGACTCAGAGAAGCAAAGCACCGGAGAAGCTGCACTCCTTCTATGAGGTCAAGGAGGA  617
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3416  GGACTCAGAGAAGCAAAGCACCGGAGAAGCTGCACTCCTTCTATGAGGTCAAGGAGGA  3475

Qy    618  GATTGAAGGGCCGTGTTTGGCTTCGTAAAAGAGTGCAGCAACAAGAAACAAGATCTT  677
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3476  GATTGAAGGGCCGTGTTTGGCTTCGTAAAAGAGTGCAGCAACAAGAAACAAGATCTT  3535

Qy    678  GTGCCTGCCAAGTTCATCCCCTACGGAGCAGAACTGGGCCCAGGCATACAGGGAGGCG  737
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3536  GTGCCTGCCAAGTTCATCCCCTACGGAGCAGAACTCGGGCCCAGGCATACAGGGAGGCG  3595

Qy    738  AGACATCCTGCCGGCGTGTTTGGCTTCACGGCGTCTGACCAGTTTGAGAC  797
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3596  AGACATCCTGCCGGCGTGTTTGGCTTCACGGCGTCTGACCAGTTTGAGAC  3655

Qy    798  CCGAAGACCCTCATCCTCATCCTGGAGCTGTGCTCATCCGAGGAGCTGCTGGACCGCCT  857
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3656  CCGCAAGACCCTCATCCTCATCCTGGAGCTGTGCTCATCCGAGGAGCTGCTGGACCGCCT  3715

Qy    858  GTACAGGAAGGGCGTGGTGACGAGCGCCGAGGTCAAGGTCTCACATCCAGAGCTCGTGGA  917
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3716  GTACAGGAAGGGCGTGGTGACGAGCGCCGAGGTCAAGGTCTCACATCCAGAGCTCGTGGA  3775

Qy    918  GGGGGCTGCACTACCTGCACAGCCATGGCGTTCTCCACCTGGACATAAAGCCCTCTACAAT  977
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3776  GGGGGCTGCACTACCTGCACAGCCATGGCGTTCTCCACCTGGACATAAAGCCCTCTACAAT  3835

Qy    978  CCTGATGGTGCATCCTGCCCGGAAGACATTAAAATCTGCACTTTGCCCAGAA  1037
           |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3836  CCTGATGGTGCATCCTGCCCGGAAGACATTAAAATCTGCACTTTGCCCAGAA  3895

Qy   1038  CATCACCCCAGCAGAGCTGCAGTTGACCAGTACGGCTCCCCTGAGTTCGTCGTTCCCCCGA  1097
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3896  CATCACCCCAGCAGAGCTGCAGTTCAGCCAGTACGGCTCCGGTCCCCTGAGTTCGTCGTTCCCCCGA  3955

Qy   1098  GATCATCCAGCAGAACCCTGTGAGCGAAGCCTCCGACATTTGGGCCATGGGTGTCATCTC  1157
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3956  GATCATCCAGCAGAACCCTGTGAGCGAAGCCTCCGACATTTGGGCCATGGGTGTCATCTC  4015
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(left column — rotated)

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Qy   4443  CTCTGGGCCCGAGCTGCTCCCCTGCCTGGCCGAGAGAGGCCTCCTACTCAGAATCTGAGGT  4502
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Db   4707  CTCTGGGCCCGAGCTGCTCCCCTGCCTGGCCGAGAGAGGCCTCCTACTCAGAATCCGAGGT  4766

Qy   4503  GAAGGACTACCTGTGGCAGATGTTGAGTGCCACCCAGTACCTGCACAACCAGCACATCCT  4562
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4767  GAAGGACTACCTGTGGCAGATGTTGAGTGCCACCCAGTACCTGCACAACCAGCACATCCT  4826

Qy   4563  GCACCTGGACCTGAGGTCCGAGAACATGATCATCACCGAATACAACCTGCTCAAGGTCGT  4622
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4827  GCACCTGGACCTGAGGTCCGAGAACATGATCATCACCGAATACAACCTGCTCAAGGTCGT  4886

Qy   4623  GGACCTGGGCAATGCACAGAGACCTCAGCAGCAGAGAAGGTGCTGCCCTCAGACAGTTCAA  4682
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4887  GGACCTGGGCAATGCACAGAGACCTCAGCAGCAGAGAAGGTGCTGCCCTCAGACAGTTCAA  4946

Qy   4683  GGACTACCTAGAGACCATGGCTCCAGAGCTCCTGGAGGGCCAGGGGCTGTGTTCCACAGAC  4742
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4947  GGACTACCTAGAGACCATGGCTCCAGAGCTCCTGGAGGGCCAGGGGCTGTGTTCCACAGAC  5006

Qy   4743  AGACATCTGGGCCATCGGTGTGGACAGCCTTCATCATGCTGAGCGCGCGAGTACCCGGTGAG  4802
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5007  AGACATCTGGGCCATCGGTGTGGACAGCCTTCATCATGCTGAGCGCGCGAGTACCCGGTGAG  5066

Qy   4803  CAGCGAGGGTGCACGCGACCTGCAGAGAGGACTGGCCAAGGGGTGGTCCGGCTGAGCCG  4862
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5067  CAGCGAGGGTGCACGCGACCTGCAGAGAGGACTGGCCAAGGGGTGGTCCGGCTGAGCCG  5126

Qy   4863  CTGCTACGGCGGGGCGTGTCCGGGGCGCCGTGCGCTTCCTGCGCAGCACTCGTGTCGCCCA  4922
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5127  CTGCTACGGCGGGGCGTGTCCGGGGCGCCGTGCCTTTCCTGCGCAGCACTCGTGTGCGCCCA  5186

Qy   4923  GCCCTGGGGCGGCCGGCCCTGCCAGTCCCAGTCCCGTTGCTCAGTGGCTAACAGAGGAGGG  4982
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5187  GCCCTGGGGCGGCCGGCCCTGCCAGTCCCAGTCCCGTTGCTCAGTGGCTAACAGAGGAGGG  5246

Qy   4983  CCCGGCCTGTTCGCGGCCCGCCCGTGACCCTCCCTACCGCGCGGCGTCGGCGTCTTCGT  5042
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5247  CCCGGCCTGTTCGCGGCCCGCCCGTGACCTTCCCTACCGCGCGGCGTCGGCGTCTTCGT  5306

Qy   5043  GGCCAATCGCGAGAAGCGCGGCGCGCGGCACAACCTGGCCCAGGTGCG  5102
           ||||||||||||||||||||||||||||||||||||||||||||||||
Db   5307  GCGCAATCGCGAGAAGCGCGGCGCGCGGCACAACCTGGCCCAGGTGCG  5366

Qy   5103  CTGAGGGGTCGCGGCCGGCCCGCGCCACACCCCTTGGTCTCCCCGGTCGCTGCTGGAGCGCGGCA  5162
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5367  CTGAGGGGTCGCGGCCGGCCCGCGCCACACCCCTTGGTCTCCCCGGTCGCTGCTGACAGCGCGCCA  5426

Qy   5163  ATAAAAAACGCACAGCCGGGCGGGGAGAAAAA  5190
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Db   5427  ATAAAAAACCACAGCCCGGGCGGGGAGAAAA  5454
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RESULT 5
US-10-077-130-1

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; Sequence 1, Application US/10077130
; Publication No. US20020168742A1
; GENERAL INFORMATION:
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Acton, Susan L.
; TITLE OF INVENTION: 59079 and 12599, Protein Kinase Family
; TITLE OF INVENTION: Members and Uses Therefor
; FILE REFERENCE: MPI2001-047P1RCP1(M)
; CURRENT APPLICATION NUMBER: US/10/077,130
; CURRENT FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: 60/269201
; PRIOR FILING DATE: 2001-02-15
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSEQ for Windows Version 4.0
;
; SEQ ID NO 1
;  LENGTH: 8106
;  TYPE: DNA
;  ORGANISM: Homo sapiens
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[DNA sequence alignment — two blocks of query (Qy) and database (Db) sequences with match bars, numbered by position]

RESULT 6
US-10-077-130-4
; Sequence 4, Application US/10077130
; Publication No. US20020168742A1
; GENERAL INFORMATION:
; APPLICANT: Kapeller-Liebermann, Rosana
; APPLICANT: Acton, Susan L.
; TITLE OF INVENTION: 59079 and 12599, Protein Kinase Family
; TITLE OF INVENTION: Members and Uses Therefor
; FILE REFERENCE: MPI2001-047P1RCP1(M)
; CURRENT APPLICATION NUMBER: US/10/077,130
; CURRENT FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: 60/269201
; PRIOR FILING DATE: 2001-02-15
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 24120
; TYPE: DNA

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Qy   1158 CTACCTCAGCCTGCTCATCCCCATTTGCCGGCGAGAGTGACCGTGCCACCCTCCT 1217
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Db   4016 CTACCTCAGCCTGCTCATCCCCATTTGCCGGCGAGAGTGACCGTGCCACCCTCCT 4075

Qy   1218 GAACGTCTTGGAGGGCGCCGTGTCATGGAGCAGCCCATGCTGCCACCTCAGCGAAGA 1277
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4076 GAACGTCCTGGAGGGCGCCGTGTCATGGAGCAGCCCATGCTGCCACCTCAGCGAAGA 4135

Qy   1278 CGGCCAAAGACTTCATCAAGGCTACGCTGCAGAGAGCCCCTCAGGCCCGGCTAGTGCGGC 1337
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4136 CGGCCAAAGACTTCATCAAGGCTACGCTGCAGAGAGCCCCTCAGGCCCGGCTAGTGCGGC 4195

Qy   1338 CCAGTGCCTCTCCCACCCTGGTTCCTGAAATCCATGCCTGCGGAGGAGCCCACTTCAT 1397
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4196 CCAGTGCCTCTCCCACCCTGGTTCCTGAAATCCATGCCTGCGGAGGAGCCCACTTCAT 4255

Qy   1398 CAACACCAAGCAGTCAAGTTCCTCCTGGCCCGAAGTCGCTGGCAGCGTTCCTGATGAG 1457
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4256 CAACACCAAGCAGTCAAGTTCCTCCTGGCCCGAAGTCGCTGGCAGCGTTCCTGATGAG 4315

Qy   1458 CTACAAGTCCATCCTGGTGATCGGCTCCATCCTGAGCTCCTGGGGGCCCACCCGACAG 1517
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4316 CTACAAGTCCATCCTGGTGATCGGCTCCATCCTGAGCTCGTCGCGGGGCCCACCCGACAG 4375

Qy   1518 CCCCTCCCTCGGGGTAGCCCGGCACCCTGCAGGGACACTGGTGCCTCCTCCAGTTCCTC 1577
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4376 CCCCTCCCTCGGCGTAGCCCGGCACCCTGCAGGGACACTGGTGCCTCCTCCAGTTCCTC 4435

Qy   1578 CTCCTCCTGACAACGAGCTTCGCCCCATTTGCCCGGGCTAAGTCACTGCCACCCTCCCC 1637
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4436 CTCCTCCTGACAACGAGCTTCGCCCCATTTGCCCGGGCTAAGTCACTGCCACCCTCCCC 4495

Qy   1638 GGTGACACACTCCACCACTGCTGCACCCCCGGGGCTTCCTGCGGGCCTCGGCCCAGCCTGCC 1697
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Db   4496 GGTGACACACTCCACCACTGCTGCACCCCCGGGGCTTCCTGCGGGCCTCGGCCCAGCCTGCC 4555

Qy   1698 TGAGGAAGCCGAGGCCAGTGAGGCGCTTCCACCGGAGCGCTTCCGGCTCCGACGTCCCGA 1757
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Db   4556 TGAGGAAGCCGAGGCCAGTGAGGCGCTTCCACCGGAGCGCTTCCGGCTCCGACGTCCCGA 4615

Qy   1758 GGGTGCCGGGGCCACCGGGGCCACCGCCCAGGGTGGCTGCTCGGGCGCACAGCGTCATCGGGGCGCAGCCT 1817
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Db   4616 GGGTGCCGGGGCCACCGGGGCCACCGCCCAGGGTGGCTGCTCGGGCGCACAGCGTCATCCGGCAGCCT 4675

Qy   1818 GTTCTACCACCAGGCCGGGTGAGAGCCCTGAGCACGGCCCTGGCCCCGGGGGAGCAGGCG 1877
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4676 GTTCTACCACCAGGCCGGGTGAGAGCCCTGAGCACGGCCCTGGCCCCGGGGGAGCAGGCG 4735

Qy   1878 GCACCCGGCCCGGCCCGGCGCGGCCACCTGCACGGCTGGGCGCTACATTGCGGGGCGCTGCCAGG 1937
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4736 GCACCCGGCCCGGCCCGGCGCGGCCACCTGGCCGGCTGGGCGTACATTGCGGGGCGCTGCCAGG 4795

Qy   1938 CCTGGCGCAGCCCTCTGGCCCCTCATTGAGACTGCCCTCCGGGTGCTGGAGGAGGCGCGCAGGGAGGAGCA 1997
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4796 CCTGGCGCAGCCCACTGGCCCCTCATTGAGACTGCCCTCGGGTGCTGGAGGAGGCGCGCAGGGAGGAGCA 4855

Qy   1998 GGCCACCCTCTGGCCAAAGCCCCTCATTCGGACACTGCCCTCCGGACTCTCCGAGCACCCCCG 2057
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4856 GGCCACCCTCTGGCCAAAGCCCCTCATTCGGACACTGCCCTCCGGACTCTCCGAGCACCCCCG 4915

Qy   2058 CCCCTCCTCCGGGAGGCTTGGGCCCCTGCCACAGCAGCACCGCGCCTCCAGGGACTCTCCGGGGGGC 2117
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4916 CCCCTCCTCCGGGAGGCTTGGGCCCCTGCCACAGCAGCACCGCGCCTCCAGGGACACCCCGGGGGGC 4975

Qy   2118 CCCTATCAGGGACATGGGCACCCTGCCTGAGGCACACCCTCCAGGCTCCAACATGACTCTCCGGGGGC 2177
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4976 CCCTTCCTCCGGGACGCTGCCTGAGGCCACACCGTGAACTCTCCAGGCACCCCCCTCCGGGGGGC 5035

Qy   2178 CCCTATCAGGGACATGGGCACCCTGCCTGAGGCTCCAAGCAGCTTCCATCCACTGGTGGCCA 2237
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5036 CCCTATCAGGGACATGGGCACCCTGCCTGAGGCTCCAAGCAGCTTCCATCCACTGGTGGCCA 5095

Qy   2238 CCCAGGCACTGCTCAGCCAGAGAGGCCATCCCGGACCAGCCCTTGGGGGCAGCCAGCCCC 2297
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5096 CCCAGGCACTGCTCAGCCAGAGAGGCCATCCCGGACCAGCAGGGGGCAGCCAGCCCC 5155

Qy   2298 TTTCTGCCACCCCAAGCAGCAGGGTTCTGCCCCTCAGGAGGGCTGCGAGCCCACCCAGCAGT 2357
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5156 TTTCTGCCACCCCAAGCAGCAGGGTTCTGCCCCTCAGGAGGGCTGCGAGCCCACCCAGCAGT 5215

Qy   2358 TGCCCCATGCCCTCCTTCCTCCTGGCTCCTTCCCTGCCTCCCTGCCAAAGAGGCCCCTTAGTACC 2417
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5216 TGCCCCATGCCCTCCTTCCTGGCTCCTTCCCTGCCTCCCTGCCAAAGAGGCCCCTTAGTACC 5275

Qy   2418 CTCAAGCCCCTTCTTGGACAGCCCCAGGCACCCCTGCCCTGCCCTGCCAAAGCAAGCCCCCC 2477
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5276 CTCAAGCCCCTTCTTGGACAGCCCCAGGCACCCCTGCCCTGCCCTGCCAAAGCAAGCCCCCC 5335

Qy   2478 ATTGGACTCTAAGATGGGCCTGGAGACATCTCTCTTCCTGGGAGGCCAAAACCCGGCCC 2537
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5336 ATTGGACTCTAAGATGGGCCTGGAGACATCTCTTCCTGGGAGGCCAAAACCCGGCCC 5395

Qy   2538 CTGCAGTTCCCCAGGGTGGGCACAGAGCCTGCCCCTCCCCAGTGAGCTCCCTCAGGGT 2597
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5396 CTGCAGTTCCCCAGGGTCAGCCTCCCCCAGGGTGGGCACAGAGCCTGCCCCTCCCCAGTGAGCTCCCTCAGGGT 5455

Qy   2598 GGGCTCCTCCCAGTGTGGGCACAGAGCCTGCCCCTCCCTGGATGCGAGGGGCTGGACCCA 2657
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5456 GGGCTCCTCCCAGTGTGGGCACAGAGCCTGGCCCTGCGGATGCGGAGGGGCTGGACCCA 5515

Qy   2658 GGAGGCTGAGGATCTGTCCAGTCCGACTCCACACCACTTGCAGCGGCCTCAGGAACAGGTGAC 2717
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5516 GGAGGCTGAGGATCTGTCCAGTCGGACTCCACACCCACTTGCAGCGGCCTCAGGAACAGGTGAC 5575

Qy   2718 CATGGGCAAGTTCTCCCTGGTGTCGGGGGGTAGCAGCGTGGCTGGCTATGGCAC 2777
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5576 CATGGGCAAGTTCTCCCTGGTGGTTCGGCGGGGGTACGCAGCGGTGGCTGGCTATGGCAC 5635

Qy   2778 CTTTGCCTTTGGTGGAGATGCAGGGGGCATGCTGGGGCAGGGGCCCATGTGGGCCAGGAT 2837
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5636 CTTTGCCTTTGGTGGAGATGCAGGGGGCATGCTGGGGCAGGGGCCCATGTGGGCCAGGAT 5695

Qy   2838 AGCCTTGGGCTGTGTCCCAGTCGGCAGCGTCTGCGTCCCGGCACAGCGTCATCCGGGAGTCCCA 2897
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5696 AGCCTGGGCTGTGTCCCAGTCGGCAGCGTCTGCGTCCCGGCACAGCGTCATCCGGGAGTCCCA 5755

Qy   2898 GTCGGAGGAGCGAGCAGCAGGGGCCAGGGCCCACTGCCCCAGGTCAGTGCAAGGCC 2957
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5756 GTCGGAGGAGCGAGCAGCAGGGGCCAGGGCTCGAGAGCCCCACTGCCCCAGGTCAGTGCAAGGCC 5815

Qy   2958 TGTGCCTGAGGTGGCAGCAGGGCTCCACCGGAGCTCTTCCAGAGCCCACCCCATGGGAGGA 3017
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5816 TGTGCCTGAGGTGGCAGCAGGGCTCCACCGGGTCTCTTCCAGAGCCCACCCCATGGGAGGA 5875

Qy   3018 CACAATATCCCTGGACATTCCATTGAGACTGCCCTGGACGTCAGTTGATGCGGAGGCGGCCGA 3077
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5876 CACAATATCCCTGGACATTCCATTGAGACTGCCCTGGACGTGTCAGTTGATGCGGAGGCGGCCGA 5935

Qy   3078 CACCACTTGGGCCCTCGGCCAAAGCCCCTCATTCGGACACTGGCCCTTGAGACTGCGGAGGAGCA 3137
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5936 CACCACTTGGGCCCTCGGCCAAAGCCCCTCATTCGGACACTTTATGATCTTCAGGAAAGTCCCCAAGTCCGCTCA 5995

Qy   3138 CGATATCAAGTACCTCCATTGAGACTTCCGGCCCCCACGCAGCGGAGATCACAGAGGAGTCACGTA 3197
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5996 CGATATCAAGTACCTCCATTGAGTTTATGATCTTCAGGAAAGTCCCCAAGTCCGCTCA 6055

Qy   3198 GCCCTGGCCAGGTGAACTGGGCCCCCACGCAGCGGAGATCACAGAGGAGTCACGTG 3257
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6056 GCCCTGGCCAGGTGAACTGGGCCCCCACGCAGCGGAGGAGAGTCACGTG 6115

Qy   3258 TGTGACGCGCCTGCTGGCAGCGAGCCAAGTGGTCTCCGCGTC 3317
          ||||||||||||||||||||||||||||||||||||||||||
Db   6116 GCCCTTGGCCAGGTGAACTGGGCCCCCACGCAGCGGAGATCAGAGGA 6175

Qy   3318 TGTGACGCGCCTGCTGGCAGCGAGCCAAGTGGTCTCCGCGTC 3377
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;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: 5'UTR
;   LOCATION: (1)...(71)
;   NAME/KEY: CDS
;   LOCATION: (72)...(23978)
;   NAME/KEY: 3'UTR
;   LOCATION: (23979)...(24120)
US-10-077-130-4

Query Match        94.9%;  Score 4940.4;  DB 14;  Length 24120;
Best Local Similarity  99.9%;  Pred. No. 0;
Matches 4944;  Conservative  0;  Mismatches  6;  Indels  0;  Gaps  0;

Qy      258 CCCAGGGCCCCATCCATGCAGGTAACCATCGAGGATGTGCAGGCACAGCAGGCGGAAC 317
            ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db    19130 CGCACGGCCCCCATCCATGCAGGTAACCATCGAGGATGTGCAGGCACAGCAGGCGGAAC 19189

Qy      318 GGCCCAATTCGAGGTATCATTGAGGGCGACCCACAGCGCCTGGTGACCTGGTACAAGGA 377
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    19190 GGCCCAATTCGAGGTATCATTGAGGGCGACCCACAGCGCCTGGTGACCTGGTACAAGGA 19249

Qy      378 CAGCGTTCCAGCTGGTGGTGACAGCACCCGGCTTAGCCAGCAGCAAGAAGGCACCACATACTC 437
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    19250 CAGCGTTCCAGCTGGTGGTGACAGCACCCGGCTTAGCCAGCAGCAAGAAGGCACCACATACTC 19309

Qy      438 CCTGGTTGCTGAGGCATGTGGGCCTCGAAGGATGCCGGCGTTTACACCTGCCTGGCCCAAAA 497
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    19310 CCTGGTTGCTGAGGCATGTGGGCCTCGAAGGATGCCGGCGTTTACACCTGCCTGGCCCAAAA 19369

Qy      498 CACTGGTTGGCCAGGTGCTCTGCAAGGCAGAGCTGCTGGTGCTTGGGGGGGACAATGAGCC 557
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    19370 CACTGGTTGGCCAGGTGCTCTGCAAGGCAGAGCTGCTGGTGCTTGGGGGGGACAATGAGCC 19429

Qy      558 GGACTCAGAGAGCAAAGCCACCGGAGGAAGCTGCACCTCCTTCATGAGGTCAAGGAGGA 617
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    19430 GGACTCAGAGAGCAAAGCCACCGGAGGAAGCTGCACCTCCTTCATGAGGTCAAGGAGGA 19489

Qy      618 GATTGAAGGGGCGTGTTTGGCTTCGTAAAAAGAGTGCAGCACAAAAAGAAGATCTT 677
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    19490 GATTGAAGGGGCGTGTTTGGCTTCGTAAAAAGAGTGCAGCACAAAAAGAAACAAGATCTT 19549

Qy      678 GTGCGCTGCCAAGTTCATCCCCTACGGACGAGAACTCGGGCCCAGGCCATACAGGGAGCG 737
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    19550 GTGCGCTGCCAAGTTCATCCCCTACGGACGAGAACTCGGGCCCAGGCCATACAGGGAGCG 19609

Qy      738 AGACATCCTGGCCGCGCTGAGCCACCCGCTGGTCACGGGCTGCTCGGACCAGTTGAGAC 797
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    19610 AGACATCCTGGCCGCGCTGAGCCACCCGCTGGTCACGGGCTGCTCGGACCAGTTTGAGAC 19669

Qy      798 CCGCAAGACCCTCATCCTGCCCGGGAAGACATTAAAATCTGCGACTTTGGCTTTGGACCGGCT 857
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    19670 CCGCAAGACCCTCATCCTCATCCTGCCCGGGAAGACATTAAAATCTGCGACTTTGGCTTTGGACCGGCCT 19729

Qy      858 GTACAGGAAGGGCGTGGTGACAGAGCCGAGTTCAGGAGGTCAGGTCAGTCACAGCTGGTGA 917
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    19730 GTACAGGAAGGGCGTGGTGACAGAGCCGAGTTCAGGAGGTCAGGTCACAGCTGGTGA 19789

Qy      918 GGGGCTGCACTACCTGCACAGCCATGGCCATTCCTCCACCTGGACATAAAGCCCTCTAACAT 977
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    19790 GGGGCTGCACTACCTGCACAGCCATGGCCATTCCTCCACCTGGACATAAAGCCCTCTAACAT 19849

Qy      978 CCTGATGGTGCATCCTGCCCGGGAAGACATTAAAATCTGCGACTTTGGCTTTGCCCAGAA 1037
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    19850 CCTGATGGTGCATCCTGCCCGGGAAGACATTAAAATCTGCGACTTTGGCTTTGCCCAGAA 19909

Qy     1038 CATCACCCCAGCAGAGCTGCAGTTCAGCGCCAGTACGGCTCCCCTGAGTTCGTCTCCCCGA 1097
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    19910 CATCACCCCAGCAGAGCTGCAGTTCAGCGCCAGTACGGCTCCCCTGAGTTCGTCTCCCCGA 19969

Qy     1098 GATCATCCAGCAGAACCCTGTGAGCGGAAGCCTCCAGCATTTGGGCCATGGGTGTCATCTC 1157
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    19970 GATCATCCAGCAGAACCCTGTGAGCGGAAGCCTCCAGCATTTGGGCCATGGGTGTCATCTC 20029
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Qy     1158 CTACCTCAGCTGACCTGCTCATCCCCATTGCCGGCGGAGAGTGACCGTGCCACCCTCCT 1217
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    20030 CTACCTCAGCTGACCTGCTCATCCCCATTGCCGGCGGAGAGTGACCGTGCCACCCTCCT 20089

Qy     1218 GAACGTCCTGGAGGGCGCGTGTCATGGAGCAGCCCATGGCTGTGCCCACCTCAGCGAAGA 1277
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    20090 GAACGTCCTGGAGGGCGCGTGTCATGGAGCAGCCCATGGCTGTGCCCACCTCAGCGAAGA 20149

Qy     1278 CGCCAAAGACTTCATCAAGGCTACGCTCGAGAGAGCCCCTCAGCCCCGCCTAGTGCGGC 1337
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    20150 CGCCAAAGACTTCATCAAGGCTACGCTGCAGAGAGCCCCTCAGCCCCGCCTAGTGCGGC 20209

Qy     1338 CCAGTGCCTCTCCCACCCTGGTTCCTGAAATCATGCTGCCGCGGAGGAGGCCCACTTCAT 1397
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    20210 CCAGTGCCTCTCCCACCCTGGTTCCTGAAATCATGCTGCCGCGGAGGAGGCCCACTTCAT 20269

Qy     1398 CAACACCAAGCAGCTCAAGTTCCTCCTGGCCCGAAGTGCTGGCAGCGTTCCCTGATGAG 1457
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    20270 CAACACCAAGCAGCTCAAGTTCCTCCTGGCCCGAAGTGCTGGCAGCGTTCCCTGATGAG 20329

Qy     1458 CTACAAGTCCATCCTGGTGATGCGGCTCCATCCCTGAGTGCTGCGGGGCCCACCCGACAG 1517
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    20330 CTACAAGTCCATCCTGGTGATGCGGCTCCATCCCTGAGTGCTGCGGGGCCCACCCGACAG 20389

Qy     1518 CCCCTCCCTCGGGCGTAGCCCGGCACCTGCAGGGACACTGGTTGGCTCCTCCAGTTCCTC 1577
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    20390 CCCCTCCCTCGGGCGTAGCCCGGCACCTGCAGGGACACTGGTTGGCTCCTCCAGTTCCTC 20449

Qy     1578 CTCCTCCTCTGACAACGAGCTCGCCCATTGCCGGGGTAAGTCACTCCCACCCTCCCC 1637
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    20450 CTCCTCCTCTGACAACGAGCTCGCCCATTGCCGGGGTAAGTCACTGCCACCCCTCCCC 20509

Qy     1638 GGTGACACATTCACCACTGCTGCACCCCCGGGGTTCCTGCGGCCCTCGGCCAGCCTGCC 1697
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    20510 GGTGACACACTCACCACTGCTGCACCCCCGGGGTTCCTGCGGCCCTCGGCCAGCCTGCC 20569

Qy     1698 TGAGGAAGCCAGTGCGCCGCCACCGGGCGCTCACCGAGCCCCAGCTCGCTCGATCTCCCGA 1757
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    20570 TGAGGAAGCCAGTGCGCCGCCACCGGGCGCTCACCGAGCCCCAGCTCGCTCGATCTCCCGA 20629

Qy     1758 GGGTGCCGGGCCACCCGGGTGCGTGCCCCAGGGCTGCTGCCCCCGGGGAGCAGGCTCAGCCT 1817
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    20630 GGGTGCGCGGGCCACCCGGGTGCGTGCCCCAGGGCTGCTGCCCCACAGCGTCATCCGCAGCCT 20689

Qy     1818 GTTCTTACCACCAGGGCGGTGAGACGCCCTGGCTCGACGGGCCCTGGCCCCGGAGCAGGCG 1877
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    20690 GTTCTTACCACCAGGGCGGTGAGACGCCCTGGCTCGACGGGCCCTGGCCCCGGAGCAGGCG 20749

Qy     1878 GCACCCGGCCGCCGGGCGCGGCGGCACCTGCTGAAGGGCGGCTACAATTGCGGGGGCGCTGCCAGG 1937
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    20750 GCACCCGGCCGCCGGGCGCGGCGGCACCTGCTGAAGGGCGGGTACATTGCGGGGGCGCTGCCAGG 20809

Qy     1938 CCTGGGCGAGCCACTGATGAGCCCTGGCTCGACTCGGGCCGCCAGGGAGGAGCA 1997
            |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    20810 CCTGCGGCGAGCCACTGATGAGCCACTGAGACCGCCGCTCGGGCCGCCAGGGAGGAGCA 20869

Qy     1998 GGCCACCCTCCTGGCCAAAGCCCCCTCATTCGAGACTGCCTTCCGGCTGCTCCCTCTGG 2057
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    20870 GGCCACCCTCCTGGCCAAAGCCCCCTCATTCGAGACTGCCTTCCGGCTGCTCCCTCTGG 20929

Qy     2058 CACCCACTTGGCCCCTGGCCACAGCCACTCCTGGAACATGACTCCCGAGCACCCCCG 2117
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    20930 CACCCACTTGGCCCCTGGCCACAGCCACTCCTGGAACATGACTCTCCGAGCACCCCCCG 20989

Qy     2118 CCCCTCCTCGGAGGCTGCGGTGAGGCACAGCCTTCAGCCCCCTCCCCGA 2177
            |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    20990 CCCCTCCTCGGAGGCTGCGGTGAGGCACAGCCTTCAGCCCCCTCCCCGGGGGGC 21049

Qy     2178 CCCTATCAGGGACATGGGCACCCTCCAAGCAGCTTCCATCCACTGGTGCCA 2237
            ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    21050 CCCTATCAGGGACATGGGCACCCTCCAAGCAGCTTCCATCCACTGGTGCCA 21109
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Right panel:

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Db  22190  TGTGGACGCGCTGGTGCTGGCAGAGGTGCTGCCGTGGGCAGGCAGGCGCAAGTGGTCCTCCGCCGTC  22249
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   3378  ACGCAGCCTCCACTTCCCTGGGAGGCACTGCGCCGCTGGATGAGCGCTGCGAGAGCTGGG          3437
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Db  22250  ACGCAGCCCTCTTCCACTTCCCTGGGAGGCACTCGCCGTGCCGTGGATGAGCTGCAGAGCTGGG      22309
           |||||||||||||||||||||||||||||||||||||||||||||||||
Qy   3438  GCTGCGTGAGAGAGTGAAGCGCTCCGTGGAGCACATCTCCCGGATCCTGAGGGCGAGGCC          3497
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  22310  GCTGCCTGCAGAGAGTGAAGCGCTCCGTGGACACATCTCCCGGATCCTGAAGGGCAGGCC          22369
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   3498  GGAAGGTCTGGAGAAGGAGGGGCCCCCAGGAGAAGGCAGGCCCAAAGCAAGCCCCC              3557
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  22370  GGAAGGTCTGGAGAAGGAGGGGCCCCCAGGAGAAGAGCCAGGCCCTTGCTTCCTTCCGGCT         22429
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   3558  CTCAGGTCTGAAGAGCTGGGACCGGAGGGCCGAGCGGCCAACATTCCTAAGGAGGCTCTCAGATGAGAC 3617
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  22430  CTCAGTCTCAAGAAGCTGGGACCGGAGGGCCGACATTCCTAAGGAGGCTCTCAGATGAGAC        22489
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   3618  TGTGGTCCTGGGCCAGTCAGTGACACTGGCCTCCAGTGTCAGCCAGTCAGCTGCCCA            3677
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  22490  TGTGTCCTGGGGCCAGTCAGTGACACTGGCCTGCCCAGTGTCAGCCAGTCAGCTGCCCA          22549
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Qy   3678  GGCCACCTGGAGCAAAGACGAGCGCCCCTGAGAGCAGCAGCAGCCGTGTCCTCATCTCTGC        3737
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  22550  GGCCACCTGGAGCAAAGACGAGCGCCCCTGAGAGCAGCAGCAGCCGTGTCCTCATCTCTGC        22609
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   3738  CACCCTCAAGAACTTCCAGCTTCTGACCATCCTGGTGGTGGCTGAGGACCTGGGTGT            3797
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  22610  CACCCTCAAGAACTTCCAGCTTCTGACCATCCTGGTGGTGGCTGAGGACCTGGGTGT            22669
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   3798  GTACACCTGCAGCGTGAGGCAATGCGCTGGGACAGTGACCACCACGGGCGTCCTCCGGAA         3857
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  22670  GTACACCTGCAGCGTGAGGCAATGCGCTGGGACAGTGACCACCACGGGCGTCCTCCGGAA         22729
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   3858  GGCAGAGCGCCCTCATCTTCGCCACACTTCCGCGAGGTGTACGCGGATGGGGT                3917
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Db  22730  GGCAGAGCGCCCTCATCTTCGCCATGCCCGATATCGGGGAGGTGTACGCGGATGGGGT          22789
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Qy   3918  GCTGCTGGTCTGGAAGCCCGTGAATCCTGTGACCTTGTGACCTACCATTGTGCAGTGCAGT        3977
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Db  22790  GCTGCTGGTCTGGAAGCCCGTGAATCCTGTGACCTACCATTGTGCAGTGCAG                22849
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Qy   3978  CCTAGAAGCGCAGCTGACCACACATCTTTGACTGCTGCTACCTGAC                      4037
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  22850  CCTAGAAGCGCAGCTGACCACACATCTTTGACTGCTGCTACCTGAC                      22909
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4038  CAGCAAGCTCTCCCGGGTGCGCACCTACACACCTTCCGCACGGCATGTGTCAGCAAGGCAGG       4097
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  22910  CAGCAAGTCTCCCGGGTGCGCACCTACACACCTTCCGCACGGCATGTGTCAGCAAGGCAGG        22969
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4098  AATGGGTCCCTACAGCAGCCCCTCCGGAGCAAGTCCTCCTGGGAGGGCCCACCTGGC            4157
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Qy   4158  CTCTGAGGAGGAGCCAGGCCAGGGGGTCAGCACCCCTGCCAGCACAAAGACCTTCGC            4217
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Db  23030  CTCTGAGGAGGAGCCAGGCGCGGTCAGCACCCCTGCCCAGCACAACAAAGACCTTCGC          23089
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Qy   4218  ATTCCAGACACAGATCCAGAGGCCGCTTCAGCGGTGGTGCGGCAATGCTGGGGAAGGC           4277
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  23090  ATTCCAGACACAGATCCAGAGGCCGTTCAGCGGTGGTGCGGCAATGCTGGGGAAGAGGC         23149
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4278  CAGCGGCGGCGGGCCGCTGGAGATCATCCCCTAAGGACTCATCCCCTAACCCCTACCACCCCAAGGACAGCAGT 4337
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  23150  CAGCGGCGGGGGGCCGCTGGAGATCATCCCCTAAGGACTCATCCCCTAACCCCTACCACCCCAAGGACAAGACAGCAGT 23209
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4338  GCTGCGCGAATACGAGCCCTCAAGGCCTGCCACCTGGCTGCACGC                       4397
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  23210  GCTGCGCGAATACGAGGGCCCTCAAGGGCCTGCCACCTGGCTGCACGC                     23269
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4398  AGCCTACCTCAGCCCCGGCACCTGGTGCTCATCTTGGAGTCTTGTCTCTGGGCCCGAGCT          4457
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Left panel:

```
Qy   2238  CCCAGGCACTGCTCAGCCAGAGAGGCCATCCCCGGACAGCCCTTGGGGCAGCCAGCCC            2297
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  21110  CCCAGGCACTGCTCAGCCAGAGAGGCCATCCCCGGACAGCCCTTGGGGCAGCCAGCCC            21169
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   2298  TTTCTGCCACCCCAAAGCAGAGGTTCTGCCCCCCAGAGAGGGCTGCAGCCCCCACCCAGCAGT       2357
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Db  21170  TTTCTGCCACCCCAAGCAGAGGGTTCTGCCCCCCAGAGAGGGCTGCAGCCCCCACCCAGCAGT       21229
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   2358  TGCCCCATGCCCTCCTGCTCCTCCCTCCAGATCTTGCAAAGAGGGCCCCTTAGTACC            2417
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Db  21230  TGCCCATGCCCTCTCCTGGCTCCTTCCCTCCAGATCTTGCAAAGAGGGCCCCTTAGTACC         21289
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   2418  CTCAAGCCCCTTCTTGGGACAAGCCCCAGGCACCCCCTGCCCCTGCCAAAGCAAGCCCCCC        2477
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  21290  CTCAAGCCCCTTCTTGGGACAGCCCCAGGCACCCCCTGCCCCTGCCAAAGCAAGCCCCCC         21349
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   2478  ATTGGACTCTAAGACATGGGGCCTGGAGACATCTCTCCTGGGAGGCAAAACCCGGCCC           2537
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  21350  ATTGGACTCTAAGACATGGGGCCTGGAGACATCTCTCCTGGGAGGCAAAACCCGGCCC           21409
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   2538  CTGCAGTTCCCCAGGGTCAGCCTCCCAGGCCGAGCTCTTCCCAAGTGAGCTCCCTCAGGGT        2597
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  21410  CTGCAGTTCCCCAGGGTCAGCCTCCCAGGCCGAGCTCTTCCCAAGTGAGCTCCCTCAGGGT        21469
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   2598  GGGCTCCTCCCAGGTGGGCACAGAGCCTGGCCCCTGGATGCGGAGGGCTGGACCCA            2657
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  21470  GGGCTCCTCCCAGGTGGGCACAGAGCCTGGCCCCTGGATGCGGAGGGCTGGACCCA            21529
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   2658  GGAGGCTGAGATCTGTCCGACTCCACACCCACCTTGCAGCGGCCTCAGGAACAGGTGAC         2717
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Db  21530  GGAGGCTGAGGATCTGTCCGACTCCACACCCACCTTGCAGCGGCCTCAGGAACAGGCGAC         21589
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   2718  CATGCGCAAGTCTCTCCCTGGGTGGTCGCGGGGCGTGGCTGGCTGTATGGCAC                2777
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  21590  CATGCGCAAGTCTCTCCCTGGGTGGTCGCGGGGCGTGGCTGGCTGTATGGCAC                21649
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   2778  CTTTGCCTTGGTGGAGATGCAGGGGCATGCTGGGGCAGGGGCCATGTGGGCCAGGAT           2837
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  21650  CTTTGCCTTTGGTGGAGATGCAGGGGCATGCTGGGGCAGGGGCCATGTGGGCCAGGAT          21709
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   2838  AGCCTGGGCTGTGTCCCAGTCGGAGAGGGAGCAGGAGGAGGAGGAGGCCAGGGCTGAGTCCCA       2897
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  21710  AGCCTGGGCTGTGTCCCAGTCGGAGAGGGAGCAGGAGGAGGAGGAGGCCAGGGCTGAGTCCCA       21769
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   2898  GTCGGAGAGCAGCAGCAGGAGGGCTCCCACGCTGAGAGCCCACTGCCCCAGGTCAGTGCAAGGCC     2957
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  21770  GTCGGAGAGGCGGCAGCAGGAGGGCTCCCACGCTGCCCCAGGTCAGTGCAAGGCC            21829
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   2958  TGTGCCTGAGGTTCGGCAGGGGCTCCCCACCAGGAGCTCTCCAGAGCCCACCCATGGGAGGA        3017
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Db  21830  TGTGCCTGAGGTTCGGCAGGGGCTCCCACCAGGAGCTCTCCAGAGCCCACCCATGGGAGGA         21889
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Qy   3018  CATCGGCAGGTCTCCCGGTGCAGATCCGGGACCTGTCAGGTGATGCGGAGGCGGCCGA           3077
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Db  21890  CATCGGCAGGTCTCCCATTGGCAGATCCGGGACCTGTCAGGTGATGCGGAGGCGGCCGA          21949
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   3078  CACAAATATCCCTGGACATTTCCGAGGTGACATCCCGGCCTACCTCAAACCTCTCAGACCTGTA      3137
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Db  21950  CACAATAATCCCTGGACATTTCCGAGGTGACCCGCCCTACCTCAACCTCTCAGACCTGTA        22009
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   3138  CGATATCAAGTACCTTCCCATTCGAGGTTTATGATCTTCAGGAAAGTCCCCAAGTCCGCTCA       3197
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  22010  CGATATCAAGTACCTCCCATTCGAGTTTATGATCTTCAGGAAAGTCCCCAAGTCCGCTCA        22069
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Qy   3198  GCCAGAGCCGCCCTTCGAGAGCTGGGGCGAGAGTCGGCACGTTCCCGGAGCCCACGTG           3257
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  22070  GCCAGAGCCGCCCTTCGAGGGGCTGGGGCGGAGCGGCGGTCCCGGAGCCCCACGTG            22129
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   3258  GCCCTGCCAGTGAACTGGGCCCCCACCAGGCCCCGCAGGGGCTGGATCACAGAGGAGTCAGAGGA    3317
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  22130  GCCCTGCCAGTGAACTGGGCCCCCACCAGGCCCCGCGCTGGATCACAGAGGAGTCAGAGGA        22189
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   3318  TGTGGACGCGCTGCTGGCAGAGGCTGCCGTGGGCAGGGAAGCGCAAGTGCTTCCTGCCGTC         3377
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; SEQ ID NO 3
; LENGTH: 5007
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (97)...(4926)
US-10-307-019-3

Query Match             94.4%;  Score 4915.8;  DB 15;  Length 5007;
Best Local Similarity   99.9%;  Pred. No. 0;
Matches 4920;  Conservative  0;  Mismatches  0;  Indels  7;  Gaps  0;

Qy    258 CCCAGGGCCCCATCCATGCAGTAACCATGGATGTGCAGCACAGACAGGCGGAAC 317
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     81 CGCACGGCCCCATCCATGCAGTAACCATGGATGTGCAGCACAGACAGGCGGAAC 140

Qy    318 GGCCCAATTCGAGGCTATCATTGAGGGGACCCAGCCCTCGGTGACCTGGTACAGGA 377
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    141 GGCCCAATTCGAGGCTATCATTGAGGGGACCCAGCCCTCGGTGACCTGGTACAGGA 200

Qy    378 CAGCGTCCAGCTGGTGGGACAGCACCCGGCTTAGCCAGCAAGAAGGCACCACATACTC 437
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    201 CAGCGTCCAGCTGGTGGGACAGCACCCGGCTTAGCCAGCAAGAAGGCACCACATACTC 260

Qy    438 CCTGTGTCTGAGGCATGTGCCTCGAAGGATGCGGGCTTTACACCTGCCTGCCCAAAA 497
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    261 CCTGTGTCTGAGGCATGTGCCTCGAAGGATGCGGGCTTTACACCTGCCTGCCCAAAA 320

Qy    498 CACTGGTGGCCAGTGCTCTGCAAGGCAGAGTGCTGTGCTTGTGGGGGACAATGAGCC 557
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    321 CACTGGTGGCCAGTGCTCTGCAAGGCAGAGTGCTGTGCTTGTGGGGGACAATGAGCC 380

Qy    558 GGACTCAGAGAAGCAAAGCCACCGGAGAAGCTGCACTCCTTCTATGAGGTCAAGGAGGA 617
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    381 GGACTCAGAGAAGCAAAGCCACCGGAGAAGCTGCACTCCTTCTATGAGGTCAAGGAGGA 440

Qy    618 GATTGGAAGGGGCGTGTTTGGCTTCGTAAAAAGAGTGCAGCACAAAGGAAACAAGATCTT 677
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    441 GATTGGAAGGGGCGTGTTTGGCTTCGTAAAAAGAGTGCAGCACAAAGGAAACAAGATCTT 500

Qy    678 GTGGCTGCCAAGTTCATCCCGCTACGGAGCAACTCGGGGCCATACAGGGAGCG 737
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    501 GTGGCTGCCAAGTTCATCCCGCTACGGAGCAACTCGGGGCCATACAGGGAGCG 560

Qy    738 AGACATCCTGGCCCGCTGAGCCACCCGGTCACGGGGCTGCTGACCAGTTTGAGAC 797
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    561 AGACATCCTGGCCCGCTGAGCCACCCGGTCACGGGGCTGCTGACCAGTTTGAGAC 620

Qy    798 CCGCAAGACCCTCATCCTCATCCTGAGCTGTGCTCATCCGAGGAGCTGCTGGACCCGCCT 857
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    621 CCGCAAGACCCTCATCCTCATCCTGAGCTGTGCTCATCCGAGGAGCTGCTGGACCCGCCT 680

Qy    858 GTACAGGAAGGGGCTGGTGACGGAGGCCGAGGTCAAGGTCACATCCAGCAGCTGGTGGA 917
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    681 GTACAGGAAGGGGCTGGTGACGGAGGCCGAGGTCAAGGTCACATCCAGCAGCTGGTGGA 740

Qy    918 GGGGCTGCACTACCTGCACAGCCGGAAGACATTAAAATCTGGACTTTGGCTTTGCCCAGAA 977
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    741 GGGGCTGCACTACCTGCACAGCCGGAAGACATTAAAATCTGGACTTTGGCTTTGCCCAGAA 800

Qy    978 CCTGATGGTGCATCCTGCCCGGGAAGACATTAAAATCTGCGACTTTGGCTTTGCCCAGAA 1037
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Db    801 CCTGATGGTGCATCCTGCCCGGGAAGACATTAAAATCTGCGACTTTGGCTTTGCCCAGAA 860

Qy   1038 CATCACCCCAGCAGAGCTGCAGTTCAGCCAGTACGGCTCCCCTGAGTTCGTCTCCCCCGA 1097
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    861 CATCACCCCAGCAGAGCTGCAGTTCAGCCAGTACGGCTCCCCTGAGTTCGTCTCCCCCGA 920

Qy   1098 GATCATCCAGCAGAACCCTGTGAGCGAAGCCTCCGACATTTGGGCATGGGTGTCATCTC 1157
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    921 GATCATCCAGCAGAACCCTGTGAGCGAAGCCTCCGACATTTGGGCATGGGTGTCATCTC 980
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Db  23270 AGCCTACCTCAGCCCCCGGCACCTGTGTCTCATCTTGGAGCTGTCTGGGCCGGAGCT 23329
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Qy   4458 GCTCCCTGCTGGCCAGGAGGGGCCTCCTACTCACTGAGGTGAAGGACTACCTGTG 4517
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  23330 GCTCCCTGCCTGGCCGAGAGGGGCCTCCTACTCACTGAGAATCCGAGAATCCGAGGACTACCTGTG 23389

Qy   4518 GCAGATGTTGAGTGGCCACCCAGTACCTGCACAACCAGCACATCCTGCACCTGGACCTGAG 4577
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Db  23390 GCAGATGTTGAGTGGCCACCCAGTACCTGCACAACCAGCACATCCTGCACCTGGACCTGAG 23449

Qy   4578 GTCCGAGAACATGATCATCACCGAATACAACCTGCTCAAGGTCGTGGACCTGGGCAATGC 4637
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Db  23450 GTCCGAGAACATGATCATCACCGAATACAACCTGCTCAAGGTCGTGGACCTGGGCAATGC 23509

Qy   4638 ACAGAGCCTCAGCCAGGAGAGGTGCTGCCCTCAGACAAGTTCAAGGACTACCTAGAGAC 4697
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  23510 ACAGAGCCTCAGCCAGGAGGAAGGTGCTGCCCTCAGACAAGTTCAAGGACTACCTAGAGAC 23569

Qy   4698 CATGGCTCCAGAGTCCTGAGGGGCCAGGGGCGTCGTTCCACAGCACAGACATCTGGGCCAT 4757
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  23570 CATGGCTCCAGAGTCCTGAGGGGCCAGGGGCGTGTTCCACAGCACAGACATCTGGGCCAT 23629

Qy   4758 CGGTGTGACAGCCTTCATCATGCTGAGCGGCGAGTACCCGGTGAGCAGCAGGGTGCACG 4817
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  23630 CGGTGTGACAGCCTTCATCATGCTGAGCGGCGAGTACCCGGTGAGCAGCAGGGTGCACG 23689

Qy   4818 CGACCTGCAGAGAGACTGCGCAAGGGGCTGGTCCGGCTGACCGGCGTGCTACGCGGGGCT 4877
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Db  23690 CGACCTGCAGAGAGACTGCGCAAGGGGCTGGTCCGGCTGACCGGCGTGCTACGCGGGGCT 23749

Qy   4878 GTCCGGGGCGCCGTGGCCTTCCTGCGCACTCTGTCGCCCCAGCCCTGGGGCCCGGCC 4937
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Qy   4938 CTGGCCGTCCAGCTGCCTGCCAGTGCCGGTGGCTAACAGAGGAGGGGCCCGGCCTGTTCGCG 4997
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Db  23810 CTGGCCGTCCAGCTGCCTGCCAGTGCCGGTGGCTAACAGAGGAGGGGCCCGGCCTGTTCGCG 23869

Qy   4998 GCCCGGCCCGCTGACCTTCCCTACCGCGGGTTCGTGCGGCAATCGCGAGAA 5057
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Db  23870 GCCCGGCCCGCTGACCTTCCCTACCGCGGGTTCGTGCGGCAATCGCGAGAA 23929

Qy   5058 GAGACCGCGCGCTGCTGTACAAGAGCACAACCTGGCGTGACGGGTGCGTGAGGGTGCCCCG 5117
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Db  23930 GAGACCGCGCGCTGCTGTACAAGAGCACAACCTGGCGTGACGGGTGCGTGAGGGTGCCCCG 23989

Qy   5118 GCCACACCCTTGGTCTCCCCGCTGGGGTCGCTGCAGACGCGCCAATAAAAACGCACAGC 5177
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Db  23990 GCCACACCCTTGGTCTCCCCGCTGGGGTCGCTGCAGACGCGCCAATAAAAACGCCCCAGC 24049

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Db  24050 CGGGGCGAGAAAAAAAAAAAAAAAAAAAAAAAAA 24079
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RESULT 7
US-10-307-019-3
; Sequence 3, Application US/10307019
; Publication No. US20030108533A1
; GENERAL INFORMATION:
; APPLICANT: Zeng, Wenlin
; APPLICANT: Stanton, Lawrence
; APPLICANT: SCIOS, INC.
; TITLE OF INVENTION: MEDIATORS OF SIGNAL TRANSDUCTION
; FILE REFERENCE: SCIOS.021DV1
; CURRENT APPLICATION NUMBER: US/10/307,019
; CURRENT FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: 09/548,473
; PRIOR FILING DATE: 2000-04-13
; PRIOR APPLICATION NUMBER: 60/129,552
; PRIOR FILING DATE: 1999-04-16
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSEQ for Windows Version 4.0

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Db 1221 CAACACCAAGCAGCTCAAGTTCCTCTGGCCGCAGTCGCTGGCAGCGTCCCTGATGAG 1280

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Db 1341 CTCCTCCTCTGACAACGAGCTCGCCGGCACTTGCCCCGGGCCTAAGTCACTGCCACCTCCCC 1400

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Db 1461 GGTGACACACTCACCACTGCTGCACCCCGGGCCTTCCTGCGGCCCTCGGCCAGCCTGCC 1520

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Db 1701 GCACCCGGCCGGCGCGGCCGCCGGGCCACCTGCGTCTGAAGGGCGGCGCGTTGCCAGG 1760

Qy 1938 CCTGCGGCGAGCCACTGATGAGCACCGCGTGCTGGAGGAGGCCGCCAGGGAGGAGCA 1997
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Qy 1998 GGCCACCCTCTGGCCAAAGCCCCTCATTCGAGACTGCCCTCCCGGCTGCCTCTG 2057
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Db 1821 GGCCACCCTCTGGCCAAAGCCCCTCATTCGAGACTGCCCTCCCGGCTGCCTCTG 1880

Qy 2058 CACCCACTTGGCCCTCGGCCACAGCACTCCCTGGAACATGACTCTCCGAGCACCCCCC 2117
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1881 CACCCACTTGGCCCTCGGCCACAGCACTCCCTGGAACATGACTCTCCGAGCACCCCCG 1940

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Db 1941 CCCCTCCTCGGAGGCCTTGCGGTGAGGCACAGCGACTGCCTTCAGCCCCTCCCGGGGGGC 2000

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Db 2001 CCCTATCAGGGACATGGGCCACCCTCAGGGCTCCAAGCAGCTTCCATCCACTGGTTGGCCA 2060

Qy 2238 CCCAGGCACTGCTCAGCCAGAGAGGCCATCCCCGGACAGCCCTTGGGGGCAGCCCCC 2297
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Db 2061 CCCAGGCACTGCTCAGCCAGAGAGGCCATCCCCGGACAGCCCTTGGGGGCAGCCCCC 2120

Qy 2298 TTTCTGCCACCCAAGCAGAGGTTCTGCGCCACCCCATTGGCTGCAGCCCTCAGCCAGCAGT 2357
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Db 2121 TTTCTGCCACCCAAGCAGAGGTTCTGCGCCACCCCATTGGCTGCAGCCCTCAGCCAGCAGT 2180

Qy 2358 TGCCCCATGCCCTCTCCTGCTCTTCCTCCTCCTCCAGATCTTGCAAAGAGGCCCCTTAGTACC 2417
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Db 2181 TGCCCCATGCCCTCTCCTGCTCTTCCTCCTCCTCCAGATCTTGCAAAGAGGCCCCTTAGTACC 2240

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Db 2241 CTCAAGCCCCTTCTTGGGACAGCCCAGGCACCCCTGCCCCCTGCCAAAGCAAGCAGCCCCCC 2300

Qy 2478 ATTGGACTCTAAGATGGGGCCTGGAGACATCTCTCTCCTCCTGGGAGACGCAAAACCCGGCCC 2537
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2301 ATTGGACTCTAAGATGGGGCCTGGAGACATCTCTCTCCTCCTGGGAGACGCAAAACCCGGCCC 2360

Qy 2538 CTGCAGTTCCCCAGGGTCAGCTCCCCAGAGCCTTGGCCCCTCCTGGATGCGAGCGGCCTGGACCCA 2597
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2361 CTGCAGTTCCCCAGGGTCAGCTCCCCAGAGCCTTGGCCCCTCCTGGATGCGAGCGGCCTGGACCCA 2420

Qy 2598 GGGCTCCTCCCAGGTGGGCACAGAGCCTTGGCCCCTCGGGGGGCTACGGGGGCTGGCTATGGCAC 2657
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Db 2421 GGGCTCCTCCCAGGTGGGCACAGAGCCTTGGCCCCTCGGGGGGCTACGGGGGCTGGCTATGGCAC 2480

Qy 2658 GGAGGCTGAGGATCTGTCCGACTTCCACACCCACCCCGTGTCGGGGGGCTACGGGGGCTGGCTATGGCAC 2717
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Db 2481 GGAGGCTGAGGATCTGTCCGACTTCCACACCCACCCCGTGTCGGGGGGCTACGGGGGCTTATGGCAC 2540

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Db 2541 CATGCGCAAGTTCTCCCTGGTGTCGGGGGGCTTCGTGCGGGCTCCAGGAGCTCCACCAGGAGCTCTCCAGAGCGAGGA 2600

Qy 2778 CTTTGCCTTTGGTGGAGATGCAGGGGGCATGCTGGGCAGGGGCCAGGGGCAGGGGCTGAGTGTCCCA 2837
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Db 2601 CTTTGCCTTTGGTGGAGATGCAGGGGGCATGCTGGGCAGGGGCCAGGGGCAGGGGCTGAGTGTCCCA 2660

Qy 2838 AGCCTGGGCGTGTGTCCCAGTCAGAGGAGGAGCAGGAGGAGGAGCAGGAGGACCTGAGTCCA 2897
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2661 AGCCTGGGCGTGTGTCCCAGTCAGAGGAGGAGCAGGAGGAGGAGCAGGAGGACGGCTGAGTCCA 2720

Qy 2898 GTCCGGAGGAGCAGCAGCCCTGAGCACGGGCTGAGAGCCCACTGCCCCCAGTGCCCCCCGAGGCC 2957
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Db 2721 GTCCGGAGGAGCAGCAGCCCTGAGCACGGGCTGAGAGCCCACTGCCCCCAGTGCCCCCCGAGGCC 2780

Qy 2958 TGTGCCTGAGGTCGGCAGGCTCTCCACCAGGAGCTCTCCAGAGCCCATGGGAGGA 3017
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Db 2781 TGTGCCTGAGGTCGGCAGGCTCTCCACCAGGAGCTCTCCAGAGCCCATGGGAGGA 2840

Qy 3018 CATCGGGCAGGTCTCCCTGGTGCAGATCCGGGACCTGTGAGGTGATGCGGAGGCGGCCGA 3077
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Db 2841 CATCGGGCAGGTCTCCCTGGTGCAGATCCGGGACCTGTGTCAGGTGATGCGGAGGCGGCCGA 2900

Qy 3078 CACAATATCCCTGGACATTCCGAGGTGGACCCCGCCGCGCTACCTCAACCTTCAGACCTGTA 3137
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Db 2901 CACAATATCCCTGGACATTCCGAGGTGGACCCCGCCGCGCTACCTCAACCTTCAGACCTGTA 2960

Qy 3138 CGAATCAGTACTTCCATTCGAGTTTATGATCTTCAGGAAAGTCCCCAAGTCCGCTCA 3197
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Db 2961 CGAATCAGTACTTCCATTCGAGTTTATGATCTTCAGGAAAGTCCCCAAGTCCGCTCA 3020

Qy 3198 GCCAGAGCCGGCCCTCCCCTCCGGAGCCTCGGAGTTCCCGAGTTCCCGGAGCCCACGTG 3257
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Db 3021 GCCAGAGCCGCGCCCTCCCCCTCCGGAGCCTCGGAGTTCCCGAGTTCCCGGAGCCCACGTG 3080

Qy 3258 GCCCTGGCCAGGTGAACTGGGCCCCCAGGCTGAGATCACAGAGGAGTCAGAGGA 3317
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Db 3081 GCCCTGGCCAGGTGAACTGGGCCCCCACGCCAGCGCTGAGATCACAGAGGAGTCAGAGGA 3140

Qy 3318 TGTGACGCGCTGCTGGCAGGCGCCGTGGGCCAGGAGGCGCAAGTGGTTCCTCGCCGTC 3377
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Db  3141  TGTGGACGCGCTGCTGGCAGAGGCTGCCGTGGGCAGGAAGCGCAAGTGGTCCTCGCCGTC  3200

Qy  3378  ACGCAGCCTCTTCCACTTCCCTGGGAGGCACCTGCCGCGCTGGATGAGCGCTGCAGAGCTGGG  3437
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Db  3201  ACGCAGCCTCTTCCACTTCCCTGGGAGGCACCTGCCGCGCTGGATGAGCGCTGCAGAGCTGGG  3260

Qy  3438  GCTGCGTGAGAGAGTGAAGGCCTCCGTGGAGCACATCTCCCGGATCCTGAAGGGCAGGCC  3497
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Db  3261  GCTGCGTGAGAGAGTGAAGGCCTCCGTGGAGCACATCTCCCGGATCCTGAAGGGCAGGCC  3320

Qy  3498  GGAAGGTCTGAGAAGAGGAGGGCCCCCCAGGAAGAAGCCAGGCCTTGCTTCCTTCCGGCT  3557
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Db  3321  GGAAGGTCTGAGAAGAGGAGGGCCCCCCAGGAAGAAGCCAGGCCTTGCTTCCTTCCGGCT  3380

Qy  3558  CTCAGGTCTGAAGAGCTGGGACGAGCGCCGACAATTCCTAAGGGAGCTCTCAGATGAGAC  3617
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Db  3381  CTCAGGTCTGAAGAGCTGGGACGAGCGCCGACAATTCCTAAGGGAGCTCTCAGATGAGAC  3440

Qy  3618  TGTGGTCCTGGGCCAGTCAGTGACACTGGCCTGCAGTGTCAGCCGCAGGTGCCCA  3677
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Db  3441  TGTGGTCCTGGGCCAGTCAGTGACACTGGCCTGCAGTGTCAGCCGCAGTGCCCCA  3500

Qy  3678  GGCCACCTGGACGCAAAGAACGAGAGCGCCCCCTGAGAGCAGCAGCCGTGTCCTCATCTCTGC  3737
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Db  3501  GGCCACCTGGACGCAAAGAACGAGAGCGCCCCCTGAGAGCAGCAGCCGTGTCCTCATCTCTGC  3560

Qy  3738  CACCCTCAAGAACTTCCAGCTTCTGACCATCCTGGTTGGTGGCTGAGGACCTGGGTGT  3797
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Db  3561  CACCCTCAAGAACTTCCAGCTTCTGACCATCCTGGTTGGTGGCTGAGGACCTGGGTGT  3620

Qy  3798  GTACACCTGCAGCGTGAGCGTGCAATGCAGTGACCACCAGCGGCGTCCTCCTCCGGAA  3857
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Db  3621  GTACACCTGCAGCGTGAGCGTGCAATGCAGTGACCACCAGCGGCGTCCTCCTCCGGAA  3680

Qy  3858  GGCAGAGCGCCCCCTCATCTTCGGCCATGCCCGGATATCGGGAGAGGTGTACGCGGATGGGGT  3917
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Db  3681  GGCAGAGCGCCCCCTCATCTTCGGCCATGCCCGGATATCGGGAGAGGTGTACGCGGATGGGGT  3740

Qy  3918  GCTGCTGCTGTCTGGAAGCCGTGGAATCCTACGGCCCTGTGACCTACCATTGTGCAGTGCAG  3977
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Qy  3978  CCTAGAAGGCGGCAGCTGGACCACACCACTGGCCTTCCGGACATCTTCGACTTGCTGCTACCTGAC  4037
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Qy  4038  CAGCAAGCTCTCCCGGGTGGCACCTACACCTTCCGCACGGCATGTGTCAGCAAGGCAGG  4097
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Db  3861  CAGCAAGCTCTCCCGGGTGGCACCTACACCTTCCGCACGGCATGTGTCAGCAAGGCAGG  3920

Qy  4098  AATGGGTCCCTACAGCAGCCCCTGGAGCAAGTCCTCCTGGAGGGCCCAGCCACCTGGC  4157
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Db  3921  AATGGGTCCCTACAGCAGCCCCTGGAGCAAGTCCTCCTGGAGGGCCCAGCCACCTGGC  3980

Qy  4158  CTCTGAGGAGGAGAGCAGCCTCCAGAGGGGCGGCCAGGGGCTCAGCCCAACCCCTGCCCAGCACAAAGACCTTCGC  4217
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Db  3981  CTCTGAGGAGGAGAGCAGCCTCCAGAGGGGCGGCCAGGGGCTCAGCCCAACCCCTGCCCAGCACCACAAAGACCTTCGC  4040

Qy  4218  ATTCCAGACACAGATCCAGAGGGGCCGCTTCAGCGTGGTGCGGCAATGCTCGGGAGAAGGC  4277
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Db  4041  ATTCCAGACACAGATCCAGAGGGGCCGCTTCAGCGTGGTGCGGCAATGCTCGGGAGAAGGC  4100

Qy  4278  CAGCGGCGGGCGGGGCCGCTGGGCCGGCCAAGATCATCCCCTACCACCCCAAGGACAAGACAGCAGT  4337
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Db  4101  CAGCGGCGGGCGGGGCCGCTGGGCCGGCCAAGATCATCCCCTACCACCCCAAGGACAAGACAGCAGT  4160

Qy  4338  GCTCGCGGAATACGAGGGCCCTCAAGGGCCTGCGCCACCCGGCCCAGCTGCACGC  4397
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Db  4161  GCTCGCGGAATACGAGGGCCCTCAAGGGCCTGCGCCACCCGGCCCAGCTGCACGC  4220

Qy  4398  AGCTTACCTCAGCCCCGGCACCTGGTTGCTCATCTTGGACGCTGTCTGCTTGGGGCCCGAGCT  4457
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Db  4221  AGCCTACCTCAGCCCCGGCACCTGGTTGCTCATCTTGGAGCTGTCTCATCTTGGGCCCGAGCT  4280


Qy  4458  GCTCCCCTGCCTGGCCGAGAGGGCCCTCCTACTCAGAATCTGAGGTGAAGGACTACCTGTG  4517
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Db  4281  GCTCCCCTGCCTGGCCGAGAGGGCCCTCCTACTCAGAATCTGAGGTGAAGGACTACCTGTG  4340

Qy  4518  GCAGATGTTGAGTGCCACCCAGTACCTGCACAACCAGCACATCCTGCACCTGACCTGAG  4577
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Db  4341  GCAGATGTTGAGTGCCACCCAGTACCTGCACCAGCACATCCTGCACCTGACCTGAG  4400

Qy  4578  GTCCGAGAACATGATCATCACCGAATACAACCTGCTCAAGGTCGTGGACCTGGGCAATGC  4637
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Db  4401  GTCCGAGAACATGATCATCACCGAATACAACCTGCTCAAGGTCGTGGACCTGGGCAATGC  4460

Qy  4638  ACAGAGCCTCAGCCAGGAGAAGGTGCTGCCCTCAGACAGTTCAAGGACTACCTAGAGAC  4697
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Db  4461  ACAGAGCCTCAGCCAGGAGAAGGTGCTGCCCTCAGACAGTTCAAGGACTACCTAGAGAC  4520

Qy  4698  CATGGCTCCAGAGCTCCTGGAGGGCTCCTGGAGGGGTGTTCCACAGACAGACATCTGGCCAT  4757
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Db  4521  CATGGCTCCAGAGCTCCTGGAGGGCTCCTGGAGGGGTGTTCCACAGACAGACATCTGGCCAT  4580

Qy  4758  CGGTGACAGCCTTCATCATGCTGAGCGTGACCGGTGCAGCGAGTGCACG  4817
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Db  4581  CGGTGACAGCCTTCATCATGCTGAGCGTGACCGGTGCAGCGAGGGTGCACG  4640

Qy  4818  CGACCTGCAGAGAGACTGCGCAAGGGCGTGGTCCGGCTGAGCCCGTACGCGGGGCT  4877
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Db  4641  CGACCTGCAGAGAGACTGCGCAAGGGCGTGGTCCGGCTGAGCCCGTACGCGGGGCT  4700

Qy  4878  GTCCGGGGGCGCCGGGCCGTGGCCTTCCTGCGCAGCACTCGTGTGCGCCCAGCCC  4937
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Db  4701  GTCCGGGGGCGCCGGGCCGTGGCCTTCCTGCGCAGCACTCGTGTGCGCCCAGCCC  4760

Qy  4938  CTGCGCGGTCCAGCTGCCTGCTGCGCCGTGCCGGTGCCTAACAGAGGAGGGCCCGCCTGTTCGCG  4997
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Db  4761  CTGCGCGGTCCAGCTGCCTGCTGCGCCGTGCCGGTGCCTAACAGAGGAGGGCCCGCCTGTTCGCG  4820

Qy  4998  GCCCGCGCCGGTGACCTTCCCTACCGGCGGCGTGCGCCGTCTTCGTGCGCAATCGGCGAGAA  5057
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Db  4821  GCCCGCGCCGGTGACCTTCCCTACCGGCGGCGTGCGCCGTCTTCGTGCGCAATCGGCGAGAA  4880

Qy  5058  GAGACGCGCGCTGCTGTGTACAAGAGGCACAACCTGGCCCAGGTGCGCTGAGGGTGCGCCCCG  5117
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Qy  5118  GCCACACCCTGGTCTCCCCCGCTGGGGGTCGCGAGACGCGCCAATAAAAACCACAGC  5177
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RESULT 8
US-10-307-019-5
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; Sequence 5, Application US/10307019
; Publication No. US20030108533A1
; GENERAL INFORMATION:
;   APPLICANT: Zeng, Wenlin
;   APPLICANT: Stanton, Lawrence
;   APPLICANT: SCIOS, INC.
;   TITLE OF INVENTION: MEDIATORS OF SIGNAL TRANSDUCTION
;   FILE REFERENCE: SCIOS.021DV1
;   CURRENT APPLICATION NUMBER: US/10/307,019
;   CURRENT FILING DATE: 2002-11-26
;   PRIOR APPLICATION NUMBER: 09/548,473
;   PRIOR FILING DATE: 2000-04-13
;   PRIOR APPLICATION NUMBER: 60/129,552
;   PRIOR FILING DATE: 1999-04-16
;   NUMBER OF SEQ ID NOS: 9
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
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;    LENGTH: 7928
;    TYPE: DNA
;    ORGANISM: Homo sapiens
;    FEATURE:
;    NAME/KEY: CDS
;    LOCATION: (60)...(7847)
US-10-307-019-5

Query Match        94.4%;  Score 4915.8;  DB 15;  Length 7928;
Best Local Similarity  99.9%;  Pred. No. 0;
Matches 4920;  Conservative  0;  Mismatches  7;  Indels  0;  Gaps  0;

Qy    258 CCCAGGGCCCCATCCATCCATGCAGGTAACCATGCAGGATGTGCAGCACAGACAGGCGGAAC 317
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Qy    318 GGCCCAATTCGAGGTCTATCATTGAGGGCGCACCCACAGCCCTCCGTGACCTGGTTACAAGGA 377
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Db   3062 GGCCCAATTCGAGGCTATCATTGAGGGCGCACCCACAGCCCTCCGTGACCTGGTTACAAGGA 3121

Qy    378 CAGCGGTCCAGCTGGTGGACAGCACCCGGCTTAGCCAGCAGCAAGAAGGCACCACCATATC 437
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Db   3122 CAGCGTTCCAGCTGGTGGACAGCACCCGGCTTAGCCAGCAGCAAGAAGGCACCACCATACTC 3181

Qy    438 CCTGTGCTGAGGCATGGCCTCGAAGATGCCGGCGTTTACACCTGCCTGGCCCAAAA 497
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Db   3242 CACTGGTGGCCAGGTGCTCTGCAAGGCAGAGCTGCTGTGGGGGGGACAATGAGCC 3301

Qy    558 GGACTCAGAGAAGCAAAGCCACCGGAGGAAGCTGCACTCCTTCTATGAGGTCAAGGAGGA 617
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Db   3302 GGACTCAGAGAAGCAAAGCCACCGGAGGAAGCTGCACTCCTTCTATGAGGTCAAGGAGGA 3361

Qy    618 GATTGGAAGGGGCGTGTTGGCTTCGTAAAAAGAGTGCAGCACAAAGGAAACAAGATCTT 677
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Db   3362 GATTGGAAGGGGCGTGTTTGGCTTCGTAAAAAGAGTGCAGCACAAAGGAAACAAGAGTCTT 3421

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Qy    738 AGACATCCTGGCCGCGCTGAGCCGTTGGTCACGGGGGCTGCTGACCAGTTTGAGAC 797
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Db   3482 AGACATCCTGGCCGCGCTGAGCCGTTGGTCACGGGGGCTGCTGACCAGTTTGAGAC 3541

Qy    798 CCGCAAGACCCCTCATCCTCATCCTCATCCTGGAGCTGTGCTCATCCGAGGACCGGCCT 857
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Db   3542 CCGCAAGACCCCTCATCCTCATCCTGGAGCTGTGCTCATCCGAGGAGCTGCTGACCGGCCT 3601

Qy    858 GTACAGGAAGGGGCGTGGTGACGGGAGCGTGGTGACGGCCGGAGGTCTACATCCAGCAGCTGGTGGA 917
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Db   3602 GTACAGGAAGGGGCGTGGTGACGGGAGCGTGGTGACGGCCGGAGGTCTACATCCAGCAGCTGGTGGA 3661

Qy    918 GGGGGTGCACTACCTGCACAGCCCATGGCGTTCTCCACCTGGACATAAAGCCCCTCTAACAT 977
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Qy    978 CCTGATGGTGTCATCTGCCCCGGAAGACATTAAAAATCTGCGACTTGGCTTTGCCCAGAA 1037
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Db   3782 CATCACCCCCAGCAGAGCTCAGTTCAGCCAGTACGGCTCCCCTGAGTTCGTCTTCCCCCGA 3841

Qy   1098 GATCATCCAGCAGAGAACCCTGTGAGCCAAGCCTCCGACATTTGGCCATGGGTGTCATCTC 1157
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Db   3842 GATCATCCAGCAGAGAACCCTGTGAGCCAAGCCTCCGACATTTGGCCATGGGTGTCATCTC 3901

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Db   3902 CTACCTCAGCCTGACCTGCTCATCCCCATTTGCCGGCGGAGAGTGACCGTGCCACCCTCCT 3961

Qy   1218 GAACGTCCTGGAGGGGCGGGGCCGCGTGTCATGAGGAGCAGCCCCATGGCTGCCACCTCAGCGCAAGA 1277
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Qy   1278 CGCCAAAGACTTCATCAAGGCTACGCTGCAGAGAGCCCCTCAGCCCGGCCGGGCCTAGTGCCGGC 1337
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Db   4022 CGCCAAAGACTTCATCAAGGCTACGCTGCAGAGAGCCCCTCAGCCCGGCCGGGCCTAGTGCCGGC 4081

Qy   1338 CCAGTGCCTCTCCACCCTGGTTCCTGAAATCATCGCTGCCGGAGGAGGCCCACTTCAT 1397
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Db   4082 CCAGTGCCTCTCCCACCCTGGTTCCTGAAATCCATCGCTGCCGGAGGAGGCCCACTTCAT 4141

Qy   1398 CAACACCAAGCAGCTCAAGTTCCTGCCCGAAGTCGCTGCAGCGTTCCCTGATGAG 1457
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Db   4142 CAACACCAAGCAGCTCAAGTTCCTGCCCGAAGTCGCTGCAGCGTTCCCTGATGAG 4201

Qy   1458 CTACAAGTCATCCTGGTGATGGCCTCATCCCTGAGCTGCTGCGGGCCCACCCGACAG 1517
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Db   4202 CTACAAGTCATCCTGGTGATGCCTCCCATCCCTGAGCTGCTGCGGGCCCACCCGACAG 4261

Qy   1518 CCCCTTCCCTCGGCGGTAGCCCGGCCACCTCTGCAGGGACACTGGTTGGCTCTCCTCCAGTTCCTC 1577
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Db   4262 CCCCTCCCTCGGCGGTAGCCCGGCCACCTCTGCAGGGACACTGGTTGGCTCTCCTCCAGTTCCTC 4321

Qy   1578 CTCCTCCTCTGACAACGAGCTCGCCCCCATTTGCCCACCCTCCACCCCTCCCC 1637
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Db   4322 CTCCTCCTCTGACAACGAGCTCGCCCCATTTGCCGGGCTAAGTCACTGCCACCCCTCCCC 4381

Qy   1638 GGTGACACACTCACCACTGCTGCACCCCGGGGGCTTCCTGCGGCCCTCGGGCCCTGCC 1697
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Db   4382 GGTGACACACTCACCACTGCTGCACCCCGGGGGCTTCCTGCGGCCCTCGGGCCCTGCC 4441

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Db   4442 TGAGGAAGCCGAGGCCCAGTGAGCGGCTCCACCGAGGGCCCCAGTCCGCCTGCATCTCCCGA 4501

Qy   1758 GGGTGCCGGCCACCGGCCCCAGGCTGCGTGTGCCCGGCACACAGCGTCATCCGCAGCCT 1817
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Db   4502 GGGTGCCGGCCACCGGCCCCAGGCTGCGTGTGCCCGGCACACAGCGTCATCCGCAGCCT 4561

Qy   1818 GTTCTACCACCAGGCGGGTGAGAGCCCCTGAGCACGGGCCCTTGCCCGGGGAGCAGGCG 1877
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Db   4562 GTTCTACCACCAGGCGGGTGAGAGCCCCTGAGCACGGGCCCTTGCCCGGGGAGCAGGCG 4621

Qy   1878 GCACCCGGCCCCACCTCATCCTCGCCCGGCGGCGGGCTACATTGCGGGGCGCTGCCAGG 1937
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Db   4622 GCACCCGGCCCCACTCATCCTCGCCCGGCGGCGGGCTACATTGCGGGGCGCTGCCAGG 4681

Qy   1938 CCTGCCGAGCCACTGATGGAGCACCGCGTGCTGGAGGAGGCCGCCAGGGAGGAGCA 1997
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Qy   1998 GGCCACCCCTCCTGGCCAAAGCCCCTCATTCGAGACTGCCCTTGCCCTTCGGCTGCCTCTGG 2057
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Db   4742 GGCCACCCCTCCTGGCCAAAGCCCCTCATTCGAGACTGCCCTTGCCTTGCCTGCCTCTGG 4801

Qy   2058 CACCCACTTGGCCCCTGGCCACCTCCGGAACATGCACTCTCCGAGCACCCCCCC 2117
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Qy   2238 CCCAGGCACTGCTCAGCCTGGTTGCCCGCGGAGAGGCCATCCCCGGACAGCCCTTGGGGCAGCCAGCCCC 2297
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Db  4982  CCCAGGCACTGCTCAGCCAGAGAGGCCATCCCCGGACAGCCCTTGGGCGGCAGCCAGCCCC  5041

Qy  2298  TTTTGCCACCCCAAGCAGGGTTCTGCCCCCAGGAGGGCTGAGCCCACCCAGCAGT  2357
          |||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db  5042  TTTCTGCCACCCCAAGCAGGGTTCTGCCCCCAGGAGGGCTGAGCCCACCCAGCAGT  5101

Qy  2358  TGCCCCATGCCCTCTGGCTCCTTCCCTCCAGGATCTTGCAAAGAGAGGCCCCTTAGTACC  2417
          ||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db  5102  TGCCCCATGCCCTCTGGCTCCTTCCCTCCAGGATCTTGCAAAGAGAGGCCCCTTAGTACC  5161

Qy  2418  CTCAAGCCCCTTCTTGGGACAGCCCAGCACCCCTGCCCCTGCCCCCAAAGCAAGCCCCCC  2477
          ||||||||||| || |||||||||||||||||||||||||||||||||||||||||||||
Db  5162  CTCAAGCCCCTTCTTGGGACAGCCCAGCACCCCTGCCCCTGCCCCCAAAGCAAGCCCCCC  5221

Qy  2478  ATTGGACTCTAAGATGGGGCCTGAGACATCTGTCTTCCTGGAGGCCAAAACCCGGCCC  2537
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5222  ATTGGACTCTAAGATGGGGCCTGAGACATCTGTCTTCCTGGAGGCCAAAACCCGGCCC  5281

Qy  2538  CTGCAGTTCCCCAGGGTCAGCCTCCCAGGCGAGCTCTTCCCAAGTGAGCTCCCTCAGGGT  2597
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5282  CTGCAGTTCCCCAGGGTCAGCCTCCCAGGCGAGCTCTTCCCAAGTGAGCTCCCTCAGGGT  5341

Qy  2598  GGGCTCCTCCCAGTGGGCACAGACCCTGGCCCCTCCTGGATGCGGAGGGCTGGACCCA  2657
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5342  GGGCTCCTCCCAGTGGGCACAGACCCTGGCCCCTCCTGGATGCGGAGGGCTGGACCCA  5401

Qy  2658  GGAGGCTGAGGATCTGTCCGACTCCACACCTTGCAGCCGCCTCAGGAACAGGTGAC  2717
          |||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Db  5402  GGAGGCTGAGGATCTGTCCGACTCCACACCTTGCAGCCGCCTCAGGAACAGCAGCGAC  5461

Qy  2718  CATGCGCAAGTTCTCCCTGGTGTCGGGGGGCTACGCAGGCGTGGCTATGGCAC  2777
          ||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db  5462  CATGCGCAAGTTCTCCCTGGTGTCGGGGGGCTACGCAGGCGTGGCTATGGCAC  5521

Qy  2778  CTTTGCCTTTGGTGAGATGCAGGGGGCGATGCTGGGGCCCATGTGGCCAGGAT  2837
          ||||||||| ||||||||||||||||||||| ||||||||||||||||||||
Db  5522  CTTTGCCTTTGGTGAGATGCAGGGGCATGCTGGGGCCCATGTGGCCAGGAT  5581

Qy  2838  AGCTGGGGCTGTGTCCCAGTCGGAGGAGGCAGGAGGCAGGAGGCTGAGTCCCA  2897
          |||||||||||||| |||||||||||||||||||||||||||||||||||||
Db  5582  AGCTGGGGCTGTGTCCCAGTCGGAGGAGGCAGGAGGCAGGAGGCTGAGTCCCA  5641

Qy  2898  GTCGGAGGAGCAGCAGGAGGAGGCCAAGGCCCACTGCCCCAGTCAGTGCGAGGCC  2957
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5642  GTCGGAGGAGCAGCAGGAGGAGGCCAAGGCCCACTGCCCCAGTCAGTGCGAGGCC  5701

Qy  2958  TGTGCCTGAGGTCGGCAGGGCTCCCACCAGAGCCTCCCAGAGCCCACCCATGGGAGGA  3017
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5702  TGTGCCTGAGGTCGGCAGGGCTCCCACCAGAGCCTCCCAGAGCCCACCCATGGGAGGA  5761

Qy  3018  CATCCGGCCAGGTCTCCCTGTGCAGATCCGGGACCTGGGACCTGCAGTTGCGGAGGCCGGCCGA  3077
          ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db  5762  CATCCGGCCAGGTCTCCCTGTGCAGATCCGGGACCTGCAGTTGCGGAGGCCGGCCGA  5821

Qy  3078  CACAATATCCCTGGACATTTCCGAGGTTTATGATCTTCAGGAAAGTCCCGCTTCAACCTCTCAACCTGTA  3137
          ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db  5822  CACAATATCCCTGGACATTTCCGAGGTGACCCCGCTTCAACCTCTCAACCTGTA  5881

Qy  3138  CGATATCAAGTACCTCCCATTCGAGTTTATGATCTTCAGGAAAGTCCCCCTCA  3197
          ||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db  5882  CGATATCAAGTACCTCCCATTCGAGTTTATGATCTTCAGGAAAGTCCCCCTCA  5941

Qy  3198  GCCAGAGCGCCCCTCCCCCATGGGAGGCTGCCTGAGGAGGTCGGCCGAGTTCCCGGAGGCCCACGTG  3257
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5942  GCCGAGAGCGCCCCTCCCCCATGGGAGGCTGCCTGAGGAGGTCGGCCGAGTTCCCGGAGGCCCACGTG  6001

Qy  3258  GCCCTGGCCAGGTGAACTGGGCCCCCACGCAGGCCTGGAGATCACAGAGGAGTCAGAGGA  3317
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  6002  GCCCCTGGCCAGGTGAACTGGGCCCCCACGCAGGCCTGGAGATCACAGAGGAGTCAGAGGA  6061

Qy  3318  TGTGGACGGCGGCTGGTGGCGAGAGGCTGCCGTGGCGAGAAGCCCAAGGTGGTTCCTCGCCGTC  3377
          ||||| |||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db  6062  TGTGGACGGCGGCTGGTGGCGAGAGGCTGCCGTGGCGAGAAGCCCAAGGTGGTTCCTCGCCGTC  6121


Qy  3378  ACGCAGCCTTCCACTTCCTGGAGGCACCTGCCGCTGGATGAGCCTGGAGAGCTGG  3437
          ||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Db  6122  ACGCAGCCTCTTCCACTTCCTGGAGGCACCTGCCGCTGGATGAGCCTGGAGAGCTGGG  6181

Qy  3438  GCTCGTGAGAGAGTGAAGGCTCCGTGGAGCATCTCCGGATCTGAAGGGCAGGCC  3497
          ||| |||||||||||||||||||| ||||||| |||| |||| |||||||||||
Db  6182  GCTGGTGAGAGAGTGAAGGCTCGTGGAGCACATCCCGGATCCTGAAGGGCAGGCC  6241

Qy  3498  GGAAGGTCTGGAGAGGAGGGGCCCCCAGGAGAACAGCAGCCAGGCCTTGCTTGTTCCTTCCCGGCT  3557
          ||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  6242  GGAAGGTCTGGAAGGAGGGAGGGCCCCCAGGAGAAGAAGCCAGGCCTTGCTTGTTCCTTCCCGGCT  6301

Qy  3558  CTCAGGTCTGAAGACTGGAGAGCTGGAGAGCCGAGCCGCGAGCATTCCTAAGGGAGTCTCAGATGAGAC  3617
          ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  6302  CTCAGGTCTGAAGACTGGAGAGCTGGAGAGCCGAGCCGCGAGCATTCCTAAGGGAGTCTCAGATGAGAC  6361

Qy  3618  TGTGGTCCTGGGCAGTCAGTGACACTGCCTCGCCAGTGTCAGCGGCTCAGCAGCTGCCCA  3677
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  6362  TGTGGTCCTGGGCAGTCAGTGACACTGCCTCGCCAGTGTCAGCGGCTCAGCAGCTGCCCA  6421

Qy  3678  GGCCACCTGGACAAAGACCGAGCCCCCTGGAGCAGCAGCAGCCGTGTCCTCATCTCTGC  3737
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  6422  GGCCACCTGGACAAAGACCGAGCCCCCTGGAGCAGCAGCAGCCGTGTCCTCATCTCTGC  6481

Qy  3738  CACCCTCAAGAACTTCAGCTTCTGACCATCTGGTGGTGGCTGAGGACCTGGGTGT  3797
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  6482  CACCCTCAAGAACTTCAGCTTCTGACCATCTGGTGGTGGCTGAGGACCTGGGTGT  6541

Qy  3798  GTACACCTGCAGCGTGAGCAATGCGTGGGACAGTGACCACACCAGGCGTCCTCCCGAA  3857
          |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db  6542  GTACACCTGCAGCGTGAGCAATGCGTGGGACAGTGACCACACCAGGCGTCCTCCCGAA  6601

Qy  3858  GGCAGAGCGCCCCTCATCTTCGGCCATGCCCGGATATCGGGAGGTGTACGCGGATGGGGT  3917
          ||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db  6602  GGCAGAGCGCCCCTCATCTTCGGCCATGCCCGGATATCGGGAGGTGTACGCGGATGGGGT  6661

Qy  3918  GCTGCTGGTCTGGAAGCCCGTGAATCCACTACGGCCCTGTGACCTACATTGTGCAGTGCAG  3977
          |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db  6662  GCTGCTGGTCTGGAAGCCCGTGAATCCACTACGGCCCTGTGACCTACATTGTGCAGTGCAG  6721

Qy  3978  CCTAGAAGGCGGCAGCGTTGACCACACTGGCCTCCCGACATCTTTGACTGCTGCTACCTGAC  4037
          |||||||||||||||||||| ||||||||||||||||||||| |||||||||||||||||||
Db  6722  CCTAGAAGGCGGCAGCGTTGACCACACTGGCCTCCCGACATCTTTGACTGCTGCTACCTGAC  6781

Qy  4038  CAGGCAAGCTCTCCCGGGGTGGCACCTCACCTTCCCGACGCGCATGTGTCAGCAAGGCAGG  4097
          || ||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db  6782  CAGGCAAGCTCTCCCGGGGTGGCACCTTCCCGACGCGCATGTGTCAGCAAGGCAGG  6841

Qy  4098  AATGGGTCCCTACAGCAGCCCCTCCTGGAGCAAGTCTTCCTGCGGAGGGCCCAGCCACCTGGC  4157
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  6842  AATGGGTCCCTACAGCAGCCCCTCCTGGAGCAAGTCTTCCTGCGGAGGGCCCAGCCACCTGGC  6901

Qy  4158  CTCTGAGGAGGAGAGCGGTGACATTTCCGAGGTGACCCCAGTCAGTGCAAGGCCTTCGC  4217
          |||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Db  6902  CCTCTGAGGAGGAGAGCGGTGACATTTCCGAGGTGACCCCAGTCAGTGCAAGGCCTTCGC  6961

Qy  4218  ATTCCAGACACAGATCCAGAGGCCGGTGGTGCGGCAATGCTGGGAGAAGGC  4277
          ||||||||||||||||||| ||||||||||||||||||||||||||||||
Db  6962  ATTCCAGACACAGATCCAGAGGCCGGTGGTGCGGCAATGCTGGGAGAAGGC  7021

Qy  4278  CAGCGGGGGGCCGCTGGCGCCAAGATCATCCCCACCCCAAGGACAAGACAGCAGT  4337
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  7022  CAGCGGGGGGCCGCTGGCGCCAAGATCATCCCCACCCCAAGGACAAGACAGCAGT  7081

Qy  4338  GCTGCGCGAATACGAGGCCCTCAAGGGCCTCGCCACCCGACCTGCCCAGCTGCGCACGC  4397
          |||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Db  7082  GCTGCGCGAATACGAGGCCCTCAAGGGCCTCGCCACCCGACCTGCCCAGCTGCCCACGC  7141

Qy  4398  AGCCTACCTCAGCCCCGGCACCTGGTGCTCATCTTGGCTGTGCTCATCTTTGGAGCTGTGTCCTCTGGGCCCGAGCT  4457
          |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db  7142  AGCCTACCTCAGCCCCGGCACCTGGTGCTCATCTTGGCTGTGCTCATCTTTGGAGCTGTGTCTCTGGGCCCGAGCT  7201
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;   LENGTH: 4936
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-182-243-14

Query Match    Best Local Similarity   93.8%;   Score 4885.2;   DB 13;   Length 4936;
               Matches 4915;   Conservative 0;   Mismatches 0;   Indels 18;   Gaps 1;
US-10-182-243-14                        95.6%;   Pred. No. 0;

Qy    268 CCATCCATGCAGGTAACCATCGACGATGTCAGGCACGACACAGCGGAACGGCCCAATTC 327
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 CCATCCATGCAGGTAACCATCGACGATGTCAGGCACGACACAGCGGAACGGCCCAATTC 60

Qy    328 GAGGGCTTATCATTGAGGGCGACCCACAGCCTCCGTGGTACAAGGACAGCGTCCAG 387
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GAGGGCTTATCATTGAGGGCGACCCACAGCCTCCGTGGTACAAGGACAGCGTCCAG 120

Qy    388 CTGGTGGACAGCACCCGGCTTAGCAGCAGCAAGAAGGCACCACATACTCCCTGGTGCTG 447
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 CTGGTGGACAGCACCCGGCTTAGCAGCAGCAAGAAGGCACCACATACTCCCTGGTGCTG 180

Qy    448 AGGCATGTGCCTCGAAGGATGCGCGGCGTTTACACCTGCCCCAAAACACTGGTGGC 507
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 AGGCATGTGCCTCGAAGGATGCGCGGCGTTTACACCTGCCCCAAAACACTGGTGGC 240

Qy    508 CAGGTGCTCTGCAAGGCAGGAGAGTGCTGGTGCTTGGG------------GGGGAC 549
          ||||||||||||||||||||||||||||||||||||||||            |||||
Db    241 CAGGTGCTCTGCAAGGCAGGAGAGTGCTGGTGCTTGGGGGCGGCCGCTTCCCACTCCTTGGGGAC 300

Qy    550 AATGAGCCGGACTCAGAGAGCAAAGCCACCCGAGGAAGCTGCACTCCTTCTATGAGGTC 609
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 AATGAGCCGGACTCAGAGAGCAAAGCCACCCGAGGAAGCTGCACTCCTTCTATGAGGTC 360

Qy    610 AAGGAGGAGATTGGAAGGGCGTGTTTGGCTTCGTAAAAAGAGTGCAGCACAAAGGAAAAC 669
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 AAGGAGGAGATTGGAAGGGCGTGTTTGGCTTCGTAAAAAGAGTGCAGCACAAAGGAAAAC 420

Qy    670 AAGATCTTGTGGCTGCAAGTTCATCCCCTACGGACAGCAGAACTCGGGCCCAGGCATAC 729
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 AAGATCTTGTGGCTGCAAGTTCATCCCCTACGGACAGCAGAACTCGGGCCCAGGCATAC 480

Qy    730 AGGGAGGCGAGACATCCTGGCGCGCTGAGCCACCCGCTGGTCACGGGGCTGCTGGACCAG 789
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 AGGGAGGCGAGACATCCTGGCGCGCTGAGCCACCCGCTGGTCACGGGGCTGCTGGACCAG 540

Qy    790 TTTGAGACCCGCCAAGACCCTCATCCTGGAGCTGTGCTCATCCGAGGAGCTGCTG 849
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 TTTGAGACCCGCCAAGACCCTCATCCTGGAGCTGTGCTCATCCGAGGAGCTGCTG 600

Qy    850 GACCGCCCTGTACAGGAAGGGCGTGGTGACGAGGCCGAGGTCACATCCAGCAG 909
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 GACCGCCCTGTACAGGAAGGGCGTGGTGACGAGGCCGAGGTCAAGTCTACATCCAGCAG 660

Qy    910 CTGGTGGAGGGGCTGCACTACCTGCACAGCCATGGCGTTCCCACTGGACATAAAGCCC 969
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 CTGGTGGAGGGGCTGCACTACCTGCACAGCCATGGCGTTCCCACCTGGACATAAAGCCC 720

Qy    970 TCTAACATCCTGATGGTGCATCCTGCCCGGGAAGACATTAAAATCTGCGACTTTGGCTTT 1029
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 TCTAACATCCTGATGGTGCATCCTGCCCGGGAAGACATTAAAATCTGCGACTTTGGCTTT 780

Qy   1030 GCCCAGAACATCACCCCAGCAGCTGCAGTTCAGCCAGTCAGCCAGTACGGGCTCCCCTGAGTTCGTC 1089
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 GCCCAGAACATCACCCCAGCAGCTGCAGTTCAGCCAGTCAGCCAGTACGGGCTCCCCTGAGTTCGTC 840

Qy   1090 TCCCCCGGATCATCCAGCAGAACCCTGTGAGCGAAGCCTCCGACATTTGGGCCATGGGT 1149
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 TCCCCCGGATCATCCAGCAGAACCCTGTGAGCGAAGCCTCCGACATTTGGGCCATGGGT 900

Qy   1150 GTCATCTCCACCTCAGCCTGACCTGCTCATCCCCATTGCCGGGGGAGTGACCGTGCC 1209
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 GTCATCTCCACCTCAGCCTGACCTGCTCATCCCCATTTGCCGGGGGAGTGACCGTGCC 960


Qy   4458 GCTCCCCTGCCTGGCCGAGAGGGCCTCCTACTCAGAATCTGAGGTGAAGGACTACCTGTG 4517
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7202 GCTCCCCTGCCTGGCCGAGAGGGCCTCCTACTCAGAATCTGAGGTGAAGGACTACCTGTG 7261

Qy   4518 GCAGATGTTGAGTGCCACCCAGTACCTGCACAACAGCACATCCTGCACCTGACCTGAG 4577
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7262 GCAGATGTTGAGTGCCACCCAGTACCTGCACAACAGCACATCCTGCACCTGACCTGAG 7321

Qy   4578 GTCCGAGAACATGATCATCACCGAATACAACCTGCTCAAGGTCGTGGACCTGGGCAATGC 4637
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7322 GTCCGAGAACATGATCATCACCGAATACAACCTGCTCAAGGTCGTGGACCTGGGCAATGC 7381

Qy   4638 ACAGAGCCTCAGCCAGGAGAAGGTGCTGCCCTCAGACAAGTTCAAGGACTACCTAGAGAC 4697
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7382 ACAGAGCCTCAGCCAGGAGAAGGTGCTGCCCTCAGACAAGTTCAAGGACTACCTAGAGAC 7441

Qy   4698 CATGGCTTCCAGAGCTCCTGGAGGGCCAGGGGCTGTTCCACAGACAGACATCTGGGCCAT 4757
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7442 CATGGCTTCCAGAGCTCCTGGAGGGCCAGGGGCTGTTCCACAGACAGACATCTGGGCCAT 7501

Qy   4758 CGGTGTGACAGCCTTCATCATGCTGAGCGGCGAGTACCCGGTGAGCAGGAGGGTGCACG 4817
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7502 CGGTGTGACAGCCTTCATCATGCTGAGCGGCGAGTACCCGGTGAGCAGGAGGGTGCACG 7561

Qy   4818 CGACCTGCAGAGAGGACTGCGCAAGGGGCTGGTTCCGGCGCTGGTCCGGCCGCTGCTACGCGGGGCT 4877
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7562 CGACCTGCAGAGAGGACTGCGCAAGGGGCTGGTTCCGGCGCTGGTCCGGCCGCTGCTACGCGGGGCT 7621

Qy   4878 GTCCGGGGGGCGCCGTGGCCTTCCTGCGCAGCACTCTGTTGCGCCCAGCCTGGGGCCCGCC 4937
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7622 GTCCGGGGGGCGCCGTGGCCTTCCTGCGCAGCACTCTGTTGCGCCCAGCCTGGGGCCGGCC 7681

Qy   4938 CTGCGCGGTCCAGCTGCCTGCCTCGCAGTGCCCGTGGCTAACAGAGGAGGCCCGGCCTGTTCGCG 4997
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7682 CTGCGCGGTCCAGCTGCCTGCCTCGCAGTGCCCGTGGCTAACAGAGGAGGCCCGGCCTGTTCGCG 7741

Qy   4998 GCCCGCGCCCGTGACCTTCCTACCGCGCGGCGTCTTCGTGGCGCAATCGCGAGAA 5057
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7742 GCCCGCGCCCGTGACCTTCCTACCGCGCGGCGTCTTCGTGGCGCAATCGCGAGAA 7801

Qy   5058 GAGACGCGCGCTGCTGTACAGAGGCACAACCTGGCCCAGGTGCGCGTGAGGGTCGCCCCG 5117
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7802 GAGACGCGCGCTGCTGTACAGAGGCACAACCTGGCCCAGGTGCGCGTGAGGGTCGCCCCG 7861

Qy   5118 GCCACACCCTTGGTCTCCCCGCGTCGGGGGTCGCAGACGCGCCAATAAAAACGCACAGC 5177
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Db   7862 GCCACACCCTTGGTCTCCCCGCGTCGGGGGTCGCAGACGCGCCAATAAAAACGCACAGC 7921

Qy   5178 CGGGGCGA 5184
          ||||||||
Db   7922 CGGGGCGA 7928
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RESULT 9
US-10-182-243-14
; Sequence 14, Application US/10182243
; Publication No. US20040048310A1
; GENERAL INFORMATION:
; APPLICANT: PLOWMAN, GREGORY D.
; APPLICANT: WHYTE, DAVID
; APPLICANT: MANNING, GERARD
; APPLICANT: SUDARSANAM, SUCHA
; APPLICANT: MARTINEZ, RICARDO
; TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES AND PROTEIN KINASE-LIKE
; TITLE OF INVENTION: ENZYMES
; FILE REFERENCE: 038602/1366
; CURRENT APPLICATION NUMBER: US/10/182,243
; CURRENT FILING DATE: 2003-07-07
; PRIOR APPLICATION NUMBER: PCT/US01/02337
; PRIOR FILING DATE: 2001-01-25
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14

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Qy  1210  ACCCCTCTGACAGTCTGGAGGGGCGCGTGTCATGGAGCAGCCCCATGGCTGCCCACCTC  1269
          ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db   961  ACCCCTCTGACAGTCTGGAGGGGCGCGTGTCATGGAGCAGCCCCATGGCTGCCCACCTC  1020

Qy  1270  AGCGAGAGACGCCAAAGACTTCATCAAGGCTACGCTGCAGAGAGCCCCTCAGGCCCGGCCT  1329
          ||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Db  1021  AGCGAGAGACGCCAAAGACTTCATCAAGGCTACGCTGCAGAGAGCCCCTCAGGCCCGGCCT  1080

Qy  1330  AGTGCGGCCCAGTGCCTCTCCCACCCCTGGTTCTGAAATCCATGCCTGCGGAGGAGGCC  1389
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1081  AGTGCGGCCCAGTGCCTCTCCCACCCCTGGTTCTGAAATCCATGCCTGCGGAGGAGGCC  1140

Qy  1390  CACTTCATCAACACCAAGCAGCTCAAGTTCCTCCTGCCCGAAGTTCGGCTGGCAGCGGTTCC  1449
          ||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db  1141  CACTTCATCAACACCAAGCAGCTCAAGTTCCTCCTGCCCGAAGTTCGGCTGGCAGCGGTTCC  1200

Qy  1450  CTGATGAGCTACAAGTCCATCCTGGTGATGCGCTTCCATCCCTGAGCTGCTGCGGGGGCCCA  1509
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1201  CTGATGAGCTACAAGTCCATCCTGGTGATGCGCTTCCATCCCTGAGCTGCTGCGGGGGCCCA  1260

Qy  1510  CCCGACAGCCCCTCCCTGGCGTAGCCCGGCACCTGCACCTCTGCAGGACACTGGTGGCTCCTCC  1569
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1261  CCCGACAGCCCCTCCCTGGCGTAGCCCGGCACCTGCACCTCTGCAGGACACTGGTGGCTCCTCC  1320

Qy  1570  AGTTCCTCCTCCTCCTGACAACGAGCTCGCCCCATTGCCCGGCTAAGTCACTGCA  1629
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1321  AGTTCCTCCTCCTCCTGACAACGAGCTCGCCCCATTGCCCGGCTAAGTCACTGCA  1380

Qy  1630  CCCTCCCCGGTGACACACTCACCACTGCTGCACCCCCGGGGCTTCCTGCGGGCCCTTGCGGCC  1689
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1381  CCCTCCCCGGTGACACACTCACCACTGCTGCACCCCCGGGGCTTCCTGCGGGCCCTTGCGGCC  1440

Qy  1690  AGCCTGCCTGAGGAAGCCGAGGCCCAGTGAGCGTTCCACCGAGGCCCCAGCTCCGCCTCGCA  1749
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1441  AGCCTGCCTGAGGAAGCCGAGGCCCAGTGAGCGTTCCACCGAGGCCCCAGCTCCGCCTCGCA  1500

Qy  1750  TCTCCCGAGGGTGCGCGGGCACCGGGCCACCGGGGCTGCGTGCCCCGGCACAGCGTCATC  1809
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1501  TCTCCCGAGGGTGCGCGGGCACCGGGCCACCGGGGCTGCGTGCCCCGGCACAGCGTCATC  1560

Qy  1810  CGCAGCCTGTTCTACCACCAGGCGGGTGAGGAGCACGGGCCTGGCCCTGGACCCCGGGG  1869
          |||||||||||||||||||||||||||||||||||||||| |||||||||||||||||
Db  1561  CGCAGCCTGTTCTACCACCAGGCGGGTGAGGAGCACGGGCCTGGCCCTGGACCCCGGGG  1620

Qy  1870  AGCAGGCGGACACCCGGCCCGGCGGCGGCCACTGCCTGCTGAAGGGCGGCTACATTGCGGGGCG  1929
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1621  AGCAGGCGGACACCCGGCCCGGCGGCGGCCACTGCCTGCTGAAGGGCGGCTACATTGCGGGGCG  1680

Qy  1930  CTGCCAGGCCTGCGGAGCCACTGATGAGCACCGCGTGCTGTGAGGAGGAGGCCGCAGG  1989
          ||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db  1681  CTGCCAGGCCTGCGGAGCCACTGATGAGCACCGCGTGCTGTGAGGAGGAGGCCGCAGG  1740

Qy  1990  GAGGAGCAGGCCACCCTCCTGGCCAAAGCCCCCTCATTCGAGACTGCGCCTCCGGCTGCCT  2049
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1741  GAGGAGCAGGCCACCCTCCTGGCCAAAGCCCCCTCATTCGAGACTGCGCCTCCGGCTGCCT  1800

Qy  2050  GCCTCTGGCACCCACTTGGCCCCTGGCCACAGCCACTCCCTGGAACATGAGACTTCCGAGC  2109
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1801  GCCTCTGGCACCCACTTGGCCCCTGGCCACAGCCACTCCCTGGAACATGAGACTTCCGAGC  1860

Qy  2110  ACCCCCCGCCCCTCCTCTCGGAGGCCTGCGGTGAGGCACAGCGACTGCCTTCAGCCCCCTCC  2169
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1861  ACCCCCCGCCCCTCCTCTCGGAGGCCTGCGGTGAGGCACAGCGACTGCCTTCAGCCCCCTCC  1920

Qy  2170  GGGGGGCCCCTATCAGGACATGGGCACCCCTCAGGGCTCCCGGACAGCCCATCCACT  2229
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1921  GGGGGGCCCCTATCAGGACATGGGCACCCCTCAGGGCTCCCGGACAGCCCATCCACT  1980

Qy  2230  GGTGGCCACCCAGGCACTGCTCAGCCAGAGAGGCCATCCCGGACAGCAGCCCTTGGGGGCAG  2289
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1981  GGTGGCCACCCAGGCACTGCTCAGCCAGAGAGGCCATCCCGGACAGCAGCCCTTGGGGGCAG  2040

Qy  2290  CCAGCCCCTTTCTGCCACCCCAAGCAGCAGGGGTTCTGCCCCCCAGGAGGGCTGCAGCCCCCAC  2349
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Db  2041  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
          CCAGCAGTTGCCCATGCCCTCCTGGCTCCTCCTCCCCAGGATCTGCGACCGCTGCGCAGCCCCCAC  2100

Qy  2350  CCAGCAGTTGCCCATGCCCTCCTGGCTGCTCCTCCTCCCCAGGAGCCCCTGCAAAGAGGCCCCC  2409
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2101  CCAGCAGTTGCCCATGCCCTCCTGGCTCCTCCTCCTCCCCAGGATCTTGCAAAGAGGCCCCC  2160

Qy  2410  TTAGTACCCTCAAGCCCTTCTTGGACAGCCCCCTGCCCCTGCCCCTGCCAAAGCA  2469
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2161  TTAGTACCCTCAAGCCCTTCTTGGACAGCCCCCTGCCCCTGCCCCTGCCAAAGCA  2220

Qy  2470  AGCCCCCATTGGACTCTAAGATGGGCGTGAGACATCTCTTCCTTCGGGAGGCCAAAA  2529
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2221  AGCCCCCATTGGACTCTAAGATGGGCGTGAGACATCTCTTCCTTCGGGAGGCCAAAA  2280

Qy  2530  CCCGGCCCCTGCCAGTTCCCCAGGGTCAGCCTCCCAGGCGAGCCTCTTCCCCAAGTGAGCTCC  2589
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2281  CCCGGCCCCTGCAGTTCCCCAGGGTCAGCCTCCCAGGCGAGCCTCTTCCCAAGTGAGCTCC  2340

Qy  2590  CTCAGGGTGGGCTCCTCCCAGGTGGGCACAGAGCCCTGGCCCCCTGGATGCGGAGGGGC  2649
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2341  CTCAGGGTGGGCTCCTCCCAGGTGGGCACAGAGCCTGGCCCCCTGGATGCGGAGGGGC  2400

Qy  2650  TGGACCCAGGAGGAGGCTGAGGATCTTGTCCCAGGGCTAAGTCACTGCA  2709
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db  2401  TGGACCCAGGAGGAGGCTGAGGATCTGTCCCAGGGCTAAGTCACTGCA  2460

Qy  2710  CAGTGACCATGCGCAAGTTCTCCCTGGGTGGTCGGGGGGGTACGCAGGCGTGGCTGGC  2769
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2461  CAGGCGACCATGCGCAAGTTCTCCCTGGGTGGTCGGGGGGGTACGCAGGCGTGGCTGGC  2520

Qy  2770  TATGGCACCTTTGCCTTTGGTGGAGATGCAGGGGCATGCGGGGCAGGGGCCATGTGG  2829
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2521  TATGGCACCTTTGCCTTTGGTGGAGATGCAGGGGCATGCGGGGCAGGGGCCATGTGG  2580

Qy  2830  GCCAGGATAGCCTGGGCTGTGTCCCAGTGGGAGGAGGAGGAGGAGGAGGGCCAGGGCT  2889
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2581  GCCAGGATAGCCTGGGCTGTGTCCCAGTGGGAGGAGGAGGAGGAGGAGGGCCAGGGCT  2640

Qy  2890  GAGTCCAGTCGGAGGAGCAGCAGGGCTGAGAGCCTCAGTGCCCCAGGTCAGT  2949
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2641  GAGTCCAGTCGGAGGAGCAGCAGGGCTGAGAGCCTCAGTGCCCCAGGTCAGT  2700

Qy  2950  GCAAGGCCTGTGCCTGAGGTCGGCAGGGCTCCCACCAGAGCTCTCCACCAGAGCCCACCCCA  3009
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2701  GCAAGGCCTGTGCCTGAGGTCGGCAGGGCTCCCACCAGAGCTCTCCACCAGAGCCCACCCCA  2760

Qy  3010  TGGGAGGACATCGGGCACGGCCAGGTCTCCCTGGTGCGACATCCGGACCTGCAGGTCATGCGGGAG  3069
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2761  TGGGAGGACATCGGGCACGGCCAGGTCTCCCTGGTGCGATCCGGACCTGCAGGTCATGCGGGAG  2820

Qy  3070  GCGGGCGACACAATATCCCCGGACATTTCCGAGGTGGACCCCGCCTACCTCAACCTCTCA  3129
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2821  GCGGGCGACACAATATCCCCGGACATTTCCGAGGTGGACCCCGCCTACCTCAACCTCTCA  2880

Qy  3130  GACCTGTAGATATCAAGTACCTCCATTCGAGTTTATGATCTTCAGGAAAGTTCCCCAAG  3189
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2881  GACCTGTAGATATCAAGTACCTCCATTCGAGTTTATGATCTTCAGGAAAGTTCCCCAAG  2940

Qy  3190  TCCGCTCAGCCAGAGCCGCCGCCCCCATGGGCTGGCCGAGTTCCCGGAG  3249
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db  2941  TCCGCTCAGCCAGAGCCGCCGCCCCCATGGGCTGGCCGAGTTCCCGGAG  3000

Qy  3250  CCCACGTGGCCCTGCCAGTGAACTGGGCCCCCACGCAGGCTGAGATCACAGAGGAG  3309
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3001  CCCACGTGGCCCTGCCAGTGAACTGGGCCCCCACGCAGGCTGAGATCACAGAGGAG  3060

Qy  3310  TCAGAGGATGTGGACGTGCTGGCAGAGGCTGCCGTGGGCAGGCAGGCGCAAGTGGTCC  3369
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3061  TCAGAGGATGTGGACGTGCTGGCAGAGGCTGCCGTGGGCAGGCAGGCGCAAGTGGTCC  3120

Qy  3370  TCGCCGTCACGCAGCCTCTTCCACTTCCCGTGGAGGCACCTGCGCGTGGATGAGCCTGCA  3429
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Db   3121 TCGCCGTCACGCAGCCTCTTCCCACTTCCCTGGGAGGCACCTGCCGCGTGGATGAGCCTGCA 3180

Qy   3430 GAGCTGGGGCTGCCGTGAGAGAGTGAAGGCCTTCCGTGAGCACATCTCCCGGATCCTGAAG 3489
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3181 GAGCTGGGGCTGCCGTGAGAGAGTGAAGGCCTTCCGTGAGCACATCTCCCGGATCCTGAAG 3240

Qy   3490 GGCAGGCCGGAAGGTCTGGAGGAGGAGGGCCCCCAGGAAGAAGCCAGGCCTTGCTTCC 3549
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3241 GGCAGCCCGGAAGGTCTGGAGGAGGAGGGCCCCCCAGGAAGAAGAGCCAGGCCTTGCTTCC 3300

Qy   3550 TTCCGGCTCTCAAGGTCTGAAGAGTCTGAAGAGCTGGGACCGGAGCGGCCGACATTCCTAAGGGAGCTCTCA 3609
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Db   3301 TTCCGGCTCTCAAGGTCTGAAGAGTCTGGGACCGGAGCGGCCGACATTCCTAAGGGAGCTCTCA 3360

Qy   3610 GATGAGACTGTGGTCCTGGGCCAGTCAGTGACACTGGCCTGCCAGTGTCAGCCCAGCCA 3669
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Db   3361 GATGAGACTGTGGTCCTGGGCCAGTCAGTGACACTGGCCTGCCAGTGTCAGCCCAGCCA 3420

Qy   3670 GCTGCCCAGGCCACTGGACCAAAGACCGAGCCCCCCTGGAGCAGCAGCCGTGTCCTC 3729
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3421 GCTGCCCAGGCCACTGGACCAAAGACCGAGCCCCCCTGGAGCAGCAGCCGTGTCCTC 3480

Qy   3730 ATCTCTGCCACCTCAAGAACTTCCAGCTTCTGACCATCCTGGTGGTGGTGGCTGAGGAC 3789
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3481 ATCTCTGCCACCTCAAGAACTTCCAGCTTCTGACCATCCTGGTGGTGGTGGCTGAGGAC 3540

Qy   3790 CTGGGTGTGTACACCTGCAGCGTGCAATGCGCTGAGCCGATATGCGGAGCAGTGACCACCACGGGGCGTC 3849
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3541 CTGGGTGTGTACACCTGCAGCGTGCAATGCGCTGGGGACAGTGACCACCACGGGGCGTC 3600

Qy   3850 CTCCGAAGGCAGAGGCCCCTCATCTTCGCCATGCCCGGATATCGGGGAGGTGTACGCG 3909
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3601 CTCCGAAGGCAGAGGCGCGCCCCTCATCTTCGCCATGCCCGGATATCGGGGAGGTGTACGCG 3660

Qy   3910 GATGGGGTGCTGGTCTGGTCTGGAATCCTACGGCCCTGTGACTTACATTGTG 3969
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3661 GATGGGGTGCTGGTCTGCTGGAATCCTACGGCCCTGTGACCTTACATTGTG 3720

Qy   3970 CAGTGCAGCCTAGAAGGCGGCAGCTGGACCCACCACTGGCCTCCGACATCTTTGACTGCTGC 4029
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3721 CAGTGCAGCCTAGAAGGCGGCAGCTGGACCACCACTGGCCTCCGACATCTTTGACTGCTGC 3780

Qy   4030 TACCTGACCAGCAAGCTCTCCCGGGGGTGCACCTGCACCTACACCTTCCGCACGCATGTGTCAGC 4089
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3781 TACCTGACCAGCAAGCTCTCCCGGGGGGTGCACCTACACCTTCCGCACGCATGTGTCAGC 3840

Qy   4090 AAGGCAGGAATGGGTCCCTACAGCAGCCCCCTCGGACAAGTCCTCCTGGGAGGGGCCCAGC 4149
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3841 AAGGCAGGAATGGGTCCCTACAGCAGCCCCCTCGGACAAGTCCTCCTGGGAGGGGCCCAGC 3900

Qy   4150 CACCTGGCCTCTGAGGAGAGAGCCAGGGGCGTCAGCCCAACCCCTGCCCAACACAAAG 4209
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3901 CACCTGGCCTCTGAGGAGAGAGCCAGGGGCGTCAGCCCAACCCCTGCCCAGCACAAAG 3960

Qy   4210 ACCTTCGCATTCCAGACACAGATCCAGAGGGGGCGCTCAGCGTGGTGCGGCCAATGCTGG 4269
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3961 ACCTTCGCATTCCAGACACAGATCCAGAGGGGGCCGCTTCAGCGTGGTGCGGCCAATGCTGG 4020

Qy   4270 GAGAAGGCCAGCGGCGGGGCGCTGCCGCCCAAGATCATCCCCTACCACCCCAAGGACAAG 4329
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4021 GAGAAGGCCAGCGGCGGGGCGCTGCCGCCGCCCAAGATCATCCCCTACCACCCCCAAGGACAAG 4080

Qy   4330 ACAGCAGTGCTGCGGCGAATACGAGGCCCTCAAGGGCCTTGCGCCACCCGCACCTGGCCCAG 4389
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4081 ACAGCAGTGCTGCGGCGAATACGAGGCCCTTCAAGGGCCTTCGCCACCCGCACCTGGCCCAG 4140

Qy   4390 CTGCACGCAGCCTACCTGCAGCCCCCCGGCACCTGTGCTCATCTTGGAGCTGTGCTCTGGG 4449
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4141 CTGCACGCAGCCAGCCTACCTGCAGCCCCCGGCACCTGTGCTCATCTTGGAGCTGTGCTCTGGG 4200

Qy   4450 CCCGAGCTGCTGCTCCCCTGCCCTGGCCGGAGGGGCCTCCTACTCAGAATCCGAAGGTGAAGGAC 4509
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4201 CCCGAGCTGCTGCTCCCCTGCCCTGGCCGGAGAGGGGCCTCCTACTCAGAATCCGAGGTGAAGGAC 4260
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Qy   4510 TACCTGTGGCAGATGTTGAGTGCCACCCAGTACCTGCGACGACACACCATCCTGCGACCTG 4569
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4261 TACCTGTGGCAGATGTTGAGTGCCACCCAGTACCTGCACAACCAGCACCATCCTGCGACCTG 4320

Qy   4570 GACCTGAGGTCCAGAACATGATCATCACCGGAATACAACCTGCTCAAGGTCGTGGACCTG 4629
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4321 GACCTGAGGTCCGAGAACATGATCATCACCGGAATACAACCTGCTCAAGGTCGTGGACCTG 4380

Qy   4630 GGCAATGCACAGAGCCTCAGCCAGGAGAAGGTGCGCCCTCAGACAAGTTCAAGGACTAC 4689
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4381 GGCAATGCACAGAGCCTCAGCCAGGAGAAGGTGCTGCCCTCAGACAAGTTCAAGGACTAC 4440

Qy   4690 CTAGAGACCATGGCTCCAGAGCTTCCTGGAGGCGCCAGGGGGTGTTCCACAGACAGACATC 4749
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4441 CTAGAGACCATGGCTCCAGAGCTTCCTGGAGGCGCCAGGGGGTGTTCCACAGACAGACATC 4500

Qy   4750 TGGGCCATCGGTGTGACAGCCTTCATCATGTGAGCGGCCAGTACCCGGTGAGCAGCGAG 4809
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4501 TGGGCCATCGGTGTGACAGCCCTTCATCATGTGAGCGGCCAGTACCCGGTGAGCAGCGAG 4560

Qy   4810 GGTGCACGCGACCTGCAGAGACGACTGCGCAAGGGGCTGGTTCCGGTGGTGAGCCGTGCTAC 4869
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4561 GGTGCACGCGACCTGCAGAGAGACTGCGCAAGGGGGCTGGTTCCGGTGGTGAGCCGTGCTAC 4620

Qy   4870 GCGGGGCGTGTCCGGGGGGCGCCGTGGCCTTCCTGCGCCTTCCTGCGCAGCACTCTGTGCGCCCAGCCCTGG 4929
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4621 GCGGGGCTGTCCGGGGGGCGCCGTGGCCTTCCTGCGCCTTCCTGCGCAGCACTCTGTGCGCCCAGCCCTGG 4680

Qy   4930 GGCCGGCCCTGCGCCTGCCGCTGCCTGCCAGTCGGCTGCCCGTGGCTAACAGGAGGAGGGCCCGGCC 4989
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4681 GGCCGGCCCTGCGCCTGCCGCTGCCTGCCAGTGCCCGTGGCTAACAGAGGAGGGCCCGGCC 4740

Qy   4990 TGTTCGCGGCCCGGCCCCGTGACCTTCCCTACCGCGGCGGTCTTCGTGCGCAAT 5049
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4741 TGTTCGCGGCCCGGCCCCGTGACCTTCCCTACCGCGGCGGTCTTCGTGCGCAAT 4800

Qy   5050 CGCGAGAAGAGACGCGCGCGCGTGCTGTACAAGAGCCACAACCTGGCCCAGGTGCGCTGAGGG 5109
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4801 CGCGAGAAGAGACGCGCGCGCGTGCTGTACAAGAGCCACAACCTGGCCCAGGTGCGCTGAGGG 4860

Qy   5110 TCGCCCCGGCCACACCCTTGGTCTCCCCGCGTGGGGGTGCGTGCAGACGCGGCCAATAAAAA 5169
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4861 TCGCCCCGGCCACACCCTTGGTCTCCCCGCGTGGGGGTGCGTGCAGACGCGCGGCCAATAAAAA 4920

Qy   5170 CGCACAGCCGGGCGAG 5185
          ||||||||||||||||
Db   4921 CGCACAGCCGGGCGAG 4936
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RESULT 10
US-10-077-130-3
; Sequence 3, Application US/10077130
; Publication No. US2002016874 2A1
; GENERAL INFORMATION:
; APPLICANT: Kapeller-Liberman, Rosana
; APPLICANT: Acton, Susan L.
; TITLE OF INVENTION: 59079 and 12599, Protein Kinase Family
; TITLE OF INVENTION: Members and Uses Therefor
; FILE REFERENCE: MPI2001-047P1RCP1(M)
; CURRENT APPLICATION NUMBER: US/10/077,130
; CURRENT FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: 60/269201
; PRIOR FILING DATE: 2001-02-15
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 7893
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-077-130-3

Query Match      93.0%;    Score 4841;    DB 14;    Length 7893;

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Best Local Similarity   99.9%;   Pred. No. 0;
Matches 4844;   Conservative   0;   Mismatches   5;   Indels   0;   Gaps   0;

Qy    258  CCCAGGGCCCCATCCATCGCAGTCAACCATGCAGGATGTGCAGGCACAGACAGGCGGAAC  317
           ||||| |||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db   3045  CGCACGGCCCCCATCCATCGCAGTCAACCATGCAGGATGTGCAGGCACAGACAGGCGGAAC  3104

Qy    318  GGCCCAATTCGAGGCTATCATTGAGGGCGACCCAGCCCTCGGTGACCTGGTACAAGGA  377
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3105  GGCCCAATTCGAGGCTATCATTGAGGGCGACCCACAGCCCTCGGTGACCTGGTACAAGGA  3164

Qy    378  CAGCGTCCAGCTGGTGGACAGCACCCGGCTTAGCCAGCAGCAAGAAGGCACCACATACTC  437
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3165  CAGCGTCCAGCTGGTGGACAGCACCCGGCTTAGCCAGCAGCAAGAAGGCACCACATACTC  3224

Qy    438  CCTGGTGTCTGAGGCATGTGGCCTCGAAGGATGCCCGGCGTTACACCTGCCTGGCCCAAA  497
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3225  CCTGGTGTCTGAGGCATGTGGCCTCGAAGGATGCCCGGCGTTACACCTGCCTGGCCCAAA  3284

Qy    498  CACTGGTTGGCCAGGTGCTTGCAAGGCAGAGCGAGCTGCACTCCTTCTATGAGGTCAAGG  557
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3285  CACTGGTTGGCCAGGTGCTTGCAAGGCAGAGCGAGCTGCACTCCTTCTATGAGGTCAAGG  3344

Qy    558  GGACTCAGAGAAGCAAAGCACCGAGGAAGCTGCACTCGGGCCCAGGCATACAGGGACGCG  617
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3345  GGACTCAGAGAAGCAAAGCACCGAGGAAGCTGCACTCGGGCCCAGGCATACAGGGACGCG  3404

Qy    618  GATTGGAAGGGGCGTGTTTGGCTTCGTAAAAAGAGTGCAGCACAAAGGAAACAAGATCTT  677
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3405  GATTGGAAGGGGCGTGTTTGGCTTCGTAAAAAGAGTGCAGCACAAAGGAAACAAGATCTT  3464

Qy    678  GTGCGCTGCCAAGTTCATCCCCACGGACGCAGAACTCGGGCCCAGGCATACAGGGAGGCG  737
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3465  GTGCGCTGCCAAGTTCATCCCCACGGACGCAGAACTCGGGCCCAGGCATACAGGGAGGCG  3524

Qy    738  AGACATCCTGGCCGCCTGAGCCACCCGGCTGGTCACGGGCTGCTGGACCAGTTTGAGAC  797
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3525  AGACATCCTGGCCGCCTGAGCCACCCGGCTGGTCACGGGCTGCTGGACCAGTTTGAGAC  3584

Qy    798  CCGCAAGACCCTCATCCTCATCCTGAGCTGTGCTCATCCAGGAGAGTGCTGACACGGCCT  857
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3585  CCGCAAGACCCTCATCCTCATCCTGAGCTGTGCTCATCCAGGAGAGTGCTGACACGGCCT  3644

Qy    858  GTACAGGAAGGGCGTGGTGACGAGGCCGAGGTCAAGGTCTACATCCAGCAGCTGGTGGA  917
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3645  GTACAGGAAGGGCGTGGTGACGAGGCCGAGGTCAAGGTCTACATCCAGCAGCTGGTGGA  3704

Qy    918  GGGGCTGCACTACCTTGCACAGCCAATGGCGTTCTCCACCTGGACATAAAGCCCTCTAACAT  977
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3705  GGGGCTGCACTACCTTGCACAGCCAATGGCGTTCTCCACCTGGACATAAAGCCCTCTAACAT  3764

Qy    978  CCTGATGGTGCATCCTGCCCGGGAAGCATTAAAATCTGCGACTTTGGCTTTGCCCAGAA  1037
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3765  CCTGATGGTGCATCCTGCCCGGGAAGCATTAAAATCTGCGACTTTGGCTTTGCCCAGAA  3824

Qy   1038  CATCACCCCAGCAGAGCTGCGAGTTCAGCCAGTACGGCTCCCCTGAGTTCGTCTCCCCGA  1097
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3825  CATCACCCCAGCAGAGCTGCGAGTTCAGCCAGTACGGCTCCCCTGAGTTCGTCTCCCCGA  3884

Qy   1098  GATCATCCAGCAGAGACCCTGTGAGCGGAAGCCTCCGACATTTGGGCATTTGGCCAACCTC  1157
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3885  GATCATCCAGCAGAGACCCTGTGAGCGGAAGCCTCCGACATTTGGGCATTTGGCCAACCTC  3944

Qy   1158  CTACCTCAGCCTGACCTGCTCATCCCCATTTGCCGGCGAGAGTGACCGTGCCACCCCCT  1217
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3945  CTACCTCAGCCTGACCTGCTCATCCCCATTTGCCGGCGAGAGTGACCGTGCCACCCCCT  4004

Qy   1218  GAACGTCCTGAGGGGCGCGTGTCATGGACGCAGCCCCATGGCTGCCACCTCAGCGGAAGA  1277
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4005  GAACGTCCTGAGGGGCGCGTGTCATGGACGCAGCCCCATGGCTGCCACCTCAGCGGAAGA  4064

Qy   1278  CGCCAAAGACTTCATCAAGGCTACGCTGCGAGAGAGCCCCTCAGGCCCGGCCTAGTGCGGC  1337
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||


Db   4065  CGCCAAAGACTTCATCAAGGCTACGCTGCGAGAGAGCCCCTCAGGCCCGGCCTAGTGCGGC  4124

Qy   1338  CCAGTGCCTCCTCCCACCCCTTGGTTCTGAAATCCATGCTGCGGAGGAGGCCCACTTCAT  1397
           |||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db   4125  CGCAGTGCCTCCTCCCACCCCTTGGTTCTGAAATCCATGCTGCGGAGGAGGCCCACTTCAT  4184

Qy   1398  CAACACCAAGCAGCTCAAGTTCCTTCCTGGCCCGAAGTCGCTGGCAGCGTTCCTGATGAG  1457
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4185  CAACACCAAGCAGCTCAAGTTCCTTCCTGGCCCGAAGTCGCTGGCAGCGTTCCTGATGAG  4244

Qy   1458  CTACAAGTCATCCTGGTGATGCGGCTCCATCCTCCTGAGCTGCTGCTGGGGGCCCACCGACAG  1517
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4245  CTACAAGTCATCCTGGTGATGCGGCTCCATCCTCCTGAGCTGCTGCTGGGGGCCCACCGACAG  4304

Qy   1518  CCCCTCCCTGGGCGTAGCCCGGCACCTCTTGCAGGGACACTGGTGGCTCCTCCAGTTCCTC  1577
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4305  CCCCTCCCTGGGCGTAGCCCGGCACCTCTTGCAGGGACACTGGTGGCTCCTCCAGTTCCTC  4364

Qy   1578  CTCCTCCTGACACGACGAGCTCGCCCCATTGCCCGGGCTAAGTCACTGCCACCCTCCCCC  1637
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4365  CTCCTCCTGACACGACGAGCTCGCCCCATTGCCCGGGCTAAGTCACTGCCACCCTCCCCC  4424

Qy   1638  GGTGACACACTCACCACTGCTGACACCCCCGGGGCTTCCTGCGGCCCTCGGCGAGCCTGCC  1697
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4425  GGTGACACACTCACCACTGCTGACACCCCCGGGGCTTCCTGCGGCCCTCGGCGAGCCTGCC  4484

Qy   1698  TGAGGAAGCCGAGGCCAGTGAGCGCTCACCGAGGCCCCAGCTTCCGCTTCCCTGCATCTCCCGA  1757
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4485  TGAGGAAGCCGAGGCCAGTGAGCGCTCACCGAGGCCCCAGCTTCCGCTTCCCTGCATCTCCCGA  4544

Qy   1758  GGGTGCCGGGCCACCCGGGCCGCCCCAGGGTGCGTGCCGGTGCCGGTGCATCCGGGGGCAGGCCT  1817
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4545  GGGTGCCGGGCCACCCGGGCCGCCCCAGGGTGCGTGCCGGTGCCGGTGCATCCGGGGGCAGGCCT  4604

Qy   1818  GTTCTACCACCAGGCGCGGTGAGAGCCCTGGACCACGGGGCCCTGGCCCGGGGAGGAGCAGGCG  1877
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4605  GTTCTACCACCAGGCGCGGTGAGAGCCCTGGACCACGGGGCCCTGGCCCGGGGAGGAGCAGGCG  4664

Qy   1878  GCACCCGGCCCGGGCCGCTTCATCCTCATCCTGAGCTGTGCTCATTGGGGGGCGCTACATTGGGGGGCGCTGCCAGG  1937
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4665  GCACCCGGCCCGGGCCGCTTCATCCTCATCCTGAGCTGTGCTCATTGGGGGGCGCTACATTGGGGGGCGCTGCCAGG  4724

Qy   1938  GTACAGGAAGGGCGTGGTGACGAGGCCGAGGTCAAGGTCTACATCCTGCGGAGCTGCTGATGGAGCACCGGCGTGCTGGAGGAGCA  1997
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4725  CCTGCGGAGCCGCCACTGATGGAGCACCGGCGTGCTGGAGGAGCA  4784

Qy   1998  GGGGCCACCCTCCTGGCCCAAAGCCCCTCTAACATGGCCACCCTCCTGGCCCAAAGCCCCTCTAACATGGCCCTTGTGGCCA  2057
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4785  GGCCACCCTCCTGGCCCAAAGCCCCTCTAACATGGCCCTTGTGGCCA  4844

Qy   2058  CACCCACTTGGCCCCTGGCCCCGCCACAGCCACTCCCTGGACAATGACTCCCTGGACACCCCCCG  2117
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4845  CACCCACTTGGCCCCTGGCCCCGCCACACTGCCTTCCAGCAACATGACTCCCTGGACACCCCCCG  4904

Qy   2118  CCCCTCCTGGAGGCTGCGGTGAGGCACAGCACGACTGCCTTCAGCCCCTCCGGGGGGC  2177
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4905  CCCCTCCTGGAGGCTGCGGTGAGGCACAGCACGACTGCCTTCAGCCCCTCCGGGGGGC  4964

Qy   2178  CCCTATCAGGGACATGGGGCACCCTGCAAGGAGCTCCAAGCAGTTCATTCCATCCACTGGTGCCA  2237
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4965  CCCTATCAGGGACATGGGGCACCCTGCAAGGAGCTCCAAGCAGTTCCATCCACTGGTGGCCA  5024

Qy   2238  CCCAGGCACTGCTCAGCCAGAGAGCCCATCCCGGACAGCAGCCCTTGGGGGCAGCAGCCCC  2297
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5025  CCCAGGCACTGCTCAGCCAGAGAGCCCATCCCGGACAGCAGCCCTTGGGGGCAGCAGCCCC  5084

Qy   2298  TTTCTGCCACCCCAAGCAGGGTTCGCCCCACCTCAGCCGGAAGACCCCCACCCCAGCAGT  2357
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5085  TTTCTGCCACCCCAAGCAGGGTTCTGCCCCACCTCAGCCGGAGAGGGGGCTGCACCCCAGCAGT  5144

Qy   2358  TGCCCCATGCCTCCTCCGGCTCCTTCCCTCCAGGATCTTGCAAAGAGGCCCCTTAGTACC  2417
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5145  TGCCCCATGCCTCCTCCGGCTCCTTCCCTCCAGGATCTTGCAAAGAGGCCCCTTAGTACC  5204
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Qy  2418  CTCAAGCCCCTTCTTGGGACAGCCCCAGGCACCCCTGCCCAAAGCAAGCCCCC  2477
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5205  CTCAAGCCCCTTCTTGGGACAGCCCCAGGCACCCCTGCCCAAAGCAAGCCCCC  5264

Qy  2478  ATTGGACTCTAAGATGGGGCCTGAGACATCTCTTCCTCTGGGAGGCCAAACCCGGCCC  2537
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5265  ATTGGACTCTAAGATGGGGCCTGAGACATCTCTTCCTCTGGGAGGCCAAACCCGGCCC  5324

Qy  2538  CTGCAGTTCCCCAGGTCAGCCTCCCAGGGCTCTTCCCAAGTGAGCTCCCTCAGGGT  2597
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5325  CTGCAGTTCCCCAGGTCAGCCTCCCAGGGCTCTTCCCAAGTGAGCTCCCTCAGGGT  5384

Qy  2598  GGGCTCCTCCCCAGGTCGGCACAGAGCCTGGCCCCTCCCTGGATGCGGAGGGCTGACCCA  2657
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5385  GGGCTCCTCCCCAGGTCGGCACAGAGCCCTGGCCCCTCCCTGGATGCGGAGGGCTGGACCCA  5444

Qy  2658  GGAGGCTGAGATCTGTCCGACTCCACACCCACCTTGCAGCCGGCCTCAGGAACAGGTGAC  2717
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5445  GGAGGCTGAGATCGTCCGACTCCACACCCACCTTGCAGCCGGCCTCAGGAACAGCGAC  5504

Qy  2718  CATGGGCAAGTTCTCCCTGGGTGTTCGCGGGGTGGTTCGCGGGGTCGCGGGGCTATGCAC  2777
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5505  CATGGGCAAGTTCTCCCTGGGTGTTCGCGGGGTGGTTCGCGGGGCTGGCTATGCAC  5564

Qy  2778  CTTTGCCTTTGGTGAGATGCAGGGGCATGCTGGGGCAGGGGCCCATGTGGGCCAGGAT  2837
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5565  CTTTGCCTTTGGTGAGATGCAGGGGCATGCTGGGGCAGGGGCCCATGTGGGCCAGGAT  5624

Qy  2838  AGCCTGGCTGTGTCCAGTCGGAGGAGCAGCAGGAGGAGCCAGGGCTGAGTCCCA  2897
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5625  AGCCTGGCTGTGTCCAGTCGGAGGAGCAGCAGGAGGAGCCAGGGCTGAGTCCCA  5684

Qy  2898  GTCGGAGGAGGAGCAGGAGGAGCCCAGGGCTGAGAGCCCACTGCCCCAGGTCAGTGCAAGGCC  2957
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5685  GTCGGAGGAGGAGCAGGAGGAGCCCAGGGCTGAGAGCCCACTGCCCCAGGTCAGTGCAAGGCC  5744

Qy  2958  TGTGCCTGAGGTCGGCAGGGCTCCCACCAGGAGCTCTCCAGGAGCTCTCCAGAGCCCCATGGGAGGA  3017
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5745  TGTGCCTGAGGTCGGCAGGGCTCCCACCAGGAGCTCTCCAGAGCCCCATGGGAGGA  5804

Qy  3018  CATCGGGCAGTCTCCCTGTGTGCAGATCCGGAGCCTGGTCAGGTGATGCGGAGGCGGCCGA  3077
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5805  CATCGGGCAGTCTCCCTGTGTGCAGATCCGGAGCCTGGTCAGTGCGGAGGCGGCCGA  5864

Qy  3078  CACAATATCCCTGGACATTCCGAGGTGACATTCCGAGGTGACCCCGCCTACCTCAAACCTTCTCAGACCCTGTA  3137
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5865  CACAATATCCCTGGACATTCCGAGGTGACCCCGCCTACCTCAACCTTCTCAGACCCTGTA  5924

Qy  3138  CGATATCAAGTACCTCCCATTCCCCATTCGAGTTTATGATCTTCAGGAAAGTCCCCAAGTTCCCAGTCCGTCA  3197
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5925  CGATATCAAGTACCTCCCATTCGAGTTTATGATCTTCAGGAAAGTCCCCAAGTCCCAGTCCGTCA  5984

Qy  3198  GCCAGAGCCGGCCGCCTCCCCGCCCCCATGGCTGAGGAGAGTCTGGCGCCGAGTTCCCGGAGCCCACGTG  3257
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5985  GCCAGAGCCGGCCGCCTCCCCGCCCCCATGGCTGAGGAGAGTCTGGCCGGAGTTCCCGAGCCCACGTG  6044

Qy  3258  GCCCTTGGCCAGGTGAACTGGGCCCCCACGCAGCCTGAGATCACAGAGAGTCAGAGGA  3317
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  6045  GCCCTTGGCCAGGTGAACTGGGCCCCCACGCAGCCTGAGATCACAGAGAGTCAGAGGA  6104

Qy  3318  TGTGGACGGCGGCTGCTGGCAGAGGGTGCCGTGGCGCAGAGGCGCAAGTGGTCCTCCGCCGTC  3377
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  6105  TGTGGACGGCGGCTGCTGGCAGAGGGTGCCGTGGCCAGGAAGCGCAAGTGGTCCTCCGCCGTC  6164

Qy  3378  ACGCAGCCTCCTTCCACTTCCCGTGAGGAGCCCTGCCTGGTGCGTGAGAGTCACATCTCCCGGAGCCTGAAGGGGCAGGGGC  3437
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  6165  ACGCAGCCTCCTTCCACTTCCACGTGAGGAGCCCTGCCTGGTGCGTGAGAGTCACATCTCCCGGAGCCTGAAGGGGCAGGGGC  6224

Qy  3438  GCTGCGTGAGAGTGAAGGCCTTGGCCTGGGATCTCCCGTGAGCACATCTCCCGGAGCCTGAAGGGGCAGGGGCC  3497
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  6225  GCTGCGTGAGAGTGAAGGCCTTGGCCTGGGATCTCCCGGAGCCTGAAGGGGCAGGGGCC  6284
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Qy  3498  GGAAGGTCTGGAGAAGGAGGGGCCCCCAGGAAGAAGCCAGGCCTTGCTTCCTTCCGGCT  3557
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  6285  GGAAGGTCTGGAGAAGGAGGGGCCCCCAGGAAGAAGCCAGGCCTTGCTTCCTTCCGGCT  6344

Qy  3558  CTCAGGTCTGAAGAGCTGGGACCGAGCGGCCGACATTCCTAAGGAGCTCTCAGATGAGAC  3617
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  6345  CTCAGGTCTGAAGAGCTGGGACCGAGCGGCCGACATTCCTAAGGAGCTCTCAGATGAGAC  6404

Qy  3618  TGTGGTCTGGGCCAGTCAGTGACACTGGCCTGTGCCCAGTGTGCAGCCAGCTGCCCA  3677
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  6405  TGTGGTCTGGGCCAGTCAGTGACACTGGCCTGTGCCCAGTGTGCAGCCAGCTGCCCA  6464

Qy  3678  GGCCACCTGGAGCAAAGACGGAGCCCCCCTGGGAGAGACAGCAGCCGTGTCCTCATCTCTGC  3737
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  6465  GGCCACCTGGAGCAAAGACGGAGCCCCCCTGGGAGAGACAGCAGCCGTGTCCTCATCTCTGC  6524

Qy  3738  CACCCTCAAGAACTTCAGCTTCAGCATCCTGGTGGTGGCTGAGAGACCTGGGTGT  3797
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  6525  CACCCTCAAGAACTTCAGCTTCAGCATCCTGGTGGTGGCTGAGAGACCTGGGTGT  6584

Qy  3798  GTACACCTGCAGCGTGAGCAATGCGCTGTGGGACAGTGACCACCACCAGCGCGTCTCCGAA  3857
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  6585  GTACACCTGCAGCGTGAGCAATGCGCTGTGGGACAGTGACCACCACCAGCGCGTCCTCCGAA  6644

Qy  3858  GGCAGAGCGCCCCTCATCTTCGCCATGCCCGGATATCGGGGAGGTGTACGCGGGATGGGGT  3917
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  6645  GGCAGAGCGCCCCTCATCTTCGCCATGCCCGGATATCGGGGAGGTGTACGCGGGATGGGGT  6704

Qy  3918  GCTGCTGGTTCTGGAAGCCCGTGACCTACGGCCCGTGTGAACTCTTGACTGTCAGTGCAG  3977
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  6705  GCTGCTGGTTCTGGAAGCCCGTGACCTACGGCCCGTGTGACCTACATTGTGCAGTGCAG  6764

Qy  3978  CCTAGAAGGCGGCAGCTGGACCACATCTGCTCTGCGTCTACCTGACTGCGTCTACCTGAC  4037
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  6765  CCTAGAAGGCGGCAGCTGGACCACATCTGCTCTGCGTCTACCTTGACTGCGTCTACCTGAC  6824

Qy  4038  CAGCAAGCTCCTCCGGGTGGCCACCTACACCTTCCGCACGGCATGTGTCAGCAAGGCAGG  4097
          ||||||||||||||||||||||||||||||||||  ||||||||||||||||||||||
Db  6825  CAGCAAGCTCTCCCGGGTGGCCACTACACCTTCCGCACGGCATGTGTCAGCAAGGCAGG  6884

Qy  4098  AATGGGTCCCTACAGCAGCCCCTCGGCAAGTCTCCTCTGGGAGGGCGCCCAGCCACCTGGC  4157
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  6885  AATGGGTCCCTACAGCAGCCCCTCGGCAAGTCTCCTCTGGGAGGGCGCCCAGCCACCTGGC  6944

Qy  4158  CTCTGAGGAGGAGCCAGGAGGCGGTCAGCCCTTCGCCCAGCCACACAGACCTTCGC  4217
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  6945  CTCTGAGGAGGAGCCAGGAGGCGGTCAGCCCTTCAGCGCCCAGCCACACAGACCTTCGC  7004

Qy  4218  ATTCCAGACACAGATCCCAGAGGGGCGCCGCTTCAGCCGCGGTGGTCGGCAATGCTGGGAGAGGC  4277
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  7005  ATTCCAGACACAGATCCCAGAGGGGCGCCGCTTCAGCCGCGGTGGTCGGCAATGCTGGGAGAGGC  7064

Qy  4278  CAGCGGCGGCGGCGCCCTCCCCAAGATCATCCCCACCCCAAGGACAAGACAGCAGCAGT  4337
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  7065  CAGCGGCGGCGGCGCCCTGCCCCAAGATCATCCCTACCACCCCAAGGACAAGACAGCAGT  7124

Qy  4338  GCTGCGGAATACGAGGCCCTCAAGGAGCTGCACCCCGCCACCTGCCACCTGCACGCG  4397
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  7125  GCTGCGGAATACGAGGCCCTCAAGGAGCTGCACCCCGCCACCTGCCACCTGCACGCG  7184

Qy  4398  AGCCTACCTCAGCCCCCGGCACCTGGTGCTCATCTTGGAGTCTGTGCTGTCTGGGCCCGAGCT  4457
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  7185  AGCCTACCTCAGCCCCCGGCACCTGGTCTCATCTTGGAGTCTGTGCTGTCTGGGCCCGAGCT  7244

Qy  4458  GCTCCCCTGCCTGCCGAGGGGCCTTCCTCTACTCAGAATCTGAGGACTACCTGTG  4517
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  7245  GCTCCCCTGCCTGCCGAGGGGCCTTCCTCTACTCAGAATCTGAAGGACTACCTGTG  7304

Qy  4518  GCAGATGTTGAGTGCCACCCAGTACCTGCACAACCAGCACATCCTGGACCTGAG  4577
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  7305  GCAGATGTTGAGTGCCACCCAGTACCTGCACAACCAGCACATCCTGGACCTGAG  7364

Qy  4578  GTCCGAGAACATGATCATCCACCGAATACAACCTGCTCAAGGTCGTCGTGGGCAATGC  4637
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Qy    438  CCTGGTGCTGAGGCATGTGGCCTGAAGGATGCCGGCGTTACACCTGCCTGCTGGCCAAAA   497
           |||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Db  19239  CCTGGTGCTGAGGCATGTGGCCTGAAGGATGCCGGCGTTTACACCTGCCTGCTGGCCAAAA  19298

Qy    498  CACTGGTGGCCAGGTGCTCTGCAGAGCAGAGAGCTGCTGGTGCTTGGGGGGACAATGAGCC   557
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  19299  CACTGGTGGCCAGGTGCTCTGCAGAGCAGAGAGCTGCTGGTGCTTGGGGGGACAATGAGCC  19358

Qy    558  GGACTCAGAGAAGCAAAGCACCGGAGAAGCTGCACTCCTTCTATGAGGTCAAGGAGGAGA   617
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  19959  GGACTCAGAGAAGCAAAGCACCGGAGAAGCTGCACTCCTTCTATGAGGTCAAGGAGGAGA  19418

Qy    618  GATTGGAAGGGCGTGTTGGCTTCGTAAAAGAGTGCGCACAAAAGGAAACAAGATCTT   677
           ||||||||||||| ||||| ||||||||||||||||| ||||||||||| |||||||
Db  19419  GATTGGAAGGGCGTGTGTT GGCTTCGTAAAAGAGTGCGCAGACAAAAGGAAACAAGATCTT  19478

Qy    678  GTGCGCTGCCAAGTTCATCCCCTACGGAGCAGAACTCGGGGCCCAGGCATACAGGGAGCG   737
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  19479  GTGCGCTGCCAAGTTCATCCCCTACGGAGCAGAACTCGGGGCCCAGGCATACAGGGAGCG  19538

Qy    738  AGACATCCTGGCCGCGTGAGCCCGCTGGTCACCCGCTGGTCACGGGCGTGCTGGACCAGTTTGAGAC   797
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  19539  AGACATCCTGGCCGCGTGAGCCCGCTGGTCACCCGCTGGTCACGGGCGTGCTGGACCAGTTTGAGAC  19598

Qy    798  CCGCAAGACCCTCATCCTCATCTGGAGCTGTGCTGCTCATCCGGAGCGTGCTGGACCGCCT   857
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  19599  CCGCAAGACCCTCATCCTCATCTGGAGCTGTGCTGCTCATCCGGAGCGTGCTGGACCGCCT  19658

Qy    858  GTACAGGAAGGGCGTGGTGAGCGGCCGGAGGCCGGAGGTCAAGGTCTCATCCACCTGGTGGA   917
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  19659  GTACAGGAAGGGCGTGGTGAGCGGCCGGAGGCCGGAGGTCAAGGTCTCATCCACCTGGTGGA  19718

Qy    918  GGGGCTGCACTACCTGCACAGCCATGGCGTTCTCCACCTGGACATAAAGCCCTCTAACAT   977
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  19719  GGGGCTGCACTACCTGCACAGCCATGGCGTTCTCCACCTGGACATAAAGCCCTCTAACAT  19778

Qy    978  CCTGATGGTGCATCCGCCCGGGAAGACATTAAAATCTGCGACTTTGGCTTTGCCCAGAA  1037
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  19779  CCTGATGGTGCATCCGCCCGGGAAGACATTAAAATCTGCGACTTTGGCTTTGCCCAGAA  19838

Qy   1038  CATCACCCCAGCAGAGCTGCAGTTCAGCCAGTACGGGCTCCCCCGAGTTCGTCTCCCCGA  1097
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  19839  CATCACCCCAGCAGAGCTCAGCCAGTACGGGCTCCCCTGAGTTCGTCTCCCCCCGA  19898

Qy   1098  GATCATCCAGCAGAACCCTGTGAGCGGAAGCCTTCCGACATTTGGGCCCATGGGTGTCATCTC  1157
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  19899  GATCATCCAGCAGAACCCTGTGAGCGGAAGCCTCCGACATTTGGGCCCATGGGTGTCATCTC  19958

Qy   1158  CTAACTTCAGCCTGACCTGCTCATCCCCATTTGCCGGCGAGAGTGACCGTGCCACCCCCCT  1217
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  19959  CTAACTTCAGCCTGACCTGCTCATCCCCATTTGCCGGCGAGAGTGACCGTGCCACCCCCCT  20018

Qy   1218  GAAGGTCCTGGAGGGGCGCGTGTCATGGAGCAGCCCCATGGCTGCCCACCTCAGCGAAGA  1277
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  20019  GAAGGTCCTGGAGGGGCGCGTGTCATGGAGCAGCCCCATGGCTGCCCACCTCAGCGAAGA  20078

Qy   1278  CGGCCAAAGACTTCATCAAGCTACAGCTCTGCAGAGCGCCCGGGCTAGTGCGGC  1337
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  20079  CGGCCAAAGACTTCATCAAGCTACAGCTCTGCAGAGCGCCCGGGCCTAGTGCGGC  20138

Qy   1338  CCAGTGCCTCTCCCACCCCTGGTTCCTGAAATCATGCGCCTGCGGGAGGAGGCCCACTTCAT  1397
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  20139  CCAGTGCCTCTCCCACCCCTGGTTCCTGAAATCATGCGCCTGCGGGAGGAGGCCCACTTCAT  20198

Qy   1398  CAACACCAAGCAGTTCCTTCCTGGCCGAAGTCGCTGCGAAGTCGCTGCCTGATGAG  1457
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  20199  CAACACCAAGCAGTTCCTTCCTGGCCGAAGTCGCTGCGAAGTCGCTGCCTGATGAG  20258

Qy   1458  CTACAAGTCCATCCTGGTGATGCCTCCATCCCTGACCTGGTGCTGCGGGGCCCACCCGACAG  1517
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  20259  CTACAAGTCCATCCTGGTGATGCCTCCATCCCTGACCTGGTGCTGCGGGGCCCACCCGACAG  20318
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RESULT 11
US-10-077-130-6
; Sequence 6, Application US/10077130
; Publication No. US20020168742A1
; GENERAL INFORMATION:
; APPLICANT: Kapeller-Liebermann, Rosana
; APPLICANT: Acton, Susan L.
; TITLE OF INVENTION: 59079 and 12599, Protein Kinase Family
; TITLE OF INVENTION: Members and Uses Therefor
; FILE REFERENCE: MPI2001-047P1RCP1(M)
; CURRENT APPLICATION NUMBER: US/10/077,130
; CURRENT FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: 60/269201
; PRIOR FILING DATE: 2001-02-15
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 23907
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-077-130-6

Query Match     93.0%;  Score 4841;  DB 14;  Length 23907;
Best Local Similarity   99.9%;  Pred. No. 0;
Matches 4844;  Conservative 0;  Mismatches 0;  Indels 5;  Gaps 0;

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Qy    258  CCCAGGGCCCCATCCATGCGAGGTAACCATCGAGGATGTGCAGGCACAGACAGGCGGAAC   317
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  19059  CGCACGGCCCCTCCCCACCCCATCCATGCGAGGTAACCATCGAGGATGTGCAGGCACAGACAGGCGGAAC  19118

Qy    318  GGCCCAATTGCGAGGCTATCATTGAGGGCGACCCCACAGCCCTCTCCGTGACCTGGTACAGGA   377
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  19119  GGCCCAATTGCGAGGCTATCATTGAGGGCGACCCCACAGCCCTCTCCGTGACCTGGTACAGGA  19178

Qy    378  CAGCGGTCCAGCTGGTGGACAGCAGCACCCGGCTTAGCCAGCAAGAAGGCACCACCACATACTC   437
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Db  19179  CAGCGGTCCAGCTGGTGGACAGCAGCACCCGGCTTAGCCAGCAGCAAGAAGGCACCACCACATACTC  19238
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Db   7365  GTCCGAGAACATGATCATCACCGAATACAACCTGCTCAAGGTCGTGGACCTGGGCAATGC   7424
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Qy   4638  ACAGAGCCTCAGCCAGGAGAAGGTGCTGCCCTCAGACAAGTTCAAGGACTACCTAGAGAC   4697
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Db   7425  ACAGAGCCTCAGCCAGGAGAAGGTGCTGCCCTCAGACAAGTTCAAGGACTACCTAGAGAC   7484

Qy   4698  CATGGCCCCAGAGCTCCTGGAGGGGCTGTTCACAGACAGACACATCTGGGCCAT   4757
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7485  CATGGCTCCAGAGCTCCTGGAGGGGCCAGGGGCTGTTCCACAGACAGACACATCTGGGCCAT   7544

Qy   4758  CGGTGTGACAGCCTTCATCATGTGAGCGCCGAGTACCCGGTGAGCAGCGAGGGTGCACG   4817
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Db   7545  CGGTGTGACAGCCTTCATCATGTGAGCGCCGAGTACCCGGTGAGCAGCGAGGGTGCACG   7604

Qy   4818  CGACCTGCAGAGAGACTGCCCAAGGGGCTGGTCCGGCTCAGCCGCTGCTACGCGGGGCT   4877
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Db   7605  CGACCTGCAGAGAGACTGCGCGCAAGGGGCTGGTCCGGCTGTCCGGCTGCTACGCGGGGCT   7664

Qy   4878  GTCCGGGGCGCCGTGCCTTCCTGCGCAGCACTCTGTGCGCCAGCCCTGGGGCCGCC   4937
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Db   7665  GTCCGGGGGCGCCCGTGCCTTCCTGCGCAGCACTCTGTGCGCCAGCCCTGGGGCCGCC   7724

Qy   4938  CTGCGGCGTCCAGCTGCCTGCGAGTGCCCGTGCCTACAGAGGAGGGCCCGGCCTGTTCGCG   4997
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Db   7725  CTTGCGCCTCCAGCTGCCTGCGAGTGCCTACAGAGAGGAGGAGGGCCCGGCCTGTTCGCG   7784

Qy   4998  GCCCGCCCGTGACCTTCCCTACCGCGCGGCGTCTTCGTGCGCAATCGCAGAGAA   5057
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7785  GCCCGGCCCGTGACCTTCCCTACCGCGCGGCCGTCTTCGTGCGCAATCGCAGAGAA   7844

Qy   5058  GAGACCGCGCGCTGCTGTACAAGAGAGCACAACCTGCCCAGGTGCGCTGA   5106
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Db   7845  GAGACGCGCGCGCTGCTGTACAAGAGAGCACAACCTGCCCAGGTGCGCTGA   7893
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Qy      1518 CCCCTCCCTCGGCGTAGCCCGGCCGCACCTCTGAGGGACACTGGTGGCTCCTCCAGTTCCTC 1577
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Qy      1578 CTCCTCCTCTGACAACGAGCTCGCCCGGGCTAAGTCACTGCCACCCTCCCC 1637
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Qy      1638 GGTGACACACTCACCACTGCTCGTGCACCCCCGGGGCTTCCTGCGGGCCCTCGGCGCCTCGCC 1697
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Db     20439 GGTGACACACTCACCACTGCTCGTGCACCCCCGGGGCTTCCTGCGGGCCCTCGGCCAGCCTGCC 20498

Qy      1698 TGAGGAAGCCGAGGCCAGTGAGCGCTCCACCGAGGCCCAGCTCCGCCTGCATCTCCCGA 1757
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Db     20499 TGAGGAAGCCGAGGCCAGTGAGCGCTCCACCGAGGCGCTCCACCGAGCCCTGCATCTCCCGA 20558

Qy      1758 GGGTGCCGGGCACCGGCCGCCCAGGGCTCGTGCCCGCACAGCGTCATCGCAGCCT 1817
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Db     20559 GGGTGCCGGGCACCGGCCGCCCAGGGCTGCCCGCACAGCGTCATCGCAGCCT 20618

Qy      1818 GTTCTACCACCAGGCGGGTGAGAGCCTGAGCACGGGGCCCTCGGCTGCCTCCCTCTGG 1877
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Db     20619 GTTCTACCACCAGGCGGGTGAGAGCCTGAGCACGGGGCCCTGGCCCTCGGCTGCCTCCCTCTGG 20678

Qy      1878 GCACCCGGCCCGCGCGGCCACCTGCTGCACATTGCGGGGGGCGCTGCCAGG 1937
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Qy      1938 CCTGCGGGAGCCACTGATGGAGCACCGCGTGTCGGAGGAGGAGGAGGAGCA 1997
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Qy      1998 GGCCACCCTCTGGCCAAAGCCCCTCATTCGAGACTGCCCTCCGGCTGCCTCGG 2057
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Db     20799 GGCCACCCTCTGGCCAAAGCCCCTCATTCGAGACTGCCCTCCGGCTGCCTCGG 20858

Qy      2058 CACCCACTTGGCCCCTGGCCACAGCAGCCACTCCCTGAAACATGACTCTCCGAGACACCCCG 2117
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Qy      2118 CCCCTCCTCGGAGGCCTCGGTGAGGCACAGCACGCCGACTGCCTTCAGCCCCCTCCGGGGGGC 2177
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Qy      2178 CCCTATCAGGGACATGGGGCACCCTCAGGGCTCCAAGCAGCTTCCATCCACTGGTGGCCA 2237
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Qy      2238 CCCAGGCACTGCTCAGCCAAGCAGAGGCCATCCCGAGAGGGCTGCAGCCCAGCAGT 2297
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Qy      2298 TTTCTGCCACCCCAACCAGGGTTCTGCCCCCCGAGAGGGCTGCAGCCCCCACCCAGCAGT 2357
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Db     21099 TTTCTGCCACCCCAAGCAGAGGGTTCTCGCCCCCCGAGAGGGCTGCAGCCCCCACCCAGCAGT 21158

Qy      2358 TGCCCCATGCCCTCCTGGCTCTTCCCCGAGATCTTGCAAAGAGGCCCCTTAGTACC 2417
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Qy      2418 CTCAAGCCCCTTCTTGGGACAGCCCCAGGCACCCCCGCCCAAAGCAAGCCCCCC 2477
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Db     21219 CTCAAGCCCCTTCTTGGGACAGCCCCAGGCACCCCCGCCCAAAGCAAGCCCCCC 21278

Qy      2478 AATTGGACTCTAAGATGGGGGCCTGGACATCTCTTCCTCCTGGGAGGCCAAAACCCGGCCC 2537
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Qy      2538 CTGCAGTTCCCAGGGTCAGCCTCCCGAGCTCTTCCCAAGTGAGCTCCCTCAGGGGT 2597
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Db     21339 CTGCAGTTCCCAGGGTCAGCCTCCCGAGCTCTTCCCAAGTGAGCTCCCTCAGGGGT 21398

Qy      2598 GGGCTCCTCCCCAGGTGGGCACAGAGCCTGGCCCTCCCTGGATGCGGAGGGGCTGGACCCA 2657
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Qy           GGGCTCCTGAGGATCTGTCCGACTTCCACCCACCTTGCAGCCGGCCGCTCAGAGGCTGGAACAGGTGAC 2717
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Db     21399 GGGCTCCTCCAGTGGTGGCACAGAGCCTGGCCCTCCCTGGATGCGGAGGGGCTGGACCCA 21458

Qy      2658 GGAGGCTGAGGATCTGTCCGACTTCCACACCACCTTGCAGCCGGCCGCTCAGGAACAGGCGAC 2717
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Qy      2718 CATGCGCAAGTTCTCCCTGGTGTCGCGGGGCTACGCCAGCAGCGTGGCTGGCTGGCTATGGCAC 2777
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Db     21519 CATGCGCAAGTTCTCCCTGGTGTCGCGGGGCTACGCCAGCAGCGTGGCTGGCTGGCTATGGCAC 21578

Qy      2778 CTTTGCCTTTGGTGGAGATGCAGGGGCCATGCTGGGGCAGGGGCCCATGTGGGCCAGGAT 2837
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Qy      2838 AGCCTGGCGTGTCCCAGTCGGAGGAGGAGGAGCAGGAGGCCAGGGCTGAGTCCCA 2897
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Qy      2898 GTCGGAGGAGCACGCAGAGGAGGACCCTGAGGAGCGTGAGGCTGAGAGCCCCACTGCCCCAGGTCCAGGCC 2957
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Db     21699 GTCGGAGGAGCAGCAGGAGGACCCTGAGGAGCGTGAGGCTGAGAGCCCCACTGCCCCAGTGTCAGGCAAGGCC 21758

Qy      2958 TGTGCCTGAGGTCGGTCGGCAGGGCTCCCACCAGGAGCTCTTCCAGAGCCCCATGGGAGGA 3017
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Qy      3018 CATGGGCAGGTCCCTGGTGCAGATCCGGACCTGTCAGGTGATGCGGAGGCGGCCGA 3077
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Qy      3318 ACGCAGCCCTTCACTTCCCTGGGAGCACTTCCCCGATGAGCCCGTCCTGCCCGTC 3377
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Db     22119 ACGCAGCCCTTCACTTCCCTGGGAGCACTTCCCCGATGAGCCCGTCCTGCCCGTC 22178

Qy      3378 GCTGCGTGAGAGTGAAGGCGCCGCTGGGAGCATCTCCCGGCACATCTCCCGGATCCTGAAGGGCAGGGC 3437
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Db     22179 GCTGCGTGAGAGTGAAGGCGCCGCTGGGAGCATCTCCCGGCACATCTCCCGGATCCTGAAGGGCAGGGC 22238

Qy      3438 GGAAGGTCTGGAGAGGAGGGGCCCCCAGGAGAGCCAGGCCTTCCTTGCTT 3497
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Db     22239 GGAAGGTCTGGAGAGGAGGGGCCCCAGGAGAGCCAGGCCTTCCTTGCTT 22298

Qy      3498 GGAAGGGTCTGGACGACGGAAGCGGCCGACATTCCTAAGGGAGCTCTAAGGAGCTCTCAGATGAGAC 3557
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     22299 GGAAGGGTCTGGAGGAGGAAGCGGCCAGGCCTTGCTTCCTTCCGGCT 22358

Qy      3558 CTCAGGTCTGAGAGCTTGGCAGGAGCTGGACGCGCCGACATTCCTAAGGGAGCTCTCAGATGAGAC 3617
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Db     22359 CTCAGGTCTGAGAGCTCGGAGACCGAGCGGCCGACATTCCTAAGGGAGCTCTCAGATGAGAC 22418

Qy      3618 TGTTGGTCCTCGGGGCCAGTGACACCGGCTGCCAGCAGTGTCAGCAGCTGCCCAGGGT 3677
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     22419 TGTTGGTCCTCGGGGCCAGTGACACTGGCCAGTGTCAGCAGCTGCCCAGGGT 22478

Qy      3678 GGCCACCTGGAGCAAAGACGGAGCCCCCTGGAGAGCAGCAGCGCCCCCTGTCCTCATCCTCTGC 3737
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Db  22479 GGCCACCTGGAGCAAAGACGGAGCGAGCCCCCCTGGAGAGCAGCAGCCGTGTCCTCATCTTGC 22538

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Qy   3798 GTACACCTGAGCGTGAGCAATGCTGGGGACGTGACCACACGGGCGTCCTCCGGAA 3857
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Qy   3858 GGCAGAGCGCCCCTCATCTTCGCCATGCCCGATATCGGGGAGTGTACGCGGATGGGT 3917
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Qy   3918 GCTGCTGGTCTGGAAGCCCGTGGAATCCTACGGGCCCTGTGACCTACATTGTGCAGTGCAG 3977
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Db  22719 GCTGCTGGTCTGGAAGCCCGTGGAATCCTACGGGCCCTGTGACCTACATTGTGCAGTGCAG 22778

Qy   3978 CCTAGAAGGGCGCAGCTGGACCACACTGGCCTCCGACATCTTTGACTGCTGCTACCTGAC 4037
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Qy   4158 CTCTGAGGAGGAGAGCCAGGAGGCCGGTCAGCCCAGCACCCCTGCCCAGCACAAAGACCTTCGC 4217
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Qy   4278 CAGCGGGCGGGCGCTGGCCGCCAAGATCATCCCCTAACCCCAAGGACAAGACAGCAGT 4337
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Qy   4398 AGCCTACCTCAGCCCCCGGACCTGGTGCTGCATCTTGGAGCTGTCTGGGGCCCCGAGCT 4457
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Db  23199 AGCCTACCTCAGCCCCCGGACCTGGTGCTGCATCTTGGAGCTGTCTGGGGCCCCGAGCT 23258

Qy   4458 GCTCCCCTGCCTGCCTGCCGAGAGGGGCCTCCTACTCAGAATCTGAGGTGAAGGACTACCTGTG 4517
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Db  23259 GCTCCCCTGCCTGCCTGCCGAGAGGGGCCTCCTACTCAGAATCTGAGGTGAAGGACTACCTGTG 23318

Qy   4518 GCAGATGTTGAGTGCCACCAGTACCTGCACAACCAGCACATCCTGACCTGGACCTGAG 4577
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Qy   4578 GTCCGAGACAGATCATCACCGAATACAACCTGCTCAAGGTCGTGGACCTGGGCAATGC 4637
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Qy   4638 ACAGAGCCTCAGCCAGGAGAAGGTGCTGCCCTCAGACAAGTTCAAGGACTACCTAGAGAC 4697
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Db  23499 CATGGTCTCCAGAGTCTCCAGAGCTCCTGAGGGCCAGGGGGGTGTTCCACAGACAGCATCTGGGCCAT 23558

Qy   4758 CGGTGTGACAGCCTTCATCATGTGTGAGCGCGAGTACCCCGGTGAGCGGGTGCACG 4817
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Db  23559 CGGTGTGACAGCCTTCATCATGTGTGAGCGCGAGTACCCCGGTGAGCGGGTGCACG 23618
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Qy   4818 CGACCTGCAGAGAGACTGCGCGCAAGGGGCTGGTCCGGCTGAGCAGCCGCTACGCGGGGGCT 4877
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Db  23859 GAGACGGCGCGCTGCTGTACAAGAGGCACAACCTGCCCAGGTGCGGCTGA 23907
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RESULT 12
US-10-307-019-2
; Sequence 2, Application US/10307019
; Publication No. US20030108533A1
; GENERAL INFORMATION:
;   APPLICANT: Zeng, Wenlin
;   APPLICANT: Stanton, Lawrence
;   APPLICANT: SCIOS, INC.
;   TITLE OF INVENTION: MEDIATORS OF SIGNAL TRANSDUCTION
;   FILE REFERENCE: SCIOS.021DV1
;   CURRENT APPLICATION NUMBER: US/10/307,019
;   CURRENT FILING DATE: 2002-11-26
;   PRIOR APPLICATION NUMBER: 09/548,473
;   PRIOR FILING DATE: 2000-04-13
;   PRIOR APPLICATION NUMBER: 60/129,552
;   PRIOR FILING DATE: 1999-04-16
;   NUMBER OF SEQ ID NOS: 9
; SEQ ID NO 2
;   LENGTH: 4175
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)...(4053)
US-10-307-019-2

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  Query Match        79.6%;    Score 4146.6;   DB 15;   Length 4175;
  Best Local Similarity  99.9%;   Pred No. 0;
  Matches 4149;  Conservative 0;  Mismatches 4;  Indels 0;  Gaps 0;

Qy   1055 TGCAGTTCAGCCAGTACGGCTCCCCGAGTTCGTCTCCCCGAGATCATCCAGCAGAGAACC 1114
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Qy   1175 GCTCATCCCCATTTGCCGGCGAGAGTGACCGTGCACCCTCCTGAACGTCCTGGAGGGGC 1234
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Db    125 GCTCATCCCCATTTGCCGGCGAGAGTGACCGTGCACCCTCCTGAACGTCCTGGAGGGGC 184

Qy   1235 GCGTGTCATGGAGCAGCCCCATGGCGTGCCACCTCAGCGAAGACGCGCCAAAGACTTCATCA 1294
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Db    185 GCGTGTCATGGAGCAGCCCCATGGCGTGCCACCTCAGCGAAGACGCGCCAAAGACTTCATCA 244

Qy   1295 AGGCTACGCTGCAGAGAGCCCGTCAGGCCGGCCAGTGCGGCCACG 1354
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Qy 1355 CCTGGTTCCTGAAATCCATGCTGCGGAGGAGGCCACTTCATCAACACCAAGCAGCTCA 1414
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Qy 2255 CAGAGAGGCCATCCCGGACAGCCCTTGGGGGCAGCCAGCCCCTTTCTGCCACCCCAAGC 2314
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Db 1865 AGGGCAGGGCTGAGAGCCCACTGCCCCAGTCAGTGGGCCTGTGCCTGAGGTCGGCA 1924

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Db  3605 AGAAGGTGCTGCCCTCAGACAAGTTCAGGACTACCTAGAGACCATGGCTCCAGAGCTCC 3664

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Qy  4835 TGCGCAAGGGCGTGGTCCGGCTGAGCCGCGTCTACGCGGGGCTGTCCCGGGGCCCGTG 4894
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RESULT 13
US-10-311-034-46
; Sequence 46, Application US/10311034
; Publication No. US20040023242A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: YUE, Henry
; APPLICANT: LAL, Preeti
; APPLICANT: BANDMAN, Olga
; APPLICANT: BOROWSKY, Mark L.
; APPLICANT: AU-YOUNG, Janice
; APPLICANT: LU, Yan
; APPLICANT: GANDHI, Ameena R.
; APPLICANT: TRIBOULEY, Catherine M.
; APPLICANT: CHAWLA, Narinder K.
; APPLICANT: YAO, Monique G.
; APPLICANT: LU, Dyung Aina M.
; APPLICANT: GREENWALD, Sara R.
; APPLICANT: RAMKUMAR, Jayalaxmi
; APPLICANT: GRIFFIN, Jennifer A.
; APPLICANT: KEARNEY, Liam
; APPLICANT: BURFORD, Neil
; APPLICANT: NGUYEN, Danniel B.
; APPLICANT: TANG, Y. Tom
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: HE, Ann
; APPLICANT: THORNTON, Michael
; APPLICANT: HAFALIA, April
; APPLICANT: ARVIZU, Chandra S.
; APPLICANT: GURURAJAN, Rajagopal
; APPLICANT: LO, Terence P.

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Db  2465 AGGGGCCCCAGGAGAAGAGCCAGGCTTGCTTCCTTCCGGCTCTCAGGTCTGAAGAGCT 2524
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Qy  4355 CCCTCAAGGGCTGCGCCACCCCGCCACCCTGGCCACGCAGCCTACCTCAGCCCCCC 4414

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; APPLICANT: KHAN, Farrah A.
; APPLICANT: RECIPON, Shirley A.
; APPLICANT: AZIMZAI, Yalda
; APPLICANT: POLICKY, Jennifer L.
; APPLICANT: DING, Li
; APPLICANT: GRETHER, Megan
; APPLICANT: ELLIOTT, Vicki S.
; APPLICANT: THANGAVELU, Kavitha
; APPLICANT: BATRA, Sajeev
; APPLICANT: ISON, Craig H.
; TITLE OF INVENTION: HUMAN KINASES
; FILE REFERENCE: PI-0125 PCT
; CURRENT APPLICATION NUMBER: US/10/311,034
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: 60/212,073; 60/213,467; 60/215,651; 60/216,605; 60/218,372; 2000-0
    60/228,056
; PRIOR FILING DATE: 2000-06-15; 2000-06-23; 2000-06-30; 2000-07-07; 2000-07-13; 2000-0
    25
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PERL Program
; SEQ ID NO 46
; LENGTH: 3225
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20040023242A1 3016969CB1
US-10-311-034-46

Query Match   61.4%;   Score 3197.8;   DB 17;   Length 3225;
Best Local Similarity   99.9%;   Pred. No. 0;
Matches 3210;   Conservative   0;   Mismatches   0;   Indels   2;   Gaps   1;

Qy  1979 AGGCCGCCAGGGAGGAGGAGCCACCCTCCTGGCCAAAGCCCCTCATTCGAGACTGCCC 2038
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Db   253 TTCCATCCACTGGTGGCCACCCAGGCACTGCTCAGCCAGGACACTGCTCAGCCCGGACAGCC 312

Qy  2279 CTTGGGGCAGCCAGCCCCTTTCTGCCACCCAAGCAGGGTTCTGCCCCCCAGGAGGGCT 2338
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   313 CTTGGGGCAGCCAGCCCCTTTCTGCCACCCAAGCAGGGTTCTGCCCCCCAGGAGGGCT 372

Qy  2339 GCAGCCCCCACCCAGCAGTGCCCCATGCCCTCCTTCCTGGCCTCCCTTCCCTCCAGGATCTTGCA 2398
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   373 GCAGCCCCCACCCAGCAGTGCCCCATGCCCTCCTTCCTGGCCTCCCTTCCCTCCAGGATCTTGCA 432

Qy  2399 AAGAGGCCCCCTTAGTACCCTCAAGCCCCTTCTT-GGGACAGCCCCAGGCACCCCCTGCC 2457
         |||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db   433 AAGAGGCCCCCTTAGTACCCTCAAGCCCCTTCTTGGGGACAGCCCCAGGCACCCCCTGCC 492

Qy  2458 CCTGCCAAAGCAAGCCCCCATTGGACTCTAAGATGGGGCCTGGAGACATCTCTTCCT 2517
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   493 CCTGCCAAAGCAAGCCCCCATTGGACTCTAAGATGGGGCCTGGAGACATCTCTTCCT 552

Qy  2518 GGGAGGCCAAAACCCGGCCCCTGAGTTCCCCAGGTCAGCCTCTCCCAGGCGAGCTCTTCC 2577
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   553 GGGAGGCCAAAACCCGGCCCCTGAGTTCCCCAGGTCAGCCTCTCCCAGGCGAGCTCTTCC 612

Qy  2578 CAAGTGAGCTCCCTCAGGGTGGCTCTCCCAGCGTGGGCACAGAGCCTGGCTGGCCCTCCCTG 2637
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   613 CAAGTGAGCTCCCTCAGGGTGGCTCTCCCAGCGTGGGCACAGAGCCTGGCTGGCCCTCCCTG 672

Qy  2638 GATGCGGAGGGCTGGACCCAGGAGGCTGAGGATCGTCGAGGATCTGTCCGACTCCACACCCACCTTGCAG 2697
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   673 GATGCGGAGGGCTGGACCCAGGAGGCTGAGGATCGTCGAGGATCTGTCCGACTCCACACCCACCTTGCAG 732

Qy  2698 CGGCCTCCAGGAACAGGTGACCAGTGCCAAGTTCTCCCTGGGTGGTCGCGGGGGCTACGCA 2757
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   733 CGGCCTCCAGGAACAGGTGACCAGTGCCAAGTTCTCCCTGGGTGGTCGCGGGGGCTACGCA 792

Qy  2758 GGCGTGGCTGGCTATGGCACCTTTGCCTTTGGTGGAGATGCAGCAGGGGGCATGCTGGGGCAG 2817
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   793 GGCGTGGCTGGCTATGGCACCTTTGCCTTTGGTGGAGATGCAGCAGGGGGCATGCTGGGGCAG 852

Qy  2818 GGGCCCATGTGGGCCAGGATAGCCTGGGCTGTGTCCCAGTCGGAGGAGCAGCAGCAGGAG 2877
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   853 GGGCCCATGTGGGCCAGGATAGCCTGGGCTGTGTCCCAGTCGGAGGAGCAGCAGCAGGAG 912

Qy  2878 GAGGGCCAGGGCTGAGTCCCAGTCGGAGGAGCAGCAGCAGGGCTGAGAGCCCCACTG 2937
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   913 GAGGGCCAGGGCTGAGTCCCAGTCGGAGGAGCAGCAGCAGGGCTGAGAGCCCCACTG 972

Qy  2938 CCCCAGGTCAGTGCAAGGCCTGTGCCTGAGGTCGGCAGGGTCTCCACCAGGAGTCTTCCA 2997
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   973 CCCCAGGTCAGTGCAAGGCCTGTGCCTGAGGTCGGCAGGGTCTCCACCAGGAGTCTTCCA 1032

Qy  2998 GAGCCCACCCCATGGAGGACATCGGGACCAGGTCTCCCTGGTGCAGATCCGGGACCTGTCA 3057
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Db  1033 GAGCCCACCCCATGGAGGACATCGGGACCAGGTCTCCCTGGTGCAGATCCGGGACCTGTCA 1092

Qy  3058 GGTGATGCGGAGGGCGCCGACACAATATCCCTGGACATTTCCGAGGTGGACCCCGCCTAC 3117
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1093 GGTGATGCGGAGGGCGCCGACACAATATCCCTGGACATTTCCGAGGTGGACCCCGCCTAC 1152

Qy  3118 CTCAACCTCTCAGACCTGTACGATATCAAGTACCTCCCATTCGAGTTTATGATCTTCAGG 3177
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1153 CTCAACCTCTCAGACCTGTACGATATCAAGTACCTCCCATTCGAGTTTATGATCTTCAGG 1212

Qy  3178 AAAGTCCCCAAGTCCGTCAGCCAGAGCGCCCCTCCCCATGGCTGAGGAGGAGCTGGCC 3237
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1213 AAAGTCCCCAAGTCCGTCAGCCAGAGCGCCCCTCCCCATGGCTGAGGAGGAGCTGGCC 1272

Qy  3238 GAGTCCCGGAGCCCACGTGGCCCTGGCCAGGTGAACTGGGCCCCCACGCAGGCCCTGGAG 3297
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Db  1273 GAGTCCCGGAGCCCACGTGGCCCTGGCCAGGTGAACTGGGCCCCCACGCAGGCCCTGGAG 1332

Qy  3298 ATCACAGAGGAGTCAGGAGGATGTGGACGCGGCTGCTGGCAGAGGCGTGCCGTGGGCAGGAAG 3357
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Db  1333 ATCACAGAGGAGTCAGGAGGATGTGGACGCGGCTGCTGGCAGAGGCGTGCCGTGGGCAGGAAG 1392

Qy  3358 CGCAAGTGGTCCTCGCCGTCACCGCAGCCTCTTCCACTTCCCTGGAGGCCTCCGTGGAGGCACCTGCGCTG 3417
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Db  1393 CGCAAGTGGTCCTCGCCGTCACCGCAGCCTCTTCCACTTCCCTGGAGGCCTCCGTGGAGGCACCTGCGCTG 1452

Qy  3418 GATGAGCCTGCAGAGCTGGGGCTGCGTGGAGAGTGAAGGCCTCCGTGGAGCACATCTCC 3477
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1453 GACGAGCCTGCAGAGCTGGGGCGTGGAGAGTGAAGGCCTCCGTGGAGCACATCTCC 1512

Qy  3478 CGGATCCTGAAGGGCAGGCCGGAAGGTCTGGAGAAGGGCCCCCCCAGGAAGAAGCCA 3537
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1513 CGGATCCTGAAGGGCAGGCCGGAAGGTCTGGAGAAGGGCCCCCCCAGGAAGAAGCCA 1572

Qy  3538 GGCCTTGCTTCCTTCCGGCTCTCAGTCTCAGGTCTGAGAGAGTCGGAGAGCTCGGGGACCGCCGAGCGCCGCACATTCCTA 3597
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Db  1573 GGCCTTGCTTCCTTCCGGCTCTCAGTCTCAGGTCTGAGAGAGTCGGAGAGCTCGGGGACCGCCGAGCGCCGCACATTCCTA 1632

Qy  3598 AGGGAGCTCTCAGATGAGACTGGTCCTGGAGCCAGTGACTGGTCCTGGCCTGGCCTGCCTGCCCTGCCCAGGTG 3657
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1633 AGGGAGCTCTCAGATGAGACTGGTCCTGGCCAGTCAGTGACTCAGTGACACTGGGCCTGCCTGCCAGGTG 1692

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Db   2773 CAGACAGACATCTGGGCCATCGGTGTGACAGCCTTCATCATGCTGAGCGCCGAGTACCCG 2832
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Db   2833 GTGAGCAGCGAGGGTGCACGCGACCTGGAGAGGACTGCGCAAGGGGCTGGTCCGGCTG 2892
Qy   4858 AGCCGCTGCTACGCGGGGCTGTCGGGGCGCCGTGGCCTTCCTGCGCAGCACTCTGTGC 4917
Db   2893 AGCCGCTGCTACGCGGGGCTGTCGGGGCGCCGTGGCCTTCCTGCGCCAGCACTCTGTGC 2952
Qy   4918 GCCCAGCCCTGGGGCCGGCCCTGCGCGTCCAGCTGCCTGCTGGCCCGTGCCTAACAGAG 4977
Db   2953 GCCCAGCCCTGGGGCCGGCCCTGCGCGTCCAGCTGCCTGCTGGCCCGTGCCTAACAGAG 3012
Qy   4978 GAGGGCCCGGCCTGTTCGGCGGCCCGGCCCGTGACCTTCCCTACCGGCGGCTGCGCGTC 5037
Db   3013 GAGGGCCCGGCCTGTTCGGCGGCCCGGCCCGTGACCTTCCCTACCGGCGGCTGCGCGTC 3072
Qy   5038 TTCGTGCGCAATCGCAGAGAGACGCGCGCTGCGTGTACAAGAGGCACAACCTGGCCCAG 5097
Db   3073 TTCGTGCGCAATCGCAGAGAGACGCGCGCTGCGTGTACAAGAGGCACAACCTGGCCCAG 3132
Qy   5098 GTGCGCTGAGGGTGCGCCCGGCCACACCCTTGTCTCCCGCTGGGGGTCGCTGCGACACG 5157
Db   3133 GTGCGCTGAGGGTGCGCCCGGCCACACCCTTGTCTCCCGCTGGGGGTCGCTGCGACACG 3192
Qy   5158 CGCCAATAAAAACGCACAGCCCGGCGAGAAAA 5190
Db   3193 CGCCAATAAAAACCACAGCCCGGCGAGAAAA 3225
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RESULT 14
US-10-425-114-26278
; Sequence 26278, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 26278
; LENGTH: 1253
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB4119-136-D3_FLI
US-10-425-114-26278

Query Match 24.0%; Score 1251.4; DB 13; Length 1253;
Best Local Similarity 99.9%; Pred. No. 1.5e-297;
Matches 1252; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy   3933 GCCCGTGGAATCCTACGGCCCGTGACCTACCATTGTGCAGTGCAGCCTAGAAGGCGGCAG 3992
Db      1 GCCCGTGGAATCCTACGGCCCTGTGACCTACCATTGTGCAGTGCAGCCTAGAAGGCGGCAG 60
Qy   3993 CTGGACCACACTGGCCTCCGACCATCTTGACTGCTGCTACCTGACCAGCAGCTCCCCG 4052
Db     61 CTGGACCACCACTGGCCTCCGACCATCTTGACTGCTGCTACCTGACCAGCAGCTCCCCG 120
Qy   4053 GGGTGGCACCTACACCTTCCGCACGCATGTCAGCAGGCACGATGGTCCTACAG 4112
Db    121 GGGTGGCACCTACACCTTCCGCACGCATGTCAGCAGGCACGATGGTCCTACAG 180
Qy   4113 CAGCCCCTCGGAGCAAGTCCTCTCGGAGGGCCCAGCCACCTGGCCTCTCGAGGAGGAGAG 4172
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Db   1753 AGCCGTGTCCTCATCTGCCACCTCAAGAACTTCCAGCTTCTGACCATCCTGGTGTG 1812
Qy   3778 GTGGCTGAGGACCTGGGTGTGTACACCTGAGCGTGAGCAATGGCTGGGACAGTGACC 3837
Db   1813 GTGGCTGAGGACCTGGGTGTGTACACCTGAGCGTGAGCAATGGCTGGGACAGTGACC 1872
Qy   3838 ACCACGGGCGTCCTCCGAAGCAGAGCGCCCCTCATCTTGCCATGCCGGATATCGGG 3897
Db   1873 ACCACGGGCGTCCTCCGAAGCAGAGCGCCCCTCATCTTGCCATGCCGGATATCGGG 1932
Qy   3898 GAGGTGTACGCGGATGGGGTGTCGTCGGTTGGTCTGGAAGCCCGTGGAATCCTACGGCCCTGTG 3957
Db   1933 GAGGTGTACGCGGATGGGGTGTCGTCGGTTGGTCTGGAAGCCCGTGGAATCCTACGGCCCTGTG 1992
Qy   3958 ACCTACAATTGTGCAGTGCAGCTAGAAGGGGCAGCTGACCAGTCTCCCGGGGTTGGCACCTACACCTTCCGCACG 4017
Db   1993 ACCTACAATTGTGCAGTGCAGCTAGAAGGGGCAGCTGACCAGTCTCCCGGGGTTGGCACCTACACCTTCCGCACG 2052
Qy   4018 TTTGACTGCTGCTACCTGACCAGCAAGCTCTCCGGGGTTGGCACCTACACCTTCCGCACG 4077
Db   2053 TTTGACTGCTGCTACCTGACCAGCAAGCTCTCCGGGGTTGGCACCTACACCTTCCGCACG 2112
Qy   4078 GCATGTGTCAGCAAGGCAGGAATGGGTCCCTACAGCAGCCCCTCGGAGCAAGTCCTCCTG 4137
Db   2113 GCATGTGTCAGCAAGGCAGGAATGGGTCCCTACAGCAGCCCCTCGGAGCAAGTCCTCCTG 2172
Qy   4138 GGAGGGCCCAGCCACCTGGCCTCTGAGGAGGAGAGCCAGGGGCGGTCAGCCCAACCCCTG 4197
Db   2173 GGAGGGGCCCAGCCACCTGGCCTCTGAGGAGGAGAGCCAGGGGCGGTCAGCCCAACCCCTG 2232
Qy   4198 CCCAGCACAAAGACCTTCGCATTCCAGACAGATCCAGAGGGCCGCGTTCAGCGTGGTG 4257
Db   2233 CCCAGCACAAAGACCTTCGCATTCCAGACACAGATCCAGAGGGCCGCGTTCAGCGTGGTG 2292
Qy   4258 CGGCAATGCTGGGAGAAGGCCAGCGGGCGGCGGCGCGCTGGCCGCCAAGATCATCCCCTACCAC 4317
Db   2293 CGGCAATGCTGGGAGAAGGCCAGCGGGCGGCGGCGCGCTGGCCGCCAAGATCATCCCCTACCAC 2352
Qy   4318 CCCAAGGACAAGACAGACAGCAGTGCTGCGCGGAATACGGAGGGCCTCAAGGGCCTGCGCCACCCG 4377
Db   2353 CCCAAGGACAAGACAGACAGCAGTGCTGCGCGGAATACGAGGGCCTCAAGGGCCTGCGCCACCCG 2412
Qy   4378 CACCTGGCCCAGCTGCACGCAGCCTACCTCAGCCCCGGCACCTGGTGTCATCTTGGAG 4437
Db   2413 CACCTGGCCCAGCTGCACGCAGCCTACCTCAGCCCCGGCACCTGGTGTCATCTTGGAG 2472
Qy   4438 CTGTGCTCTGGGCCCGGAGCTGCTCCCCGCTGCCCGGAGAGGGCCTCTACTCAGAATCT 4497
Db   2473 CTGTGCTCTGGGCCCGAGCTGCTCCCCTGCCCGGAGAGGGCCTCTACTCAGAATCC 2532
Qy   4498 GAGGTGAAGGACTACCTGTGCGCAGATGTTGAGTGCCACCAGTACCTGCACAACCAGCAC 4557
Db   2533 GAGGTGAAGGACTACCTGTGCGCAGATGTTGAGTGCCACCAGTACCTGCACAACCAGCAC 2592
Qy   4558 ATCCTGCACCTGGACCTGAGGTCCGAGAACATGATCATCACCGAATACAACCTGCTTCAAG 4617
Db   2593 ATCCTGCACCTGGACCTGAGGTCCGAGAACATGATCATCACCGAATACAACCTGCTTCAAG 2652
Qy   4618 GTCGTGACCACTGGGCAATGCAGAGCCTCAGCCAGGAGAAGTGCTGCCCCTCAGACAAG 4677
Db   2653 GTCGTGACCACTGGGCAATGCAGAGCCTCAGCCAGGAGAAGTGCTGCCCCTCAGACAAG 2712
Qy   4678 TTCAAGGACTACCTAGAGACTACCTAGCTCCAGAGCTCTGGAGGGCCAGGGGCTGTTCCA 4737
Db   2713 TTCAAGGACTACCTAGAGACCTAGAGTCCTGAGAGTCCTGGAGGGGCCAGGGGCTGTTCCA 2772
Qy   4738 CAGACAGACATCTGGGCCATCGGTGTGACAGCCTTCATCATGCTGAGCGCCGAGTACCCG 4797
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US-09-864-408A-8947
; Sequence 8947, Application US/09864408A
; Publication No. US20040009474A1
; GENERAL INFORMATION:
; APPLICANT: Leach, Martin D.
; APPLICANT: Shimkets, Richard A.
; TITLE OF INVENTION: No. US2004000947AIel human Polynucleotides and Polypeptides Enc
; FILE REFERENCE: 21402-012
; CURRENT APPLICATION NUMBER: US/09/864,408A
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: 60/206,690
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 9068
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8947
; LENGTH: 382
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1)
; OTHER INFORMATION: Wherein n may be a, c, g or t
US-09-864-408A-8947

Query Match             6.9%;    Score 358.4;  DB 11;  Length 382;
Best Local Similarity  99.7%;    Pred. No. 4.2e-78;
Matches  359;  Conservative  0;  Mismatches  1;  Indels  1;  Gaps  0;

Qy    502 GGTGGCCAGTGCTCTGCAAGGCAGGAGAGCTGCTGGTGCTTGGGGGGACAATGAGCCGGAC 561
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     13 GGTGGCCAGTGCTCTGCAAGGCAGGAGAGCTGCTGGTGCTTGGGGGGACAATGAGCCGGAC 72

Qy    562 TCAGAGAAGCAAAGCCACCGGAGAAGCTGCACTCCTTCTATGAGGTCAAGGAGGAGATT 621
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     73 TCAAAGAAGCAAAGCCACCGGAGAAGCTGCACTCCTTCTATGAGGTCAAGGAGGAGATT 132

Qy    622 GGAGAGGGGCTGTTTGGCTTCGTAAAAAGAGTGCAGCACAAAGGAAACAAGATCTTGTGC 681
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    133 GGAAGGGGGCTGTTTGGCTTCGTAAAAAGAGTGCAGCACAAAGGAAACAAGATCTTGTGC 192

Qy    682 GCTGCCAAGTTCATCCCCTACCGACAGCAGAACTCGGGCCCAGGCATACAGGAGCGAGAC 741
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    193 GCTGCCAAGTTCATCCCCTACCGACAGCAGAACTCGGGCCCAGGCATACAGGAGCGAGAC 252

Qy    742 ATCCTGGCCGCGTGAGCCACCGCTGCTGACCAGTTTGAGACCCGC 801
          |||||||||||||||||||||||||||||||||||||||||||||
Db    253 ATCCTGGCCGCGTGAGCCACCGCTGCTGACCAGTTTGAGACCCGC 312

Qy    802 AAGACCCTCATCCTCATCCTGGAGCTGTGCTCATCCGAGGAGCTGCTGGACCGCCTGTAC 861
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    313 AAGACCCTCATCCTCATCCTGGAGCTGTGCTCATCCGAGGAGCTGCTGGACCGCCTGTAC 372

Search completed: April 26, 2004, 18:26:10
Job time : 1377 secs

Db     181 CAGCCCCTCGGAGCAAGTCCTCCTGGGAGGGCCCACCTGGCCTCTGAGGAGGAGGAG 240
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Qy    4173 CCAGGGGCGGTCAGCCCAACCCTGCCCAGCACAACAAAGACCTTCGCATTCCAGACACAGAT 4232
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 CCAGGGGCGGTCAGCCCAACCCTGCCCAGCACAACAAAGACCTTCGCATTCCAGACACAGAT 300

Qy    4233 CCAGAGGGGCCGCTTCAGCGTGGTGCGGCAATGCTGGGAGAAGGCCAGCGGGGGGGCGCT 4292
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 CCAGAGGGGCCGCTTCAGCGTGGTGCGGCAATGCTGGGAGAAGGCCAGCGGGGGGGCGCT 360

Qy    4293 GGCCGCCAAGATCATCCCCAAGGACAAGACAGCAGTGCTGCGGCAATACGA 4352
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 GGCCGCCAAGATCATCCCCAAGGACAAGACAGCAGTGCTGCGGCAATACGA 420

Qy    4353 GGCCCTCAAGGGCCTGCGCCACCCGACCTGGCCCAGCTGCACGCAGCCTACCTCAGCCC 4412
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 GGCCCTTCAAGGGCCTGCGCCACCCGACCTGGCCCAGCTGCACGCAGCCTACCTCAGCCC 480

Qy    4413 CCCGGCACCTGGTGCTCATCTTGGGAGCTGTGTCCTGTGGGCCCGGAGCTGCTCCCCTGCCTGGC 4472
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 CCCGGCACCTGGTGCTCATCTTGGGAGCTGTGTCCTGTGGGCCCGGAGCTGCTCCCCTGCCTGGC 540

Qy    4473 CGAGAGGGGCCTCCTACTCAGAATCTGAGGTGAAGGACTTACCTGTGGCAGATGTTGAGTGC 4532
           ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
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Qy    4533 CACCCAGTACCTGCACAACCAGCACATCCTGACCTGGACCTGGAGTCCGAGAACATGAT 4592
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 CACCCAGTACCTGCACAACCAGCACATCCTGACCTGGACCTGGAGTCCGAGAACATGAT 660

Qy    4593 CATCACCGAATACAACCTGCTCAAGGTCGTGGACCTGGCAATGCACAGAGCCTCAGCCA 4652
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 CATCACCGAATACAACCTGCTCAAGGTCGTGGACCTGGCAATGCACAGAGCCTCAGCCA 720

Qy    4653 GGAGAAGGTGCTGCCCTCAGACAAGTTCAAGGACTTACCTAGAGACCATGGCTCCAGAGCT 4712
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 GGAGAAGGTGCTGCCCTCAGACAAGTTCAAGGACTTACCTAGAGACCATGGCTCCAGAGCT 780

Qy    4713 CCTGGAGGGCCAGGGGGCTGTTCCACAGACAGATCTGGGCCATCGGTGTGACAGCCTT 4772
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db     841 CATCAATGCTGAGCGCGCGAGTACCCGTGAGCCACCTGCACGCGAGGGTGCACGCAGGAGG 900

Qy    4833 ACTGCGGCAAGGGGCTGGTCCGGCTGAGCCGCCTGCTACCGCGGGCTGTCCGGGGGCCGCCGT 4892
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    4893 GGCCTTCCTGCGCAGCACTCTGTGCGCGCCCAGCCTGGGGCCCGGGCCGGCCCTGCGCGGTCCAGCTG 4952
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     961 GGCCTTCCTGCGCAGCACTCTGTGCGCGCCCAGCCTGGGGCCCGGGCCGGCCCTGCGCGGTCCAGCTG 1020

Qy    4953 CCTGCAGTGCCCGTGGCTAACAGAGGAGGGCCCGGCTGTTCGCGGCCCGGCCCCGTGAC 5012
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1021 CCTGCAGTGCCCGTGGCTAACAGAGGAGGGCCCGGCCCTGTTCGCGGCCCGGCCCCGTGAC 1080

Qy    5013 CTTCCCTACCGGCGCGGCTGCGCGTCTTCGTGCGCAATCGGCGGAGAGAGGACGGGCGTGCT 5072
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    5073 GTACAAGAGGCACAACCTGGCCCAGGTGCCGTGAGGGTGCCCCCGGGCCACACCCTTGGTC 5132
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Db    1141 GTACAAGAGGCACAACCTGGCCCAGGTGCCGTGAGGGTGCCCCCGGGCCACACCCTTGGTC 1200

Qy    5133 TCCCCGGCTGGGGGTCGCTGCAGAGCGCGCCAATAAAAACGCACAGCCCGGCGGCGAG 5185
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Db    1201 TCCCCGGCTGGGGGTCGCTGCAGAGCGCGCCAATAAAAACGCACAGCCCGGCGGCGAG 1253

RESULT 15

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                   GenCore version 5.1.6
          Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:      April 26, 2004, 06:37:28 ; Search time 1244 Seconds
                                        (without alignments)
                                        17781.646 Million cell updates/sec

Title:        US-10-697-263-1
Perfect score: 5207
Sequence:    1 cagcacgaggaactccttct.........aaaaaaaaaaaaaaaaaaa 5207

Scoring table:  IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched:    3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters:      6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :    N Geneseq_29Jan04:*
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              8: geneseqn2003bs:*
              9: geneseqn2003cs:*
             10: geneseqn2004s:*

                             SUMMARIES

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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| Result No. | Score | % Query Match | Length | DB ID | Description |
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| 1 | 5207 | 100.0 | 5207 | 6 | AAL43909 | Aal43909 Human kin |
| 2 | 5207 | 100.0 | 5207 | 6 | AAL43908 | Aal43908 Human kin |
| 3 | 5173.6 | 99.4 | 5454 | 6 | AAD38865 | Aad38865 Human kin |
| 4 | 4940.4 | 94.9 | 8106 | 7 | ABX11641 | Abx11641 Human ser |
| 5 | 4940.4 | 94.9 | 24120 | 7 | ABX11642 | Abx11642 Human ser |
| 6 | 4915.8 | 94.4 | 5007 | 5 | AAC62286 | Aac62286 cDNA enco |
| 7 | 4915.8 | 94.4 | 7928 | 5 | AAC62287 | Aac62287 cDNA enco |
| 8 | 4885.2 | 93.8 | 4936 | 5 | AAH46904 | Aah46904 cDNA enco |
| 9 | 4146.6 | 79.6 | 4175 | 5 | AAC62285 | Aac62285 cDNA enco |
| 10 | 3197.8 | 61.4 | 3225 | 6 | AAD26467 | Aad26467 Human kin |
| 11 | 358.4 | 6.9 | 382 | 6 | ABN79527 | Abn79527 Human kin |
| 12 | 327.6 | 6.3 | 7710 | 4 | AAF44662 | Aaf44662 Novel pro |
| 13 | 327.6 | 6.3 | 7789 | 9 | AAD30565 | Aad30565 Human kin |
| 14 | 327.6 | 6.3 | 9696 | 9 | ADE47675 | Ade47675 Human NOV |
| 15 | 327.6 | 6.3 | 9807 | 9 | ADB79958 | Adb79958 Human kin |
| 16 | 327.6 | 6.3 | 10662 | 9 | ADC99127 | Adc99127 Human KPP |
| 17 | 308.4 | 5.9 | 9930 | 9 | ADE47671 | Ade47671 Human NOV |
| 18 | 308.4 | 5.9 | 10122 | 9 | ADE47673 | Ade47673 Human NOV |
| 19 | 223.4 | 4.3 | 225 | 9 | ABN76255 | Abn76255 Human kin |
| 20 | 205.2 | 3.9 | 860 | 9 | ADE47677 | Ade47677 Human NOV |
| c 21 | 188.2 | 3.6 | 338 | 6 | ABN18263 | Abn18263 Human ORF |
| 22 | 178.2 | 3.4 | 1429 | 2 | AAX34657 | Aax34657 Murine ZI |
| 23 | 175 | 3.4 | 2079 | 4 | AAK94258 | Aak94258 Human ful |

| | | | | | |
|---|---|---|---|---|---|
| 24 | 175 | 3.4 | 2226 | 9 | ADD29770 | Add29770 Human tum |
| 25 | 173.4 | 3.3 | 1514 | 9 | ADB58463 | Adb58463 Toxicity-r |
| 26 | 173.4 | 3.3 | 1514 | 9 | ADB53052 | Adb53052 Primary r |
| 27 | 173.4 | 3.3 | 2105 | 6 | ABV72291 | Abv72291 Nucleotid |
| 28 | 173.4 | 3.3 | 2132 | 9 | AAX34656 | Aax34656 Human ZIP |
| 29 | 173.4 | 3.3 | 2132 | 7 | ACA90235 | Aca90235 Deatch as |
| 30 | 173.4 | 3.3 | 2224 | 4 | AAH16158 | Aah16158 Human cDN |
| 31 | 173.4 | 3.2 | 2224 | 3 | AAH78068 | Aah78068 Nucleotid |
| 32 | 164.8 | 3.2 | 182 | 3 | AAC25654 | Aac25654 Human sec |
| 33 | 157.2 | 3.0 | 1971 | 6 | AAD26571 | Aad26571 Human POL |
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| 40 | 153.8 | 3.0 | 1836 | 4 | AAS06721 | Aas06721 Polynucle |
| 41 | 153.8 | 3.0 | 2046 | 5 | AAH78263 | Aah78263 Nucleotid |
| 42 | 153.6 | 2.9 | 8586 | 7 | ACA57512 | Aca57512 Human adi |
| 43 | 153.6 | 2.9 | 8906 | 2 | AAT85392 | Aat85392 Human TRI |
| 44 | 153.6 | 2.9 | 8906 | 5 | AAS81211 | Aas81211 DNA encod |
| 45 | 153.6 | 2.9 | 8906 | 5 | ABA82699 | Aba82699 GTPase ge |

```
                             ALIGNMENTS

RESULT 1
AAL43909
ID   AAL43909 standard; DNA; 5207 BP.
XX
AC   AAL43909;
XX
DT   19-SEP-2002 (first entry)
XX
DE   Human kinase protein coding sequence 2.
XX
KW   Human; gene; ds; gene therapy; chromosome 1; kinase protein;
KW   myosin light chain kinase subfamily; kinase protein-mediated disease;
KW   transgenic animal.
XX
OS   Homo sapiens.
XX
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FT                  /*tag= h
FT                  /standard_name= "Single nucleotide polymorphism"
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PN   WO200240683-A2.
XX
PD   23-MAY-2002.
XX
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PF   22-OCT-2001; 2001WO-US032616.
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PR   14-NOV-2000; 2000US-00711134.
PR   17-MAY-2001; 2001US-00858664.
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PA   (PEKE ) PE CORP NY.
XX
PI   Wei M, Ketchum K, Di Francesco V, Beasley EM;
XX
DR   WPI; 2002-500223/53.
DR   P-PSDB; AA015372.
XX
PT   New kinase proteins related to myosin light chain kinase subfamily and
PT   encoding polynucleotide, useful for diagnosing, treating disease or
PT   condition mediated by the kinase protein and for identifying modulators.
XX
PS   Claim 23; Fig 3; 96pp; English.
XX
CC   The invention comprises the amino acid and coding sequences (located on
CC   chromosome 1) of a human kinase protein that is related to the myosin
CC   light chain kinase subfamily. The human kinase DNA and protein sequences
CC   of the invention are useful for identifying agents that modulate the
CC   activity of the human kinase protein. Kinase-modulating agents are useful
CC   for treating a disease or condition mediated by a human kinase protein.
CC   The human kinase DNA sequences can be used to produce transgenic animals
CC   which are useful for studying the function of kinase proteins and
CC   identifying/evaluating modulators of kinase protein activity. The present
CC   DNA sequence encodes the human kinase protein of the invention
XX
SQ   Sequence 5207 BP; 988 A; 1758 C; 1612 G; 849 T; 0 U; 0 Other;

Query Match         100.0%;  Score 5207;  DB 6;  Length 5207;
Best Local Similarity   100.0%;  Pred. No. 0;
Matches 5207;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy    1 CAGCACGAGGAACTCCTTCTGATCACCTGCCAGTCAGTGAGGTCAGAGTGGGAGGCAGTG 60
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Qy  2701 CCTCAGGAACAGGTGACCATGCGCAAGTTCTCCCGGGTGGTACGGGGGGGTACGCAGGC 2760
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         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3361 AAGTGGTCCTCGCCGGTCACGCAGCAGCTCTTCCAGCTTCCTGGAGGAGCACATCTCCCGG 3420

Qy  3421 GAGCCTGAGAGCGAGTCTGGGGCTGGGTGGCCGGAAGGTCTGGAGAGAGTGAGGCCGGGAGGCAGGGC 3480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3421 GAGCCTGAGAGCGAGTCTGGGGCTGGGTGGCCGGAAGGTCTGGAGAGAGTGAGGCCTGGGAGGCCAGGC 3480

Qy  3481 ATCCTGAAGGGCAGGCCGGAAGGTCTGAAGAGTCTGAAGAGGAGGGCCCCCAGGAGAAGCCAGAGGC 3540
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3481 ATCCTGAAGGGCAGGCCGGAAGGTCTGAAGAGTCTGAAGAGGAGGGCCCCCAGGAGAAGCCAGGC 3540

Qy  3541 CTTGCTTCCTTCCGGCTTCAGGTCTCAGGTCTGGGCCAGTCAGTGAGAGCTGGACCGAGCGCCGACATTCCTAAGG 3600
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3541 CTTGCTTCCTTCCGGCTTCAGGTCTCAGGTCTGGGCCAGTCAGTGAGAGCTGGACCGAGCGCCGACATTCCTAAGG 3600

Qy  3601 GAGGTCTCAGATGAGACTGTGGTTCCGGGCCAGCGCCACCTGGGGAGCCAGTGACACTGGCTGCCAGTGTCA 3660
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3601 GAGGTCTCAGATGAGACTGTGGTTCCGGGCCAGCGCCACCTGGGGAGCCAGTGACACTGGCTGCCAGTGTCA 3660

Qy  3661 GCCAGCCAGCTGCCCAGGGTCGGGGCACAGAGCCTCCCCTGGAGCAAAGACCGGAGCCCCTGGAGAGCAGCAGC 3720
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3661 GCCAGCCAGCTGCCCAGGGTGGCACAGAGCCTCCCCTGGAGCAAAGACCGGAGCCCCTGGAGAGCAGCAGC 3720

Qy  3721 CGTGTCCTCATCTCTGCCACCCTCAAGACTTCCAGCTTCGACAATCCTGGTGGTGGTG 3780
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3721 CGTGTCCTCATCTCTGCCACCCTCAAGACTTCCAGCTTCGACAATCCTGGTGGTGGTG 3780

Qy  3781 GCTGAGGACCTGGGTGTGTGTACACCTGCAGCGTGACAATGGCGTGGGACAGTGACCACC 3840
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3781 GCTGAGGACCTGGGTGTGTACACCTGCAGCGTGACAATGGCGTGGGACAGTGACCACC 3840

Qy  3841 ACGGGCGCTCCTCCGGAGGCAGGAGCGCCCCTCATCTTCGCCACGACCTCCGGGGGATATCCGGGGAG 3900
```

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Qy  3841 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       ACGGGGGTCCTCCGGAAGGCAGAGAGGCCCCTCATCTTCGCCATGCGGGATATCGGGGAG 3900

Qy  3901 GTGTACGCGGATGGGGGTGCTGTGGTCTGCTGGTGTGCTGGTGTCTGCTGGAAGCCCTGTGACC 3960
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       GTGTACGCGGATGGGGGTGCTGTGGTCTGCTGGTGTGCTGGTGTCTGCTGGAATCCTACGGCCCTGTGACC 3960

Qy  3961 TACATTGTGCAGTGCAGCCTAGAGGCGGCAGCTGGACCACACACTTCCGACATCTTT 4020
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       TACATTGTGCAGTGCAGCCTAGAGGCGGCAGCTGGACCACACACTTCCGACATCTTT 4020

Qy  4021 GACTGCTGCTACCTGACCAGCAAGTCTCCCGGGTGGCACCTACACCTTCCGCACGGCA 4080
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       GACTGCTGCTACCTGACCAGCAAGTCTCCCGGGTGGCACCTACACCTTCCGCACGGCA 4080

Qy  4081 TGTGTCAGGCAGGAATGGTCCCTACAGCAGCCCTGGAGCAAGTCCTCCTGGGA 4140
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       TGTGTCAGGCAGGAATGGTCCCTACAGCAGCCCTGGAGCAAGTCCTCCTGGGA 4140

Qy  4141 GGGCCCAGCCAACCTGGCCTCTGAGGAGGAGACCCAGGGCGGCAGGAGCCCAGCCCTGCCC 4200
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       GGGCCCAGCCAACCTGGCCTCTGAGGAGGAGACCCAGGGCGGCAGGAGCCCAGCCCTGCCC 4200

Qy  4201 AGCACAAAGACCTTCGCATTCGAGACACAGATCCAGAGGGGCCGCGCTTCAGCGTGGTGCGG 4260
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       AGCACAAAGACCTTCGCATTCGAGACACAGATCCAGAGGGGCCGCGCTTCAGCGTGGTGCGG 4260

Qy  4261 CAATGCTGGGAGAGGCCAGCGGCGGCGGGGCGTGGCCGCCCAAGATCATCCCCTACCACCCC 4320
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       CAATGCTGGGAGAGGCCAGCGGCGGCGGGGCGTGGCCGCCAAGATCATCCCCTACCACCCC 4320

Qy  4321 AAGGACAAGACAGCAGTGCTGCGCGGAATACCGAGGCCCTCAAGGGCCTCAAGGGCCACCCCGCAC 4380
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       AAGGACAAGACAGCAGTGCTGCGCGGAATACCGAGGCCCTCAAGGGCCTCAAGGGCCACCCCGCAC 4380

Qy  4381 CTGGCCCAGCTGCACGCGAGCTCACCTGAGCCCCCGGACCTGGTGCTCATCTTGGAGCTG 4440
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       CTGGCCCAGCTGCACGCGAGCTCACCTGAGCCCCCGGACCTGGTGCTCATCTTGGAGCTG 4440

Qy  4441 TGTGTCTGGCCGAGCTGCTCCCCTGCCTGGCCGAGAGGGCCTCTACTCCACTCAGAATCTGAG 4500
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       TGTGTCTGGCCGAGCTGCTCCCCTGCCTGGCCGAGAGGGCCTCTACTCCACTCAGAATCTGAG 4500

Qy  4501 GTGAAGGACTACCTGTGCAGATGTTGAGTGCCACCCAGTACCTGCACAACCAGCACATC 4560
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       GTGAAGGACTACCTGTGCAGATGTTGAGTGCCACCCAGTACCTGCACAACCAGCACATC 4560

Qy  4561 CTGCACCTGGACCTGAGGTCCGAGAACATGATCATCACCGAATACACAACCTGCTCAAGGTC 4620
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Db       CTGCACCTGGACCTGAGGTCCGAGAACATGATCATCACCGAATACACAACCTGCTCAAGGTC 4620

Qy  4621 GTGACCTGGCAATGCACAGGACCTCAGCCAGGAGAAGTGCTGCCCTCAGACAAGTTC 4680
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Db       GTGACCTGGCAATGCACAGGACCTCAGCCAGGAGAAGTGCTGCCCTCAGACAAGTTC 4680

Qy  4681 AAGGACTACCTAGAGACCATGGCCTCCAGAGCTCTGAGGGGGCTCTTCCACAG 4740
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       AAGGACTACCTAGAGACCATGGCCTCCAGAGCTCTGAGGGGGCTGTTCCACAG 4740

Qy  4741 ACAGACATCTGGGCCCATCGGTGTGACAGGTGTACAGCTTCATCATGCTGAGCGCCGAGTACCCGGTG 4800
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       ACAGACATCTGGGCCCATCGGTGTGACAGGTGTACAGCTTCATCATGCTGAGCGCCGAGTACCCGGTG 4800

Qy  4801 AGCAGCGAGGGTGCACGGACCTGACACCTGCCCAAGGGACTGCCAAGGGCTGGTCCGGCTGAGC 4860
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       AGCAGCGAGGGTGCACGCGGACCTGACACCTGCCCAAGGGACTGCCAAGGGCTGGTCCGGCTGAGC 4860

Qy  4861 CGCTGCTACGCGGGGCGTGTCCGGGGGCGCCGTGGCCCTTCCTGCGCCAGCACTCTGTGCGCC 4920
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       CGCTGCTACGCGGGGCGTGTCCGGGGGGCGCCTTCCTTCCTGCGCCAGCACTCTGTGCGCC 4920

Qy  4921 CAGCCCTGGGCGCCGGCCCTGCGCGTCCAGCTGCTGCGAGTGCCCGTGGCTAACAGAGGAG 4980
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4921 CAGCCCTGGGCGCCGGCCCTGCGCGTCCAGCTGCTGCGAGTGCCCGTGGCTAACAGAGGAG 4980

Qy  4981 GGGCCGGCCTGTTCGCGGCCCGGCCCGCCCGGCCCTGACCTTCCTACCGCCGCGCGTCTTC 5040
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4981 GGGCCGGCCTGTTCGCGGCCCGGCCCGCCCGGCCCTGACCTTCCTACCGCCGCGCGTCTTC 5040

Qy  5041 GTGGCAATCGCGGAAGAGACGCGCGCTGTCGTGTACAAGAGAGGCACAACCTGGCCCAGTG 5100
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5041 GTGGCAATCGCGGAAGAGACGCGCGCTGTCGTGTACAAGAGAGGCACAACCTGGCCCAGTG 5100

Qy  5101 CGCTGAGGGTCGCCCGGCCACACCCTTGGTCTCCCCGCTGGGGGTCCGCTGCAGACCGGC 5160
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5101 CGCTGAGGGTCGCCCGGCCACACCCTTGGTCTCCCCGCTGGGGGTCGCTGCGAGACCGGC 5160

Qy  5161 CAATAAAACGCACAGCCGGGCGAGAAAAAAAAAAAAAAA 5207
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Db  5161 CAATAAAAACGCACAGCCCGGCGAGAAAAAAAAAAAAAAAAAAAAA 5207
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RESULT 2
AAL43908
ID   AAL43908 standard; DNA; 5207 BP.
XX
AC   AAL43908;
XX
DT   19-SEP-2002 (first entry)
XX
DE   Human kinase protein coding sequence 1.
XX
KW   Human; gene; ds; gene therapy; chromosome 1; kinase protein;
KW   myosin light chain kinase subfamily; kinase protein-mediated disease;
KW   transgenic animal.
XX
OS   Homo sapiens.
XX
FH                    Location/Qualifiers
FT   Key
FT   CDS               109..5106
FT                     /tag= a
FT                     /product= "Human kinase protein"
XX
PN   WO200240683-A2.
XX
PD   23-MAY-2002.
XX
PF   22-OCT-2001; 2001WO-US032616.
XX
PR   14-NOV-2000; 2000US-00711134.
PR   17-MAY-2001; 2001US-00858664.
XX
PA   (PEKE ) PE CORP NY.
XX
PI   Wei M, Ketchum K, Di Francesco V, Beasley EM;
XX
DR   WPI; 2002-500223/53.
DR   P-PSDB; AAO15372.
XX
PT   New kinase proteins related to myosin light chain kinase subfamily and
PT   encoding polynucleotide, useful for diagnosing, treating disease or
PT   condition mediated by the kinase protein and for identifying modulators.
XX
PS   Claim 23; Fig 1; 96pp; English.
XX
CC   The invention comprises the amino acid and coding sequences (located on
CC   chromosome 1) of a human kinase protein that is related to the myosin
CC   light chain kinase subfamily. The human kinase DNA and protein sequences
CC   of the invention are useful for identifying agents that modulate the
CC   activity of the human kinase protein. Kinase-modulating agents are useful
CC   for treating a disease or condition mediated by a human kinase protein.
CC   The human kinase DNA sequences can be used to produce transgenic animals
CC   which are useful for studying the function of kinase proteins and
CC   identifying/evaluating modulators of kinase protein activity. The present
CC   DNA sequence encodes the human kinase protein of the invention
XX

SQ  Sequence 5207 BP; 988 A; 1758 C; 1612 G; 849 T; 0 U; 0 Other;

Query Match       100.0%;  Score 5207;  DB 6;  Length 5207;
Best Local Similarity  100.0%;  Pred. No. 0;
Matches 5207;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

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Qy       1 CAGCACGAGGAACTCCTTCTGATCACCTGGCCAGCTGAGGTCAGAGTGGGAGAGGCAGTG 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 CAGCACGAGGAACTCCTTCTGATCACCTGGCCAGCTGAGGTCAGAGTGGGAGAGGCAGTG 60

Qy      61 GTTCCATTGAAGGAGTACTCCTAACTGTCAGAAGCCTGGGCGGTCAGGATGGGGTGCTGT 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 GTTCCATTGAAGGAGTACTCCTAACTGTCAGAAGCCTGGGCGGTCAGGATGGGGTGCTGT 120

Qy     121 CGCTTGGGCTGCGGGGGGGTGTTCAGTTGCCCACCAGTGTATCTCAGGGTCTTCACCAACCAT 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 CGCTTGGGCTGCGGGGGGGTGTTCAGTTGCCCACCAGTGTATCTCAGGGTCTTCACCAACCAT 180

Qy     181 CCAAGCATGGTAGGCTGGCACCCAGGGTTGTGTGGCTGGGAGGTGGTCTCCAC 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 CCAAGCATGGTAGGCTGGCACCCAGGGTTGTGTGGCTGGGAGGTGGTCTCCAC 240

Qy     241 AGTTCCCTGCCCTCCCAGGGCCCCATCCATGCAGGTAACCATGGATGTGCAG 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 AGTTCCCTGCCCTCCCAGGGCCCCATCCATGCAGGTAACCATGGATGTGCAG 300

Qy     301 GCACAGACAGGCGGACGGCCCAATTCGAGGCTATCATTGAGGGCGACCCACAGCCCTCG 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 GCACAGACAGGCGGAACGGCCCAATTCGAGGCTATCATTGAGGGCGACCCACAGCCCTCG 360

Qy     361 GTGACCTGGTACAAGGAACAGGCTCCAGCTGGTGGACAGCACCGGCTTAGCCAGCAGCAA 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 GTGACCTGTACAAGGAACAGGCTCCAGCTGGTGGACAGCACCGGCTTAGCCAGCAGCAA 420

Qy     421 GAAGGCACCACCATACTCCCTGGGTGCTGAGGCATGTGCCTCGAAGAGTGCCGGCGTTTAC 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 GAAGGCACCACCATACTCCCTGGGTGCTGAGGCATGTGCCTCGAAGAGTGCCGGCGTTTAC 480

Qy     481 ACCTGCCTGGCCCAAAACACTGGTGGCCAGTGCTCTCGCAAGGCAGAGTCTGCTGGTGCTT 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 ACCTGCCTGGCCCAAAACACTGGTGGCCAGTGCTCTCGCAAGGCAGAGTCTGCTGGTGCTT 540

Qy     541 GGGGGGACAATGACCCGGACTCAGAGAAGCAAAGCCACCGGAGGAAGCTGCACTCCTTC 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 GGGGGGACAATGACCCGGACTCAGAGAAGCAAAGCCACCGGAGGAAGCTGCACTCCTTC 600

Qy     601 TATGAGGTCAAGGAGGAGATTGGAAGGGGCGTGTTTTGGCTTCGTAAAAAGAGTGCAGCAC 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 TATGAGGTCAAGGAGGAGATTGGAAGGGGCGTGTTTTGGCTTCGTAAAAAGAGTGCAGCAC 660

Qy     661 AAAGGAAACAAGATCTTGTGCGCTGCCAAGTTCATCCCCGGTGAGCAGCAGACTCGGGGC 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 AAAGGAAACAAGATCTTGTGCGCTGCCAAGTTCATCCCCGGTGAGCAGCAGACTCGGGGC 720

Qy     721 CAGGCATACAGGAGCGAGACATCCTGGCCGGCCACCCGCTGGTCGTGCTGTCACGGGCTG 780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 CAGGCATACAGGAGCGAGACATCCTGGCCGGCCACCCGCTGGTCGTGCTGTCACGGGCTG 780

Qy     781 CTGACCAGTTGACCCGGGAGGGGCTGCCCAAGTTCATCCGAGCTGTGCTCATCCGAG 840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 CTGGACCAGTTGACCCGGGAGGGGCTGCCCAAGTTCATCCGAGCTGTGCTCATCCGAG 840

Qy     841 GAGCTGCTGGACCCCGTGTACAGGAAGGGCGTGGTGACGGAAGGGCGTCAAGGTCTAC 900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 GAGCTGCTGGACCCCGTGTACAGGAAGGGCGTGGTGACGGAAGGGCGTCAAGGTCTAC 900

Qy     901 ATCCAGCAGCTGTGGGAGGGCGTGGCCACTACCTGCACAGCGTTCTCCACCTGGAC 960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901 ATCCAGCAGCTGTGGGAGGGCGTGGCCACTACCTGCACAGCGTTCTCCACCTGGAC 960

Qy     961 ATAAAGCCCTCTAACATCCTGATGGTGCATCCTGGCATCCTGCCCGGGGAAGACATTAAAAATCTGCGAC 1020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     961 ATAAAGCCCTCTAACATCCTGATGGTGCATCCTGGCATCCTGCCCGGGGAAGACATTAAAAATCTGCGGAC 1020

Qy    1021 TTTGGCTTTGCCCAGAACATCACCCAGCAGAGACTGCAGTTCAGCCAGTACGGCTCCCCT 1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1021 TTTGGCTTTGCCCAGAACATCACCCAGCAGAGACTGCAGTTCAGCCAGTACGGCTCCCCT 1080

Qy    1081 GAGTTCGTCTCCCCGATCATCCAGCAGCAGAACCGTGTGAGCGAAGCCTCCGACATTTGG 1140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1081 GAGTTCGTCTCCCCGGATCATCCAGCAGCAGAACCGTGTGAGCGAAGCCTCCGACATTTGG 1140

Qy    1141 GCCATGGGTGTCATCTCCACCTGCCTCAGCCTGACCTGCCTCATCCCGGCGGAGAGT 1200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1141 GCCATGGGTGTCATCTCCACCTGCCTCAGCCTGACCTGCCTCATCCCGGCGGAGAGT 1200

Qy    1201 GACCGTGCCACCCTCCTGAACGTGCTGGAGGGGCGGGTGTGTCATGGAGCGGCCCATGGCT 1260
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Db    1201 GACCGTGCCACCCTCCTGAACGTGCTGGAGGGGCGGGTGTGTCATGGAGCGGCCCATGGCT 1260

Qy    1261 GCCACCTCAGCGAAGACGCCAAAGACTTCATCAAGGCTACGCTGCGAGAGCCCCTCAG 1320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1261 GCCCACCTCAGCGAAGACGCCAAAGACTTCATCAAGGCTACGCTGCGAGAGCCCCTCAG 1320

Qy    1321 GCCCGGCCAGTGCGGCCAGTGCCTCTTCCACCCTGGTTCCTGAAATCCATGCCTGCG 1380
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1321 GCCCCGGCCAGTGCGGCCAGTGCCTCTTCCACCCTGGTTCCTGAAATCCATGCCTGCG 1380

Qy    1381 GAGGAGGCCCACTTCATCAACAGCAGCTCAAGTTCCTGCTGGCCGAAGTGCGCTGG 1440
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Qy    1441 CAGCGTTCCTGATGAGCTACAAGTCCATCCTGTGATGCGCTCCATCCTGAGCTGCTG 1500
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Db    1441 CAGCGTTCCTGATGAGCTACAAGTCCATCCTGTGATGCGCTCCATCCTGAGCTGCTG 1500

Qy    1501 CGGGGCCCACACCCGCACAGCCCCTCGGCGTAGCCCGGCTCCTGCAGGGACACTGGT 1560
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Db    1501 CGGGGCCCACACCCGCACAGCCCCTCGGCGTAGCCCGGCTCCTGCAGGGACACTGGT 1560

Qy    1561 GGCTCCTCCAGTTCCTCCTCTCGCGCCCATTTGCCCGGGGCTAAG 1620
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1561 GGCTCCTCCAGTTCCTCCTCTCGCGCCCATTTGCCCGGGGCTAAG 1620

Qy    1621 TCACTGCCACCCTGCACACTACCACTGCTGCACTGCTGCCGAGCGCCCAGCT 1680
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1621 TCACTGCCACCCTGCACACTCCCGGTGACACACTCACTGCTGCACTGCTGCCGAGCGCCCAGCT 1680

Qy    1681 CCCTGGCCAGCCTGCTGAGGAACGCGAGGCCAGTGAGCGCCGCCCACCCGGCCCCAGCAC 1740
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1681 CCCTGGCCAGCCTGCTGAGGAACGCGAGGCCAGTGAGCGCCGCCCACCCGGCCCCAGCAC 1740

Qy    1741 CGCGTCATCCCGAGGGTGCCCGGGCCGCGGGCCCACCAGGCGGGCACGGGGCCCTG 1800
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1741 CGCGTCATCCCGAGGGTGCCCGGGCCGCGGGCCCACCAGGCGGGCACGGGGCCCTG 1800

Qy    1801 AGGGTCATCCGCAGCCTGTTCTACCACGGGAGCACCACCAGGAGGACACGGGCCCTG 1860
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1801 AGGGTCATCCGCAGCCTGTTCTACCACGGGAGCACCACCAGGAGGACACGGGCCCTG 1860

Qy    1861 GCCCCGGGAGCAGGGGCACCCGGGCCGCCCGGCCACCCTGCTGAAGGGCGGTACATT 1920
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1861 GCCCCGGGAGCAGGGGCACCCGGGCCGCCCGGCCACCCTGCTGAAGGGCGGTACATT 1920

Qy    1921 GCGGGGCGTGCCAGGCGTGCGCGGAGCCGATGATGGAGACGCGGTGCTGGAGGAGGAG 1980
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1921 GCGGGGCGTGCCAGGCGTGCGCGGAGCCGATGATGGAGACGCGGTGCTGGAGGAGGAG 1980

Qy    1981 GCCGGCAGGAGGAGGAGGCCACCCTCATTGCGGTTCTCACCTGGAC 2040
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1981 GCGCGGCAGGAGGAGGAGGCCACCCTCATTGCGGTTCTCACCTGGAC 2040

Qy    2041 CGGCTGCTGCTCTGGAGGGCTGCTGCTGCCACAGCCACTCCCTGAACATGAC 2100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2041 CGGCTGCTGCTCTGGAGGGCTGCTGCTGCCACAGCCACTCCCTGAACATGAC 2100
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Qy    2101 TCTCCGAGCAGCACCCCGCCCTCCTCGGAGGCCTGCGGTGAGGCACAGCGACTGCCTTCA 2160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2101 TCTCCGAGCAGCACCCCGCCCGCCCTCCTCGGAGGCCTGCGGTGAGGCACAGCGACTGCCTTCA 2160

Qy    2161 GCCCCCTCCGGGGGGCGGGGGGCCCTATCAGGACATGGGCACCCTTCAGGGCTCCAAGCAGCTT 2220
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2161 GCCCCCTCCGGGGGGGGCCCTATCAGGACATGGGCACCCTTCAGGGCTCCAAGCAGCTT 2220

Qy    2221 CCATCCACTGTGGCCACCCAGGCACTGCTCAGCCAGAGAGGCCATCCCCGACACAGCCCT 2280
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2221 CCATCCACTGGTGGCCACCCAGGCACTGCTCAGCCAGAGAGGCCATCCCCGACACAGCCCT 2280

Qy    2281 TGGGGCAGCCAGCCCTTTCTGCCACCCCAAGCAGGGTTCTGCCCCCAGGAGGGCTGC 2340
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2281 TGGGGCAGCCAGCCCTTTCTGCCACCCCAAGCAGGGTTCTGCCCCCAGGAGGGCTGC 2340

Qy    2341 AGCCCCCACCCAGCAGTTGCCCCATGCCCTCCTTCCCTCCCTCCAGGATCTTGCAAA 2400
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2341 AGCCCCCACCCAGCAGTTGCCCCATGCCCTCCTTGCCTCCTTCCCTCCAGGATCTTGCAAA 2400

Qy    2401 GAGGCCCCCTTAGTACCCCTTCAAGCCCCTTCTTGGACAGCCCCAGGCACCCCTGCCCCT 2460
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Qy    2461 GCCAAAGCAAGCCCCCATTGGACTCTAAGATGGGGCCTGAGACAATCTCTCTTCCTCCTGGG 2520
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Qy    2521 AGGGCCAAAACCCGGCCCCTGCAGTTCCCCAGGGTCAGCCTCCCAGGCGAGCTCTTCCCAA 2580
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2521 AGGGCCAAAACCCGGCCCCTGCAGTTCCCCAGGGTCAGCCTCCCAGGCGAGCTCTTCCCAA 2580

Qy    2581 GTGAGCTCCCTCAGGGTGGGCTCCTCCCAGGTGGGCACCAGAGCCTGCCCCTCCCTGGAT 2640
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2581 GTGAGCTCCCTCAGGGTGGGCTCCTCCCAGGTGGGCACCAGAGCCTGCCCCTCCCTGGAT 2640

Qy    2641 GCGGAGGGCTGGACCCAGGAGGCTGAGGATCGTGCCGACTCCACACCTTGCAGCGG 2700
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2641 GCGGAGGGCTGGACCCAGGAGGCTGAGGATCGTGCCGACTCCACACCTTGCAGCGG 2700

Qy    2701 CCTCAGGAACAGGTGACCATGCGCAAGTTCTCCCTGGGTGGTCGCGGGGGGTACGGCAGGC 2760
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2701 CCTCAGGAACAGGTGACCATGCGCAAGTTCTCCCTGGGTGGTCGCGGGGGGTACGGCAGGC 2760

Qy    2761 GTGGCTGGCTATGGCCACCTTTGCCTTTGGCTTTGGCTGTGGAGATGCCAGGGGGCATGGGCAGGGG 2820
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2761 GTGGCTGGCTATGGCCACCTTTGCCTTTGGCTTTGGCTGTGGAGATGCCAGGGGGCATGGGCAGGGG 2820

Qy    2821 CCCATGTGGGCCAGGATAGCCTCGGGCTGTGTCCAGTCGGAGGAGGAGGCAGGAGGAG 2880
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2821 CCCATGTGGGCCAGGATAGCCTCGGGCTGTGTCCAGTCGGAGGAGGAGGCAGGAGGAG 2880

Qy    2881 GCCAGGGCTGAGTCCCAGCAGGAGGAGCAGGAGGCTGAGAGGCCCACTGCCC 2940
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2881 GCCAGGGCGTGAGTCCCAGTCGCAGCCTAGGAGGGCAGCGGCAGGGGCTGAGAGCCCCACTGCCC 2940

Qy    2941 CAGGTCAGTGCAAGGCCTGTGCCTGAGGTCGGCAGGCTCTCCACAGGAGCTCTCCAGAG 3000
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2941 CAGGTCAGTGCAAGGCCTGTGCCTGAGGTCGGCAGGCTCTCCACAGGAGCTCTCCAGAG 3000

Qy    3001 CCCACCCCATGGGAGGGACATCGGGCAGGACATCGGGCAGTCTCCCTTGGTCGAGATCCGGGACCTGTCAGGT 3060
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3001 CCCACCCCATGGGAGGGACATCGGGCAGGACATCGGGCAGTCTCCCTTGGTCGAGATCCGGGACCTGTCAGGT 3060

Qy    3061 GATGCGGAGGCGGCCGACCTGTACGGATATCAAGTCACCTCCCCATTCAAGTTTATGATCTTCAGGAAA 3120
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3061 GATGCGGAGGCGGCCGACCTGTACGGATATCAAGTCACCTCCCCATTCAAGTTTATGATCTTCAGGAAA 3120

Qy    3121 AACCTCTCAGACCTGTACGATATCAAGTCACCTCCCATTCAAGTTTATGATCTTCAGGAAA 3180
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3121 AACCTCTCAGACCTGTACGATATCAAGTCACCTCCCATTCAAGTTTATGATCTTCAGGAAA 3180

Qy    3181 GTCCCCAAGTCCGCTCAGCCAGAGCCGCCTCCCCATGGCTGAGGAGGAGCTGGCCGAG 3240

Db    3181 GTCCCCAAGTCCGCTCAGCCAGAGCCGCCCTCCCCATGGGTGAGGAGCTGAGGAGCTGGCCGGA 3240

Qy    3241 TTCCCGGAGCCCAGTGGCCCTGCCCAGGTGAACTGGGCCCCCATGGCCCAGGCCTGGGAGATC 3300
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Db    3241 TTCCCGGAGCCCACGTGGCCCTGCCCAGGTGAACTGGGCCCCCATGGGCCCAGGCCTGCTGGAGATC 3300

Qy    3301 ACAGAGAGTCAGAGGATGTGACGCGGCTGCTGGACGAGGTTGCCGGGCAGGAGGCGC 3360
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3301 ACAGAGAGTCAGAGGATGTGACGCGGCTGCTGGAGCGAGGTTGCCGGGCAGGAAGCGC 3360

Qy    3361 AAGTGGTCCTCGCCGTCACGCAGCCCTCTTCCCACTTCCCTCGGGAGGCACCTGCCGTGGAT 3420
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3361 AAGTGGTCCTCGCCGTCACGCAGCCTCTTCCACTTCCCTCGGGAGGCACCTGCCGTGGAT 3420

Qy    3421 GAGCCTGCAGAGCTGGGGCTGCGTGAGAGTGAAGGCTCCGTGAGCACATCTCCCGG 3480
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3421 GAGCCTGCAGAGCTGGGGCTGCGTGCCGTGAGAGTGAAGGCTCCGTGAGCACATCTCCCGG 3480

Qy    3481 ATCCTGAAGGGCAGGCCCGGAAGGTCTGGAGAGGAGGCCCCAGGAAGAAGCCAGGC 3540
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3481 ATCCTGAAGGGGCAGGCCCGGAAGGTCTGGAGAGGAGGAGGGGCCCCAGGAAGAAGCCAGGC 3540

Qy    3541 CTTGCTTCCTTCCGGCTCTCAGGTCTGAAGAGCTGGGCCAGTCAGTGACACTGGCCTGCCAGGTGTCA 3600
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3541 CTTGCTTCCTTCCGGCTCTCAGGTCTGAAGAGCTGGGACCAGTCAGTGACACTGGCCTGCCAGGTGTCA 3600

Qy    3601 GAGCTCTCAGATGAGACTGGTGTCTGTCTGGGCCAGTCAGTGACACTGGCCTGCCAGGTGTCA 3660
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3601 GAGCTCTCAGATGAGACTGGTGTGTCAGTCTGGGCCAGTCAGTGACACTGGCCTGCCAGGTGTCA 3660

Qy    3661 GCCCAGCCAGCTGCCCAGGCCACCTGGAGCAAAGACGAGCCCCCTGGAGAGCAGCAGCAGC 3720
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3661 GCCCAGCCAGCTGCCCAGGCCACCTGGAGCAAAGACGAGCCCCCTGGAGAGCAGCAGCAGC 3720

Qy    3721 CGTGTCCTCATCTCTGCCACCTCAGCTTCGAGTCGTGGTGTGGTGGTG 3780
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3721 CGTGTCCTCATCTCTGCCACCTCAGCTTCGAGTCTTCGAGTCGTGGTGTGGTGGTG 3780

Qy    3781 GCTGAGGAACCTGGTGTACACCTGCAGCGGTGAGCAGTGACAGTGACCACC 3840
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3781 GCTGAGGAACCTGGTGTGTACACCTGCAGCGGTGAGCAGTGACAGTGACCACC 3840

Qy    3841 ACGGGCGTCCTCCGGAAGGCAGAGCGCCCTCATCTTCGCCATGCCGGATATCGGGGAG 3900
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3841 ACGGGCGTCCTCCGGAAGGCAGAGCGAGCGCCCTCATCTTCGCCATGCCCGGATATCGGGGAG 3900

Qy    3901 GTGTACGGCGGATGGGGTCGTCTGGTTCGGGTGCTGCTGGTCGGAAGCCCGTGTGTCC 3960
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3901 GTGTACGGCGGATGGGGTCGTCTGGTTCGGGTGCTGCTGGTCGGAATCCTACGGCCCGTGTGACC 3960

Qy    3961 TACATTGTGCAGTGCAGCCTAGAGGCGGCAGCTGACCACACTGGCCTTCCGACATCTTT 4020
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3961 TACATTGTGCAGTGCAGCCTAGAGAGGCGGCAGCTGACCACCACTGGCCTCCGACATCTTT 4020

Qy    4021 GACTGCGTGCTACCTGACCAGCAAGCTCTCCCGGGGTGGCACCTACACCTTCCGCACGGCA 4080
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4021 GACTGCGTGCTACCTGACCAGCAAGCTCTCCCGGGGTGGCACCTACACCTTCCGCACGGCA 4080

Qy    4081 TGTGTGCAGGCAGGAATGGGTCCCACAGCAGCCCCTCGGAGGCAAGTCCTCCTGGGA 4140
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4081 TGTGTGCAGGCAGGAATGGGTCCCACAGCAGCCCCTCGGAGGCAAGTCCTCCTGGGA 4140

Qy    4141 GGGCCCCATGGGAGGGCGCCACCTGGCTCGCCCCAACCCCTGCCC 4200
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4141 GGGCCCCAGCCCACCTGGCTCTGAGGAGGAGCCAGGGGCGGTCAGCCCAACCCCTGCCC 4200

Qy    4201 AGCACAAAGACCTTCGCATTCGACTGGTCATCCCCGCGTGGTGTGCGG 4260
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4201 AGCACAAAGACCTTCGCATTCGACTCGACACAGATCCAGCAGGGGCGCGCTTCAGCGTGTGCGG 4260

Qy    4261 CAATGCTGGGAGAAGGCCAGCCGGCGGGGCCGCTGGCCTGGGCCGCCAAGATCATCCCCTACCACCCC 4320
           ||||||||||||||||||||||||||||||||||||||||||||||||||

Db   4261 CAATGCTGGAGAAGGCCAGCGGGCGCTGGCCGCCAAGATCATCCCTACCACCCC 4320
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   4321 AAGGACAAGACAGCAGTGCTGCGCGAATACGAGGCCTCAAGGCCTGCGCACCCGCAC 4380
Db   4321 AAGGACAAGACAGCAGTGCTGCGCGAATACGAGGCCTCAAGGCCTGCGCCACCCGCAC 4380

Qy   4381 CTGGCCCAGCTGCACGCAGCCTACCTCAGCCCCCGCACCTGGTGCTGCATCTTGGAGCTG 4440
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4381 CTGGCCCAGCTGCACGCAGCCTACCTCAGCCCCCGCACCTGGTGCTCATCTTGGAGCTG 4440

Qy   4441 TGCTCTGGGGCCCGAGTGCTCCCCTGCCTGGCCGAGAGGGCCTCCTACTCAGAATCTGAG 4500
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4441 TGCTCTGGGGCCCGAGTGCTCCCCTGCCTGGCCGAGAGGGCCTCCTACTCAGAATCTGAG 4500

Qy   4501 GTGAAGGACTACCTGTGGCAGATGTTGAGTGCCACCAGGTGCCACACCAGCACATC 4560
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4501 GTGAAGGACTACCTGTGGCAGATGTTGAGTGCCACCAGGTGCCACACCAGCACATC 4560

Qy   4561 CTGCACCTGGACCTGAGGTCCGAGAACATGATCATCACCGAATACAACCTGCTCAAGGTC 4620
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4561 CTGCACCTGGACCTGAGGTCCGAGAACATGATCATCACCGAATACAACCTGCTCAAGGTC 4620

Qy   4621 GTGGACCTGGGCAATGCAGAGAGCCTCAGCCAGGAGAAGTGTGCCCTCAGACAAGTTC 4680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4621 GTGGACCTGGGCAATGCAGAGAGCCTCAGCCAGGAGAAGTGTGCCCTCAGACAAGTTC 4680

Qy   4681 AAGGACTACCTAGAGACCATGGCTCTCAGAGCTCCTGGAGGGCCAGGGGCTGTTCCACAG 4740
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4681 AAGGACTACCTAGAGACCATGGCTCTCAGAGCTCCTGGAGGGCCAGGGGCTGTTCCACAG 4740

Qy   4741 ACAGACATCTGGGCCATCGGTGTGACAGCCTTCATCATGCTGGCCGAGTACCCGTG 4800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4741 ACAGACATCTGGGCCATCGGTGTGACAGCCTTCATCATGCTGGCCGAGTACCCGTG 4800

Qy   4801 AGCAGCGAGGGTGCACGCGACCTGACCGAGAGAGAGGGCTGCGCAAGGGCTGGTCCGGCTGAGC 4860
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4801 AGCAGCGAGGGTGCACGCGACCTGACCGAGAGAGAGGGCTGCGCAAGGGCTGGTCCGGCTGAGC 4860

Qy   4861 CCCTGCTACGCGGGGGTGTCCGGGGGCGCCGTGGCCTTCCTGCGCAGCACTCTGTGCGCC 4920
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Db   4861 CGTGCTACGCGGGGGTGTCCGGGGGCGCCGTGGCCTTCCTGCGCAGCACTCTGTGCGCC 4920

Qy   4921 CAGCCCTGGGGCGCCGCCCTGGGCGTCAGCTGGCCCGCAGCGCCCGTGGCTAACAGAGAG 4980
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4921 CAGCCCTGGGGCGCCGCCCTGGGCGTCAGCTGGCCCGCAGCGCCCGTGGCTAACAGAGAG 4980

Qy   4981 GGCCCGGCCTGTTCGGGGGCCCGGCCCCGGCCCGGCCCGTGACCTTCCCTACCCGCCGGCGGCCGGCTGCGGCCGTCTTC 5040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4981 GGCCCGGCCTGTTCGGGGGCCCGGCCCCGGCCCGGCCCGTGACCTTCCCTACCCGCCGGCGGCCGGCTGCGGCCGTCTTC 5040

Qy   5041 GTGCGCAATCGCGGAGAAGAGACGCGCGCGCGTCGTGTACAGAGGCACAACCTGGGCCAGGTG 5100
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5041 GTGCGCAATCGCGGAGAAGAGACGCGCGCGCGTCGTGTACAGAGGCACAACCTGGGCCAGGTG 5100

Qy   5101 CGCTGAGGGTGCCCCCGGCCACACCCTTGGTCTCCCCGCTGGGGGTCGCTGCAGACGCGC 5160
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5101 CGCTGAGGGTGCCCCCGGCCACACCCTTGGTCTCCCCGCTGGGGGTCGCTGCAGACGCGC 5160

Qy   5161 CAATAAAAACGCACACGCGGGCGGAGAAAAAAAAAAAAAAAAAAAAAAA 5207
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db   5161 CAATAAAAACGCACACGCGGGCGGAGAAAAAAAAAAAAAAAAAAAAAAA 5207

RESULT 3
AAD38865
ID   AAD38865   standard; cDNA; 5454 BP.
XX
AC   AAD38865;
XX
DT   23-SEP-2002   (first entry)
XX
DE   Human kinase (PKIN)-22 cDNA.
XX

Query Match     99.4%;   Score 5173.6;   DB 6;   Length 5454;
Best Local Similarity   99.8%;   Pred. No. 0;

Matches 5179; Conservative 0; Mismatches 0; Indels 9; Gaps 0;

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Qy      3  GCAGGAGGAACTCCTTCTGATCACCTGGCCAGCTGAGGTCAGAGTGGGAGGAGGCAGTGGT    62
             ||  | |||||||||||||||||||||||||||||||||||||  |||||||||||||||
Db    267  GCCCCACCAACTCCTTCTGATCACCTGGCCAGCTGAGGTCAGAGTGGGAGGAGGCAGTGGT   326

Qy     63  TCCATTGAAGGAGTACTCCTAACTGTCAGAAGCCTTGGGCGGTCAGGATGGGGTGCTGTCG   122
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    327  TCCATTGAAGGAGTACTCCTAACTGTCAGAAGCCTTGGGCGGTCAGGATGGGGTGCTGTCG   386

Qy    123  CTTGGGCGTGCGGGGGTGTTCAGTTGCCCACAGTGTATCTCAGGGTCTCACCAACCATCC   182
           |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db    387  CTTGGGCTGCGGGGGTGTTCAGTTGCCCACAGTGTATCTCAGGGTCTCACCAACCATCC   446

Qy    183  AAGCATGGTAGGCTTGGCTGGCACCCAGGTTGTGTGGCTGGGAGGTGGTCTCCACAG   242
           ||||||||||||| |||||||||||||||||||||| |||||||||||||||||||||
Db    447  AAGCATGGTAGGCGTGGCTGGCACCCAGGTTGTGTGGCTGGGAGGTGGTCTCCACAG   506

Qy    243  TTCCCTCCCTGCCTCCCAGGGCCCCATCATGCGAGGTAACCATCGAGGATGTGCAGGC   302
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    507  TTCCCTCCCTGCCTCCCAGGGCCCCATCATGCGAGGTAACCATCGAGGATGTGCAGGC   566

Qy    303  ACAGACAGGCGAACGGCCCAATTCGAGGCTATCATTGAGGGGGCGACCCACAGCCCTCGGT   362
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    567  ACAGACAGGCGAACGGCCCAATTCGAGGCTATCATTGAGGGGGCGACCCACAGCCTCGGT   626

Qy    363  GACCCTGTACAAGGACAGCGTCCAGCTGGTGGACAGCACCCGGCTTAGCGCTGGCAGCAAGA   422
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    627  GACCCTGTACAAGGACAGCGTCCAGCTGGTGGACAGCACCCGGCTTAGCGCTGGCAGCAAGA   686

Qy    423  AGGCACCACCATACTCCCTGTGCTGAGGCATGTGGCTTCGAAGGATGGCCGGCGTTTACAC   482
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    687  AGGCACCACATACTCCCTGTGCTGAGGCATATGGCTTCGAAGGATGGCCGGCGTTTACAC   746

Qy    483  CTGCCTGGCCCAAAACACTGGTGGCCAGTGCTCTGCGAAGGCAGAGCTGCTGGTGCTTGG   542
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Db    747  CTGCCTGGCCCAAAACACTGGTGGCCAGTGCTCTGCAAGGCAGAGCTGCTGGTGCTTGG   806

Qy    543  GGGGACAATGAGCCGGACTCAGAGAAGCAAAGCCACCGGAAGCTCGATAAAAAGAGTGCAGCACAA   602
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    807  GGGGGACAATGAGCCGGACTCAGAGAAGCAAAGCCACCGGAAGCTCGTAAAAAGAGTGCAGCACAA   866

Qy    603  TGAGGTCAAGGAGGAGGAGATTGTGCGCCAAGTTCATCCCCGCTGTTTGGCTTCGTAAAAGAGTGCAGCACAA   662
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    867  TGAGGTCAAGGAGGAGGAGATTGTGCGCCAAGTTCATCCCCGCTGTTTGGCTTCGTAAAAAGAGTGCAGCACAA   926

Qy    663  AGGAAACAAGATCTTGTGCGCTGCCAAGTTCATCCCCGCTGGTCACCCGCTGGTCACGGGGCTGCT   722
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    927  AGGAAACAAGATCTTGTGCGCTGCCAAGTTCATCCCCGCTGGTCACCCGCTGGTCACGGGGCTGCT   986

Qy    723  GGCATACAGGGAGCGAGACATCCTGCGCGGCTGAGCCACCCGCTGGTCACGGGGGCTGCT   782
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    987  GGCATACAGGGAGCGAGACATCCTGCGCGGCTGAGCCACCCGCTGGTCACGGGGGCTGCT   1046

Qy    783  GGACCAGTTTGAGACCGCCTGTACAGGAAGGGCGTGGTGACGGAGGCCGAGGTCATCCTGGAGCTGTGTCATCCCGAGGA   842
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1047  GGACCAGTTTGAGACCGCCTGTACAGGAAGGGCGTGGTGACGGAGGCCGAGGTCATCCTGGAGCTGTGTCATCCCGAGGA   1106

Qy    843  GCTGCTGGACCGGCCTGTACGGAGGGCGTGGTGACGGAGGCCGAGGTCAGGGTCATCCTGGGCCAAGGTCACAT   902
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1107  GCTGCTGGACCGGCCTGTACGGAGGGCGTGGTGACGGAGGCCGAGGTCAGGGTCAAGGTCACAT   1166

Qy    903  CCAGCAGCTGGTGGGAGGGGCTGCACTACCTGCACTACCTGCCAAGGCCCATGGCGTTCTTCCACCTGGACAT   962
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1167  CCAGCAGCTGGTGGGAGGGGCTGCACTACCTGCACTACCTGCCAAGGCCCATGGCGTTCTTCCACCTGGACAT   1226

Qy    963  AAAGCCCTCTAACATCCTGATGGTGCATCCTGCCGGGAAGACATTAAAATCTGCGGACTT   1022
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1227  AAAGCCCCTCTAACATCCTGATGGTGCATCCTGCCGGGAAGACATTAAAATCTGCGGACTT   1286

Qy   1023  TGGCTTTGCCCAGAACATCACCCCCAGCAGCTGCAGTTCAGCCAGCTGCCCCTGA   1082
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1287  TGGCTTTGCCCAGAACATCACCCCCAGCAGCTGCAGTTCAGCCAGCTGCCCCTGA   1346
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Qy   1083  GTTGTCTCCCCGAGATCATCCAGCAGGAACCCTGTGAGCGAAGCCTTCCGACATTGGGC   1142
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1347  GTTGTCTCCCCGAGATCATCCAGCAGGAACCCTGTGAGCGAAGCCTTCCGACATTGGGC   1406

Qy   1143  CATGGTGTCATCTCCTACCTCCTCAGCCTTGGGCGGTCAGGATGGGGTGCTGTCG   1202
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1407  CATGGTGTCATCTCCTACCTCCTCAGCCTTGGGCGGTCAGGATGGGGTGCTGTCG   1466

Qy   1203  CCGTGCCACCCTCCTGAACGTCCTGAGGGGGCGGCGTGTCATGGAGCAGCCCATGCGTGC   1262
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1467  CCGTGCCACCCTCCTGAACGTCCTGGAGGGGGCGGCGTGTCATGGAGCAGCCCATGGCTGC   1526

Qy   1263  CCACCTCAGCGAGAGACGCCAAAGACTTCATCAAGGCTACGGTGCGAGAGAGCCCTCAGGC   1322
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1527  CCACCTCAGCGAGAGACGCCAAAGACTTCATCAAGGCTACGGTGCGAGAGAGCCCCTCAGGC   1586

Qy   1323  CCGGCCTAGTGCGGCCCAGTGCCTCTCCCACCCCTGGTTCTGAAATCATGCGCGA   1382
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1587  CCGGCCTAGTGCGGCCCAGTGCCTCTCCCACCCCTGGTTCTGAAATCATGCCGCGGA   1646

Qy   1383  GGAGGCCCACTTCATCAACAACAAGCAGCTCAAGTTCCTCCTGGCCCGAGTCGCTGGCA   1442
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1647  GGAGGCCCACTTCATCAACAACAAGCAGCTCAAGTTCCTCCTGGGCCCGAGTCGCTGGCA   1706

Qy   1443  GCGTTCCTGATGAGCTACAAGTTCCATCCTGGTGATGCGCTCCATCCTGAGTGCTGCGCG   1502
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1707  GCGTTCCTGATGAGCTACAAGTTCCATCCTGGTGATGCGCTCCATCCTGAGTGCTGCGCG   1766

Qy   1503  GGGCCCACCCGACGCAGCCCCTCCTCCTCGGCGTAGCCGGATGGCCGGCCTTCCTGCGGTG   1562
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Db   1767  GGGCCCACCCGACAGCGCCCTCCTCCTCGGCGTAGCCGGACACTTGGTG   1826

Qy   1563  CTCCTCCAGTTCTCTCCTCCTCCTGACAACGAGCTCGCCCCAGTTGCCCGGGGCTAAGTC   1622
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Db   1827  CTCCTCCAGTTCTCTCCTCCTCCTGACAACGAGCTCGCCCCATTGCCCGGGGCTAAGTC   1886

Qy   1623  ACTGCCACCCTCCCGGTGACACTTCACCACTGCTGACACTGTCGACCCGAGGCCCCAGCTCC   1682
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Db   1887  ACTGCCACCCTCCCGGTGACACACTTCACCACTGCTGACACTGTCGACCCGAGGCCCCAGCTC   1946

Qy   1683  CTGGGCCATCTCCGAGGGTGCCCGGGTGCCGCGGCCACCAGGGCGGTGAGCACCGGGCCCTGGC   1742
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1947  CTGGGCCCATCTCCGAGGGTGCCCGGGTGCCGCGGCCACCAGGGCGGTGAGCACCGGGCCCTGGC   2006

Qy   1743  GCCTGCATCTCCCGAGGGTGCCCGCCACCAGGTGCGGGGCCCAGGGCTGCGTGCCCCGGCACAG   1802
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2007  GCCTGCATCTCCCGAGGGTGCCCGCCACCAGGTGCGGTGCCGGGGCTGCGTGCCCCGGCACAG   2066

Qy   1803  CGTCATCCGCAGCCTGTTCTACCACCCGGCTGAGGCGGTGCACCGGGGCCCTGGC   1862
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2067  CGTCATCCGCAGCCTGTTCTACCACCCGGCTGAGGCGGTGCACCGGGGCCCTGGC   2126

Qy   1863  CCCGGGAGCAGCAGGCCTGCCAGGCCTGCGCGGAGGCCACTGATGGAGCACCGGGGCGGCTACATTGC   1922
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2127  CCCGGGAGCAGCAGGCCTGCCAGGCCTGCGCGGAGGCCACTGATGGAGCACCGGGGCGGTACATTGC   2186

Qy   1923  GGGGCGGCTGCCAGGCCTGCCGCGGAGGCCCACTGCTGAGGGGCTGCTGGAGGAGGAGGC   1982
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2187  GGGGGCGGCTGCCAGGCCTGCCGCGGAGGCCCACTGCTGAGGGGCTGCTGGAGGAGGAGGC   2246

Qy   1983  CGCCAGGAGGAGCAGCCACCCTCCTGGCCAAAGCCCCCTCATTCGAGACTGCCCCCG   2042
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2247  CGCCAGGAGGAGCAGCCACCCTCCTGGCCAAAGCCCCCTCATTCGAGACTGCCCCCG   2306

Qy   2043  GCTGCCTGCTGGCACCCACTTGGCCCCTGGCCCGGCCACCCGAACATGACTC   2102
           |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2307  GCTGCCTGCTGGCACCCACTTGGCCCCTGGCCCGCACAGCCACTCCCTGAACATGACTC   2366

Qy   2103  TCCGAGCACCCCCCGCCCCTCCTCGGAGGGCTGCCGGTGAGGCACAGCGACTGCCTTCAGC   2162
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2367  TCCGAGCACCCCCCGCCCCTCCTCGGAGGGCTGCCGGTGAGGCACAGCGACTGCCTTCAGC   2426
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Qy          2163 CCCCTCCGGGGGGGCCCCTATCAGGGACATGGGGCACCCTCAGGGCTCCAAGCAGCTTCC 2222
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Db          2427 CCCCTCCGGGGGGGCCCCTATCAGGGACATGGGGCACCCTCAGGGCTCCAAGCAGCTTCC 2486

Qy          2223 ATCCACTGGTGGCCACCCAGGCACTGCTCAGCCAGAGAGGCCATCCCCGGACAGCCCTTG 2282
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2487 ATCCACTGGTGGCCACCCAGGCACTGCTCAGCCAGAGAGGCCATCCCCGGACAGCCCTTG 2546

Qy          2283 GGGGCAGCCAGCCCCTTTCTGCCACCCCAAGCAGGGTTCTGCCCCCCAGGAGGGCTGCAG 2342
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2547 GGGGCAGCCAGCCCCTTTCTGCCACCCCAAGCAGGGTTCTGCCCCCCAGGAGGGCTGCAG 2606

Qy          2343 CCCCCACCCAGCAGTTGCCCCATGCCCTCCTGGCTCCTTCCCTCCAGGATCTTGCAAAGA 2402
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2607 CCCCCACCCAGCAGTTGCCCCATGCCCTCCTGGCTCCTTCCCTCCAGGATCTTGCAAAGA 2666

Qy          2403 GGCCCCCTTAGTACCCTCAAGCCCCTTCTTGGGACAGCCCCAGGCACCCCCTGCCCCTGC 2462
                 |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db          2667 GGCCCCCTTAGTACCCTCAAGCCCCTTCTTGGGACAGCCCCAGGCACCCCTTGCCCCTGC 2726

Qy          2463 CAAAGCAAGCCCCCCATTGGACTCTAAGATGGGGCCTGGAGACATCTCTCTTCCTGGGAG 2522
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2727 CAAAGCAAGCCCCCCATTGGACTCTAAGATGGGGCCTGGAGACATCTCTCTTCCTGGGAG 2786

Qy          2523 GCCAAAACCCGGCCCCTGCAGTTCCCCAGGGTCAGCCTCCCAGGCGAGCTCTTCCCAAGT 2582
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2787 GCCAAAACCCGGCCCCTGCAGTTCCCCAGGGTCAGCCTCCCAGGCGAGCTCTTCCCAAGT 2846

Qy          2583 GAGCTCCCTCAGGGTGGGCTCCTCCCAGGTGGGCACAGAGCCTGGCCCCTCCCTGGATGC 2642
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2847 GAGCTCCCTCAGGGTGGGCTCCTCCCAGGTGGGCACAGAGCCTGGCCCCTCCCTGGATGC 2906

Qy          2643 GGAGGGCTGGACCCAGGAGGCTGAGGATCTGTCCGACTCCACACCCACCTTGCAGCGGCC 2702
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2907 GGAGGGCTGGACCCAGGAGGCTGAGGATCTGTCCGACTCCACACCCACCTTGCAGCGGCC 2966

Qy          2703 TCAGGAACAGGTGACCATGCGCAAGTTCTCCCTGGGTGGTCGCGGGGGCTACGCAGGCGT 2762
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Db          2967 TCAGGAACAGGTGACCATGCGCAAGTTCTCCCTGGGTGGTCGCGGGGGCTACGCAGGCGT 3026

Qy          2763 GGCTGGCTATGGCACCTTTGCCTTTGGTGGAGATGCAGGGGGCATGCTGGGGCAGGGGCC 2822
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Qy          2823 CATGTGGGCCAGGATAGCCTGGGCTGTGTCCCAGTCGGAGGAGGAGGAGCAGGAGGAGGC 2882
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Db          3087 CATGTGGGCCAGGATAGCCTGGGCTGTGTCCCAGTCGGAGGAGGAGGAGCAGGAGGAGGC 3146

Qy          2883 CAGGGCTGAGTCCCAGTCGGAGGAGCAGCAGGAGGCCAGGGCTGAGAGCCCACTGCCCCA 2942
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Db          3147 CAGGGCTGAGTCCCAGTCGGAGGAGCAGCAGGAGGCCAGGGCTGAGAGCCCACTGCCCCA 3206

Qy          2943 GGTCAGTGCAAGGCCTGTGCCTGAGGTCGGCAGGGCTCCCACCAGGAGCTCTCCAGAGCC 3002
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Db          3207 GGTCAGTGCAAGGCCTGTGCCTGAGGTCGGCAGGGCTCCCACCAGGAGCTCTCCAGAGCC 3266

Qy          3003 CACCCCATGGAGGACATCGGGCAGGTCTCCCTGGTGCAGATCCGGGACCTGTCAGGTGA 3062
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Db          3267 CACCCCATGGAGGACATCGGGCAGGTCTCCCTGGTGCAGATCCGGGACCTGTCAGGTGA 3326

Qy          3063 TGCGGAGGCGGCCGACACAATATCCCTGGACATTTCCGAGGTGGACCCCGCCTACCTCAA 3122
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Db          3327 TGCGGAGGCGGCCGACACAATATCCCTGGACATTTCCGAGGTGGACCCCGCCTACCTCAA 3386

Qy          3123 CCTCTCAGACCTGTACGATATCAAGTACCTCCCATTCGAGTTTATGATCTTCAGGAAAGT 3182
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Db          3387 CCTCTCAGACCTGTACGATATCAAGTACCTCCCATTCGAGTTTATGATCTTCAGGAAAGT 3446

Qy          3183 CCCCAAGTCCGCTCAGCCAGAGCCGCCCTCCCCCATGGCTGAGGAGGAGCTGGCCGAGTT 3242
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Qy          3243 CCCGGAGCCCACGTGGCCCTGGCCAGGTGAACTGGGCCCCCACGCAGGCCTGGAGATCAC 3302
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Qy          3303 AGAGGAGTCAGAGGATGTGGACGCGCTGCTGGCAGAGGCTGCCGTGGGCAGGAAGCGCAA 3362
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Qy          3363 GTGGTCCTCGCCGTCACGCAGCCTCTTCCACTTCCCTGGGAGGCACCTGCCGCTGGATGA 3422
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db          3627 GTGGTCCTCGCCGTCACGCAGCCTCTTCCACTTCCCTGGGAGGCACCTGCCGCTGGACGA 3686

Qy          3423 GCCTGCAGAGCTGGGGCTGCGTGAGAGAGTGAAGGCCTCCGTGGAGCACATCTCCCGGAT 3482
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Db          3687 GCCTGCAGAGCTGGGGCTGCGTGAGAGAGTGAAGGCCTCCGTGGAGCACATCTCCCGGAT 3746

Qy          3483 CCTGAAGGGCAGGCCGGAAGGTCTGGAGAAGGAGGGGCCCCCAGGAAGAAGCCAGGCCT 3542
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Db          3747 CCTGAAGGGCAGGCCGGAAGGTCTGGAGAAGGAGGGGCCCCCAGGAAGAAGCCAGGCCT 3806

Qy          3543 TGCTTCCTTCCGGCTCTCAGGTCTGAAGAGCTGGACCGAGCGCCGACATTCCTAAGGGA 3602
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Db          3807 TGCTTCCTTCCGGCTCTCAGGTCTGAAGAGCTGGACCGAGCGCCGACATTCCTAAGGGA 3866

Qy          3603 GCTCTCAGATGAGACTGTGGTCCTGGGCCAGTCAGTGACACTGGCCTGCCAGGTGTCAGC 3662
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3867 GCTCTCAGATGAGACTGTGGTCCTGGGCCAGTCAGTGACACTGGCCTGCCAGGTGTCAGC 3926

Qy          3663 CCAGCCAGCTGCCCAGGCCACCTGGAGCAAAGACGGAGCCCCCCTGGAGAGCAGCAGCCG 3722
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Qy          3723 TGTCCTCATCTCTGCCACCCTCAAGAACTTCCAGCTTCTGACCATCCTGGTGGTGGTGGC 3782
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Db          4047 TGAGGACCTGGGTGTGTACACCTGCAGCGTGAGCAATGCGCTGGGGACAGTGACCACCAC 4106

Qy          3843 GGGCGTCCTCCGGAAGGCAGAGCGCCCCTCATCTTCGCCATGCCCGGATATCGGGGAGGT 3902
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Qy          3903 GTACGCGGATGGGGTGCTGCTGGTCTGGAAGCCCGTGGAATCCTACGGCCCTGTGACCTA 3962
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Db          4167 GTACGCGGATGGGGTGCTGCTGGTCTGGAAGCCCGTGGAATCCTACGGCCCTGTGACCTA 4226

Qy          3963 CATTGTGCAGTGCAGCCTAGAAGGCGGCAGCTGGACCACACTGGCCTCCGACATCTTTGA 4022
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Qy          4023 CTGCTGCTACCTGACCAGCAAGCTCTCCCGGGGTGGCACCTACACCTTCCGCACGGCATG 4082
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4287 CTGCTGCTACCTGACCAGCAAGCTCTCCCGGGGTGGCACCTACACCTTCCGCACGGCATG 4346

Qy          4083 TGTCAGCAAGGCAGGAATGGGTCCCTACAGCAGCCCCTCGGAGCAAGTCCTCCTGGGAGG 4142
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Db          4347 TGTCAGCAAGGCAGGAATGGGTCCCTACAGCAGCCCCTCGGAGCAAGTCCTCCTGGGAGG 4406

Qy          4143 GCCCAGCCACCTGGCCTCTGAGGAGGAGAGCCAGGGGCGGTCAGCCCAACCCCTGCCCAG 4202
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4407 GCCCAGCCACCTGGCCTCTGAGGAGGAGAGCCAGGGGCGGTCAGCCCAACCCCTGCCCAG 4466

Qy          4203 CACAAAGACCTTCGCATTCCAGACACAGATCCAGAGGGGCCGCTTCAGCGTGGTGCGGCA 4262
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4467 CACAAAGACCTTCGCATTCCAGACACAGATCCAGAGGGGCCGCTTCAGCGTGGTGCGGCA 4526

Qy          4263 ATGCTGGGAGAAGGCCAGCGGGCGGGCGCTGGCCGCCAAGATCATCCCCTACCACCCCAA 4322
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4527 ATGCTGGGAGAAGGCCAGCGGGCGGGCGCTGGCCGCCAAGATCATCCCCTACCACCCCAA 4586

Qy          4323 GGACAAGACAGCAGTGCTGCGCGAATACGAGGCCCTCAAGGGCCTGCGCCACCCGCACCT 4382
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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KW   haemolytic anaemia; cellular proliferative disorder; cancer;
KW   protein kinase disorder; autoimmune disorder; diabetes mellitus;
KW   psoriasis; inflammatory bowel disease; rheumatoid arthritis;
KW   multiple sclerosis.
XX
OS   Homo sapiens.
XX
FH   Key            Location/Qualifiers
FT   5'UTR          1..71
FT                  /tag= a
FT   CDS            72..7964
FT                  /tag= b
FT                  /product= "kinase 59079"
FT                  /note= "This CDS is specifically claimed in claim 2"
FT   3'UTR          7965..8106
FT                  /tag= c
XX
PN   US2002168742-A1.
XX
PD   14-NOV-2002.
XX
PF   15-FEB-2002; 2002US-00077130.
XX
PR   15-FEB-2001; 2001US-0269201P.
XX
PA   (MILL-) MILLENNIUM PHARM INC.
XX
PI   Kapeller-Libermann R,   Acton SL;
XX
DR   WPI; 2003-298729/29.
DR   P-PSDB; ABG76186.
XX
PT   Novel isolated human protein kinase, designated 59079 or 12599
PT   polypeptide, useful as diagnostic and therapeutic agents for preventing
PT   cardiovascular diseases, proliferative disorders, and protein kinase
PT   disorders.
XX
PS   Claim 2; Page 39-48; 119pp; English.
XX
CC   The invention relates to an isolated human serine/threonine or protein
CC   kinase, 59079 or 12599 polypeptide, encoded by nucleic acid molecule
CC   comprising at least 85% identity to the nucleic acids appearing as
CC   ABX11641 and ABX11642 or their complement, a naturally occurring variant
CC   of the kinases or their fragments. Also included are a non-human host
CC   cell containing the nucleic acids, an antibody specific for the proteins,
CC   identifying a compound which binds to the kinase (by contacting the
CC   kinase or a cell expressing the kinase with a test compound and
CC   determining whether the kinase binds to the test compound) and modulating
CC   the activity of kinase using the identified compound. The kinases and
CC   their encoding nucleic acids are useful as diagnostic and therapeutic
CC   agents for preventing a disease or condition associated with an aberrant
CC   or unwanted 59079 or 12599 activity in a subject, including
CC   cardiovascular diseases such as heart failure, and myocardial infarction;
CC   disorders involving blood vessels such as atherosclerosis, and Kaposi's
CC   sarcoma; blood platelets disorder such as thrombocytopaenia, leukaemia,
CC   Hodgkin's disease, haemolytic anaemia; cellular proliferative disorders
CC   such as cancer; and protein kinase disorders such as autoimmune
CC   disorders, diabetes mellitus, psoriasis, inflammatory bowel disease,
CC   rheumatoid arthritis, and multiple sclerosis (many examples of diseases
CC   and disorders are included in the specification). The kinases, their
CC   encoding nucleic acids and antibodies are useful in screening assays,
CC   detection assays (e.g. forensic biology), and predictive medicine (e.g.
CC   diagnostic assays, prognostic assays, and monitoring clinical trials and
CC   pharmacogenomics). The kinases and their encoding nucleic acids are
CC   useful as query sequences to perform a search against public databases to
CC   identify other family members or related sequences. The present sequence
CC   encodes the kinase 59079
XX
SQ   Sequence 8106 BP; 1603 A; 2684 C; 2530 G; 1289 T; 0 U; 0 Other;

Query Match             94.9%;   Score 4940.4;   DB 7;   Length 8106;
Best Local Similarity   99.9%;   Pred. No. 0;
Matches 4944;   Conservative   0;   Mismatches   6;   Indels   0;   Gaps   0;

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Db   4587 GGACAAGACAGCAGTGCTGCCGAATACAGAGGCCCTGCCGCCACCGCACCT 4646
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Qy   4383 GGCCCAGCTGCACGCAGCCTACCTGCCCCCGGCCACCTGGTGCTCATCTTGGAGCTGTG 4442
              ||||||||||||||||||||||||||||||||||||||||||
Db   4647 GGCCCAGCTGCACGCAGCCTACCTGCCCCCGGCCACCTGGTGCTCATCTTGGAGCTGTG 4706

Qy   4443 CTCTGGGCCCCAGCTGCTGCTCCCCTGCCTGGCCGAGAGGGGCCTCCTACTCAGAATCTGAGGT 4502
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Qy   4563 GCACCTGGACCTGAGGTCCGAGAACATGATCATCACCGAATACAACCTGCTCAAGGTCGT 4622
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Qy   4623 GGACCTGGGCAATGCACAGAGCCTCAGCCAGGAGAAGGTGCTGCCCTCAGACAAGTTCAA 4682
              ||||||||||||||||||||||||||||||||||||||||||
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Qy   4683 GGACTACCTAGAGACCATGGCTCCAGAGCTCCTGAGGGGCCAGGGGCTGTTCCACAGAC 4742
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Qy   4743 AGACATCTGGGCCATCGGTGTGACAGCCTTCATCATGTGAGCGGCCAGAGTACCCGGTGAG 4802
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Qy   4803 CAGCGAGGGTGCCACGCGACCTGCGAGAGGACTGCGCAAGGGCTGGTCCGGCTGAGCCCG 4862
              ||||||||||||||||||||||||||||||||||||||||||
Db   5067 CAGCGAGGGTGCACGCGACCTGCGAGAGGACTGCGCAAGGGCTGGTCCGGCTGAGCCCG 5126

Qy   4863 CTGCTACGCGGGGGCTGTCCGGGGGCCGCCTGGCCTTCCTGCGGCAGCACTCTGTGCGCCCAA 4922
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Db   5127 CTGCTACGCGGGGGCTGTCCGGGGGCCGCCTGGCCTTCCTGCGGCAGCACTCTGTGCGCCCCA 5186

Qy   4923 GCCCTGGGGCCCGGGGCCTGCCCGTCCAGTCGCTGCCCGTCCAGTGCCGTCAGTGGCTAACAGAGAGGGG 4982
              ||||||||||||||||||||||||||||||||||||||||||
Db   5187 GCCCTGGGGCCCGGGGCCTGCCCGTCCAGTCGCTGCCCGTCCAGTGCCGTCAGTGGCTAACAGAGAGGGG 5246

Qy   4983 CCCGGCCTGTTCGCGGCCCCGGCCCGTGACCTTCCACGGCCGCGGCGGCCTCTTCGT 5042
              ||||||||||||||||||||||||||||||||||||||||||
Db   5247 CCCGGCCTGTTCGCGGCCCCGGCCCGTGACCTTCCTACCGCGGCGGCCGGTCTTCGT 5306

Qy   5043 GCGCAATCGGCGAGAAGAGACGCGCGGCTGTCGTGTACAAGAGGCACAACCTGGCCCAGGTGCG 5102
              ||||||||||||||||||||||||||||||||||||||||||
Db   5307 GCGCAATCGGCGAGAGAGAGACGCGCGCGCCTGTCGTGTACAAGAGGCACAACCTGGCCCAGGTGCG 5366

Qy   5103 CTGAGGTCGCGCCCCGCCACACCCTTGGTCTCCCCCGCGTGGGGGTCGCTGCAGACGCGCCA 5162
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Db   5367 CTGAGGTCGCCCCCGCCACACCCTTGGTCTCCCCCGCTGGGGGTCGCTGCAGACGCGCCA 5426

Qy   5163 ATAAAAACGCACAGCCGGGCGAGAAAA 5190
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Db   5427 ATAAAAACGCACAGCCGCGGGGGGAGAAAA 5454
```

RESULT 4
ABX11641
ID   ABX11641 standard; cDNA; 8106 BP.
XX
AC   ABX11641;
XX
DT   09-MAY-2003   (first entry)
XX
DE   Human serine/threonine or protein kinase 59079, cDNA.
XX
KW   Human; ss; gene; serine/threonine kinase; protein kinase; 59079;
KW   cardiovascular disease; heart failure; myocardial infarction;
KW   blood vessel disorder; atherosclerosis; Kaposi's sarcoma;
KW   blood platelet disorder; thrombocytopaenia; leukaemia; Hodgkin's disease;

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Qy    258 CCCAGGGCCCCATCCATGCAGGTAACCATCGAGGATGTGCAGGCACAGACGGCGAAC  317
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Db   3116 CGCACGGCCCCCATCCATGCAGGTAACCATCGAGGATGTGCAGGCACAGACGGCGAAC 3175

Qy    318 GGCCCAATTCGAGGCTATCATTGAGGGCGACCCACAGCCCTCGGTGACCTGGTACAAGGA  377
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Qy    378 CAGCGGTCCAGTGGCTGGACAGCACCCGGCTTAGCCAGCAGAAGGCACCACCATACTC  437
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Qy    438 CCTGGTGCTGAGGCATGGGCCTCGAAGGATGCCGGCGTTTACACCTGCCTGCCCAAAA  497
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Db   3296 CCTGGTGCTGAGGCATGGGCCTCGAAGGATGCCGGCGTTTACACCTGCCTGCCCAAAA 3355

Qy    498 CACTGGTGGCCAGTGCTCTGCAAGGCAGAGCTGCTGGTGCTTGGGGGGGACAATGAGCC  557
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Db   3356 CACTGGTGGCCAGTGCTCTGCAAGGCAGAGCTGCTGGTGCTTGGGGGGGACAATGAGCC 3415

Qy    558 GGACTTCAGAGAAGCAAAGCCACCGGACGAGGAAGCTGCACTCCTTCTATGAGGTCAAGGAGGA  617
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Db   3476 GATTGGAAGGGCGTGTTTGGCTTCGTAAAAGAGTGCAGCACAAAGGAAACAAGATCTT 3535

Qy    678 GTGCGCTGCCAAGTTCATCCCCCTACGGAGCAGAACTCGGGCCCAGGCATACAGGGAGGCG  737
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Qy    798 CCGCAAGACCCTCATCCTCATCCTGGAGCTGTGCTCATCCGAGGAGCTGCTGGACCGCCT  857
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Db   3656 CCGCAAGACCCTCATCCTCATCCTGGAGCTGTGCTCATCCGAGGAGCTGCTGGACCGCCT 3715

Qy    858 GTACAGGAAGGGCGTGGTGACGAGGCCGAGGTCAAGGTCATCATCCAGCAGTCTGGTGGA  917
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Db   3776 GGGGCTGCACTACCTGCACAGCACCTGCACAGCCATGGCCTTCCACCTGGACATAAAGCCCTCTAACAT 3835

Qy    978 CCTGATGGTGCATCCTGGCCCGGAAGCACATTAAAATCGCGGACTTTGGCTTTGCCCCAGAA 1037
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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3896 CATCACCCCAGCAGAGCTGCAGTTCAGCCAGTTACGGCGTCCCCTGAGTTCGTCTCCCCGA 3955

Qy   1098 GATCATCCAGCAGAACCCTGTGAGCAGACCCTCCGACATTTGGGCCATGGGTGTCATCTC 1157
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3956 GATCATCCAGCAGAACCCTGTGAGCAGACCCTCCGACATTTGGGCCATGGGTGTCATCTC 4015

Qy   1158 CTACCTCAGCCTGACCTGCTCATCCCATTTGCCGGGCAGAGTGACCGTGCCCACCCTCCT 1217
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4016 CTACCTCAGCCTGACCTGCTCATCCCATTTGCCGGGCAGAGTGACCGTGCCCACCCTCCT 4075

Qy   1218 GAACGTCCTGGAGGGCGGCGTGTCATGGAGCAGCCCATGGCCTGCCCACCTCAGCCGAAGA 1277
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4076 GAACGTCCTGGAGGGCGGCGTGTCATGGAGCAGCCCATGGCCTGCCCACCTCAGCCGAAGA 4135

Qy   1278 CGGCCAAAGACTTCATCAAGGCTACGGCTGCACGAGCCCTCAGGGCCCTAGGCCCTAGTGCGGC 1337
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4136 CGCCAAAGACTTCATCAAGGCTACGCTGCACGAGCCCTCAGGGCCCTAGGCCCTAGTGCGGC 4195
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Qy   1338 CCAGTGCCTCTCCACCCGTTCTGAAATCCATGCCTGCGGAGGAGGCCCACTTCAT 1397
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4196 CCAGTGCCTCTCCACCCCGGTTCCTGAAATCCATGCCTGGGGAGGAGGCCCACTTCAT 4255

Qy   1398 CAACACCAGCAGCTCAAGTTCCTCCTGGCCCGAAGTCGGCTGCAGCGTTCCTCGATGAG 1457
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4256 CAACACCAAGCAGCTCAAGTTCCTCTCCGGCCCGAAGTCGGCTTGGCAGCGTTCCTCGATGAG 4315

Qy   1458 CTACAAGTCCATCCTGGTGATGCGCTCCATCCTGAGCGTCCTGAGCTCCGCCACCGACACAG 1517
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4316 CTACAAGTCCATCCTGGTGATGCGCTCCATCCCGAGCGTCCTGAGCTCCGCCACCGACACAG 4375

Qy   1518 CCCCTCCCTGGGTAGCCGGCACCTCCGGGGCTTCCTCCCAGTTCCTC 1577
          |||||||||||||||||||||||||||||||||||||||||||||||
Db   4376 CCCTCCCTGGGTAGCCGGCACCTCCGGGGCTTCCTCCCAGTTCCTC 4435

Qy   1578 CTCCTCTCTGACAACGAGCTCGCCCCACCATTTGCCCGGGCTAAGTCACTGCCCACCTCCCC 1637
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4436 CTCCTCCTCTGACAACGAGCTCGCCCCATTTGCCCGGGCTAAGTCACTGCCCACCCTCCCC 4495

Qy   1638 GGTGACACTCCACCACTGCTGCACCCGCCACTGAGCGCTCCACCGAGGCCCAGCTCCGCTGCC 1697
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4496 GGTGACACTCCACCACTGCTGCACCCGCCAGTGAGCGCTCCACCGAGGCCCAGCTCCGCTGCC 4555

Qy   1698 TGACGAAGCCGAGGCCACTGAGCGCTCCACCGAGGCCCAGCTCCGCCTGCATCTCCCGA 1757
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4556 TGAGGAAGCCGAGGCCAGTGAGCGCTCCACCGAGGCCCAGCTCCGCCTGCATCTCCCGA 4615

Qy   1758 GGGTGCCGGGCCACCGGGCTGCGTGCCCCGGGCACAGCGTCATCCGACAGCCT 1817
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4616 GGGTGCCGGGCCACCGGGCTGCGTGCCCCGGCACAGCGTCATCCGACAGCCT 4675

Qy   1818 GTTCTACCACCAGGCGGGTGAGAGCCCTGAGCACGGGCCCTGGCCCTGGCGAGCAGGCG 1877
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4676 GTTCTACCACCAGGCGGGTGAGAGCCCTGAGCACGGGCCCTGGCCCTGGCGAGCAGGCG 4735

Qy   1878 GCACCCGGCCCGGCACCTGCTGGGCGCACCTGCTGAAGGGCGCTACATTGGCGGGGCGCTGCCAGG 1937
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4736 GCACCCGGCCCGGCCCGGCACCTGCTGAAGGGGCGCTACATTGGCCGGGGGCGCTGCCAGG 4795

Qy   1938 CCTGCGCGAGCCACTGATGAGCACCCGTGCTGAGAGGACCGCCAGGAGGAGCA 1997
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4796 CCTGCGCGAGCCACTGATGAGCACCCGTGCTGAGAGGACCGCCAGGAGGAGCA 4855

Qy   1998 GGCCACCCTCTGCCAAAGCCCCTTCATTCGAGACTGCCCTCCTGCCTCTG 2057
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   4856 GGCCACCCTCTGCCAAAGCCCCTTCATTCGAGACTGCCCTCCTGCCTCTGG 4915

Qy   2058 CACCCACTTGGCCCCTGGCCACAGCCACCACTCCCTGGAACATGACCTCCTGGAACATGACT 2117
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4916 CACCCACTTGGCCCCTGGCCACAGCCACCACTCCCTGGAACATGACTCCTGGAACATGACT 4975

Qy   2118 CCCTCCTCGGAGGGCCTGCGGTGAGGCCACAGCGACTGCCTTCAGCCCCTCCGGGGGGC 2177
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4976 CCCTCCTCGGAGGGCCTGCGGTGAGGCCACAGCGACTGCCTTCAGCCCCTCCGGGGGGGC 5035

Qy   2178 CCCTATCAGGGACATGGGCACCCTCCAGGGCTTCCAGCAGCTTCATCCAGTGGCCA 2237
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5036 CCCTATCAGGGACATGGGCACCCTCCAGGGCTCCAAGCAGCTTCCATCACTGGTGGCCA 5095

Qy   2238 CCCAGGCACTGCTCAGCCAGGAGCCATCCCCCGGGACACAGCCCTTGGGGGGCAGCCAGCCC 2297
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5096 CCCAGGCACTGCTCAGCCAGGAGCCATCCCCCGGGACACAGCCCTTGGGGGGCAGCCAGCCCC 5155

Qy   2298 TTTCTGCCACCCAAGCAGGGTTCTGCCCCCCAGAGGGCCCCACCCAGCAGT 2357
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5156 TTTCTGCCACCCAAGCAGGGTTCTGCCCCCCAGAGGGCTGCACCCCACCCAGCAGT 5215

Qy   2358 TGCCCCATGGCCTCTCGGCTCCTTCCCTCCAGGATCTTGCAAAGAGGGCCCCTTAGTACC 2417
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5216 TGCCCCATGGCCTCTCGGCTCCTTCCCTCCAGGATCTTGCAAAGAGGGCCCCTTAGTACC 5275

Qy   2418 CTCAAGCCCCTTCTTGGGACAGCCCCTGCCAAAGGCACCCCTGCCCAAAGCAAGCAGCCCCCC 2477
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Db  5276 ||||||||||||||| CTCAAGCCCCTTCTTGGGACAGCCCCAGGCACCCCCTGCCCCTGGGAGGCAAAGCAAGCCCCCCC 5335
Qy  2478 ATTGGACTCTAAGATGGGCGGCCTGGAGACATCTCTCTTCCTCCTGGGAGGCCAAAACCCGGCCC 2537
Db  5336 ||||||||||||||| ATTGGACTCTAAGATGGGCGGCCTGGAGACATCTCTCTTCCTCCTGGGAGGCCAAAACCCGGCCC 5395
Qy  2538 CTGCAGTTCCCCAGGGTCAGCCTCCCAGGCCTCCCAGGCCAGCTCTTCCCAAGTGAGCTCCCTCAGGGT 2597
Db  5396 ||||||||||||||| CTGCAGTTCCCCAGGGTCAGCCTCCCAGGCCTCCCAGGCCAGCTCTTCCCAAGTGAGCTCCCTCAGGGT 5455
Qy  2598 GGGCCACCTTGGAGCAAAGACAGGAGCCCCCCCTGGATGCGGAGGGGTGGACCCA 2657
Db  5456 ||||||||||||||| GGGCCACCTTGGAGCAAAGACAGGAGCCCCCCCTGGATGCGGAGGGGTGGACCCA 5515
Qy  2658 GGAGGCTGAGGATCTGTCCGACTCACACCCACTTGCAGCGGCCTCAGGACAGGTGAC 2717
Db  5516 ||||||||||||||| GGAGGCTGAGGATCTGTCCGACTCACACCCACTTGCAGCGGCCTCAGGAACAGGTGAC 5575
Qy  2718 CATGCGCAAGTTCTCCCTGGGTGGTCGCGGGGGCCATGCTGGGCCAGGGGCCGTGGCTGGCTATGGCAC 2777
Db  5576 ||||||||||||||| CATGCGCAAGTTCTCCCTGGGTGGTCGCGGGGGCCATGCTGGGCCAGGGGCCGTGGCTGGCTATGGCAC 5635
Qy  2778 CTTTGCCTTTGTGTGAGATGCAGGGGCATGCTGGGGCCATGTGGGCCAGGAT 2837
Db  5636 ||||||||||||||| CTTTGCCTTTGTGTGAGATGCAGGGGCATGCTGGGGCCATGTGGGCCAGGAT 5695
Qy  2838 AGCCTGGGCTGTGTCCCCAGTTGCAGATCGGGACCTGCAGGGCTGAGGGCTG 2897
Db  5696 ||||||||||||||| AGCCTGGGCTGTGTCCCCAGTTGCAGATCGGGACCTGCAGGGCTGAGGGCTG 5755
Qy  2898 GTCGGAGGAGCAGCAGGAGGCCAGGGCTGAGAGCCCACTGCCCCAGGTCAGTGCAAGGCC 2957
Db  5756 ||||||||||||||| GTCGGAGGAGCAGCAGGAGGCCAGGGCTGAGAGCCCACTGCCCCAGGTCAGTGCAAGGCC 5815
Qy  2958 TGTGCCTGAGGTCGGCAGAGGGCTCCACCCAGGAGCTCTCCAGAGCCCCACCCCATGGGAGGA 3017
Db  5816 ||||||||||||||| TGTGCCTGAGGTCGGCAGAGGGCTCCACCCAGGAGCTCTCCAGAGCCCCACCCCATGGGAGGA 5875
Qy  3018 CATCGGGCAGGTCTCCCTGGTGCAGATCGGGACCTGTCAGGTGATCGGGAGGCGGAGGCGGCCGA 3077
Db  5876 ||||||||||||||| CATCGGGCAGGTCTCCCTGGTGCAGATCGGGACCTGTCAGGTGATCGGGAGGCGGAGGCGGCCGA 5935
Qy  3078 CACAAATATCCCTGGACATTCCGAGGTGACCCGGCCCACCTCAAACCTCTCAGACCTGTA 3137
Db  5936 ||||||||||||||| CACAATATCCCTGGACATTCCGAGGTGGACCCGGCCCCGCCCTCACCTCTCAGACCTGTA 5995
Qy  3138 CGATATCAAGTACCTCCCATTCGAGTTTATGATCTTCAGGAAAGTCCCCAAGTCCCGCTCA 3197
Db  5996 ||||||||||||||| CGATATCAAGTACCTCCCATTCGAGTTTATGATCTTCAGGAAAGTCCCCAAGTCCCGCTCA 6055
Qy  3198 GCCAGAGCCGGCCCTCCCCCATGGCTGAGGAGGAGCTGGCCGAGTTCCCGGAGCCCCACGTG 3257
Db  6056 ||||||||||||||| GCCAGAGCCGGCCCTCCCCCATGGCTGAGGAGGAGCTGGCCGAGTTCCCGGAGCCCCACGTG 6115
Qy  3258 GCCCCTGGCCAGTGAACTGGGCCCCCCAGGCCCTGAGAGGCCTGAGAGGGAGTCAGAGGA 3317
Db  6116 ||||||||||||||| GCCCTGGCCAGTGAACTGGGCCCCCCAGGCCCTGAGAGGCCTGAGAGGGAGTCAGAGGA 6175
Qy  3318 TGTGGACGCGGCTGCTGGAGAGGCTTCCACTTCCACTTCCCTGGAGGGCAACCTGGCTGGG 3377
Db  6176 ||||||||||||||| TGTGGACGCGGCTGCTGGAGAGGCTTCCACTTCCACTTCCCTGGAGGGCAACCTGGCTGGG 6235
Qy  3378 ACGCAGCCTCTTCCAGTGAAGGCTCCGTGAGTCTCCCGGAGCACATCTCCGTGAGATCCTGAAGCTGCAGAGCTGAG 3437
Db  6236 ||||||||||||||| ACGCAGCCTCTTCCACTTCCCTGGGAGGCCTCCGTGAGTCTCCCGGATCCTGAAGCTGCAGAGCTGAG 6295
Qy  3438 GCTGCCGTGAGAGTGAAGGCGTGGCTGCAGAGGCAGGGC 3497
Db  6296 ||||||||||||||| GCTGCCGTGAGAGTGAAGGCGTGGCTGCAGAGGCAGGGC 6355
Qy  3498 GGAAGGTCTGGAGAAGGAGGAGGGGCCCCCAGGAAGAGAAGCCAGGCCTTGCTTCCTTCCGGCT 3557
Db  6356 ||||||||||||||| GGAAGGTCTTGGAGAAGGAGGAGGGGCCCCCAGGAAGAGAAGCCAGGCCTTGCTTCCTTCCGGCT 6415

Qy  3558 CTCAGGTCTGAAGAGACTGGGACCGAGCGCCGACCGCAGCGCCGACCGAGCGCCGACATTCCTAAGGGAGCTCTCAGATGAGAC 3617
Db  6416 ||||||||||||||| CTCAGGTCTGAAGAGACTGGGACCGAGCGCCGACCGCAGCGCCGACCGAGCGCCGACATTCCTAAGGGAGCTCTCGACATGAGAC 6475
Qy  6476 TGTGGTCTGGGCCAGTCAGTCAGTGACACTGGCCTGCCAGGTGTCAGCGCCGTGTCCTCATCTCTGC 6535
Db  3678 ||||||||||||||| TGTGGTCTGGGCCAGTCAGTCAGTGACACTGGCCTGCCAGGTGTCAGCGCCGTGTCCTCATCTCTGC 3737
Qy  6536 GGCCACCTGGAGCAAAGACAGGAGCCCCCCTGGAGACGCAGCAGCCGTGTCCTCATCTCTGC 6595
Db  3738 ||||||||||||||| GGCCACCTGGAGCAAAGACAGGAGCCCCCCTGGAGACGCAGCAGCCGTGTCCTCATCTCTGC 3797
Qy  6596 CACCCTCAAGAACTTCCAGCTTCTGACCATCCTGGTTGGTGGTGGTGGTGGACCTGGGGTGT 6655
Db  3798 ||||||||||||||| CACCCTCAAGAACTTCCAGCTTCTGACCATCCTGGTTGGTGGTGGTGGTGGACCTGGGGTGT 3857
Qy  6656 GTACACCTGCAGCGTGACGAATGCGCTGGGGACAATGCGCTGGGGACAATCGGGACACACCACCACGGGGTCCTCCGGAA 6715
Db  3858 ||||||||||||||| GTACACCTGCAGCGTGACGAATGCGCTGGGGACAATGCGCTGGGGACAATCGGGACACACCACCACGGGGTCCTCCGGAA 3917
Qy  6716 GGCAGAGCGCCCCTCATCTTCGCCATGCCCGATATCGGGGAGGTGTACGGCGGATGGGGT 6775
Db  3918 ||||||||||||||| GGCAGAGCGCCCCTCATCTTCGCCATGCCCGATATCGGGGAGGTGTACGGCGGATGGGGT 3977
Qy  6776 GCTGCTGGTCTGGAAGCCCGTGACTCTACGGCCCGTGACTCTACTGTGCAGTGCAG 6835
Db  3978 ||||||||||||||| GCTGCTGGTCTGGAAGCCCGTGACTCTACGGCCCGTGACTCTACTGTGCAGTGCAG 4037
Qy  6836 CCTAGAAGGCGGCAGCTGGAGCACACTGGCCTCCGACATCTTTGACTGCTGCTACCTGAC 6895
Db  4038 ||||||||||||||| CCTAGAGGCGGCAGCTGGAGCACACTGGCCTCCGACATCTTTGACTGCTGCTACCTGAC 4097
Qy  6896 CAGCAAGCTCTTCCGGGGTGGCACCTACACCTTCCGCACGGCATGTGTCAGCAAGGCAGG 6955
Db  4098 ||||||||||||||| CAGCAAGCTCTTCCGGGGTGGCACCTACACCTTCCGCACGGCATGTGTCAGCAAGGCAGG 4157
Qy  6956 AATGGGTCCCTACAGACAGCCCCTCGGAGCAAGTCTCCTCCTGGAGGGCCCAGCCACCTGGCC 7015
Db  4158 ||||||||||||||| AATGGGTCCCTACAGACAGCCCCTCGGAGCAAGTCTCCTCCTGGAGGGCCCAGCCACCTGGCC 4217
Qy  7016 CTCTGAGGAGGAGCAGGTGGCGGTCAGCCCGGGCTTCAGCGTGGTCGGGGAAGTGCGGAGAAGGC 7075
Db  4218 ||||||||||||||| CTCTGAGGAGGAGCAGGTGGCGGTCAGCCCGGGCTTCAGCGTGGTCGGGGAAGTGCGGAGAAGGC 4277
Qy  7076 ATTCCAGACACAGATCCCAGAGGGGCCCGCAAGATCATCCCCTACACCCCAGGACACAGAAGCAGT 7135
Db  4278 ||||||||||||||| ATTCCAGACACAGATCCCAGAGGGGCCCGCAAGATCATCCCCTACACCCCAGGACACAGAAGCAGT 4337
Qy  7136 CAGCGGCGGCGGGCCCGGCGGGCCCGGAGTTCCCGGAGGCGGCGGAGT 7195
Db  4338 ||||||||||||||| CAGCGGCGGCGGGCCCGGCGGGCCCGGAGTTCCCGGAGGCGGCGGAGT 4397
Qy  7196 GCTGCGCGGAATACGAGGCCCTCAAGGGCCTGCATCTTGGAGCTGTGCTGCTCGGGAGAAGGC 7255
Db  4398 ||||||||||||||| GCTGCGCGGAATACGAGGCCCTCAAGGGCCTGCATCTTGGAGCTGTGCTGCTCGGGAGAAGGC 4457
Qy  7256 AGCCTACCTGCCGCTCCAGCCCCTGGCCCTTCCTCCTACTCAGAATCTGAGGTGAAGGACTACCTGTG 7315
Db  4458 ||||||||||||||| AGCCTACCTGCCGCTCCAGCCCCTGGCCCTTCCTCCTACTCAGAATCTGAGGTGAAGGACTACCTGTG 4517
Qy  7316 GCTCCCCTGCCCTGCCTGCCGCCGCGGGCCCTCCACTTCCACTTCGCGGAGGGCACCTGGGGG 7375
Db  4518 ||||||||||||||| GCTCCCCTGCCCTGCCTGCCGCCGCGGGCCCTCCACTTCCACTTCGCGGAGGGCACCTGGGGG 4577
Qy  7376 GCGAGATGTTGAGTGCCACCCAGTACCTGCCACCAACCTGCACAACCAGCACATCTGCACCTGGACCTGAG 7435
Db  4578 ||||||||||||||| GCAGATGTTGAGTGCCACCCAGTACCTGCCACCAACCTGCACAACCAGCACATCTGCACCTGTG 4637
Qy  7436 GTCCGAGAACATGATCATCACCGAATACAACCTGCTCAAGGTCGTGACCTGGCAATGC 7495
Db       ||||||||||||||| GTCCGAGAACATGATCATCACCGAATCAACCTGCTCAAGGTCGTGACCTGGCAATGC
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PN   US2002168742-A1.
XX
PD   14-NOV-2002.
XX
PF   15-FEB-2002; 2002US-00077130.
XX
PR   15-FEB-2001; 2001US-0269201P.
XX
PA   (MILL-) MILLENNIUM PHARM INC.
XX
PI   Kapeller-Libermann R,   Acton SL;
XX
DR   WPI; 2003-298729/29.
DR   P-PSDB; ABG76187.
XX
PT   Novel isolated human protein kinase, designated 59079 or 12599
PT   polypeptide, useful as diagnostic and therapeutic agents for preventing
PT   cardiovascular diseases, proliferative disorders, and protein kinase
PT   disorders.
XX
PS   Claim 2; Page 58-84; 119pp; English.
XX
CC   The invention relates to an isolated human serine/threonine or protein
CC   kinase, 59079 or 12599 polypeptide, encoded by nucleic acid molecule
CC   comprising at least 85% identity to the nucleic acids appearing as
CC   ABX11641 and ABX11642 or their complement, a naturally occurring variant
CC   of the kinases or their fragments. Also included are a non-human host
CC   cell containing the nucleic acids, an antibody specific for the proteins,
CC   identifying a compound which binds to the kinase (by contacting the
CC   kinase or a cell expressing the kinase with a test compound and
CC   determining whether the kinase binds to the test compound) and modulating
CC   the activity of kinase using the identified compound. The kinases and
CC   their encoding nucleic acids are useful as diagnostic and therapeutic
CC   agents for preventing a disease or condition associated with an aberrant
CC   or unwanted 59079 or 12599 activity in a subject, including
CC   cardiovascular diseases such as heart failure, and myocardial infarction;
CC   disorders involving blood vessels such as atherosclerosis, and Kaposi's
CC   sarcoma; blood platelets disorder such as thrombocytopaenia, leukaemia,
CC   Hodgkin's disease, haemolytic anaemia; cellular proliferative disorders
CC   such as cancer; and protein kinase disorders such as autoimmune
CC   disorders, diabetes mellitus, psoriasis, inflammatory bowel disease,
CC   rheumatoid arthritis, and multiple sclerosis (many examples of diseases
CC   and disorders are included in the specification). The kinases, their
CC   encoding nucleic acids and antibodies are useful in screening assays,
CC   detection assays (e.g. forensic biology), and predictive medicine (e.g.
CC   diagnostic assays, prognostic assays, and monitoring clinical trials and
CC   pharmacogenomics). The kinases and their encoding nucleic acids are
CC   useful as query sequences to perform a search against public databases to
CC   identify other family members or related sequences. The present sequence
CC   encodes the kinase 12599
XX
SQ   Sequence 24120 BP; 4719 A; 7265 C; 8278 T; 3858 G; 0 U; 0 Other;

Query Match     94.9%;  Score 4940.4;  DB 7;  Length 24120;
Best Local Similarity   99.9%;  Pred. No.0;
Matches 4944;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy    258  CCCAGGGCCCCATCCATGCAGGTAACCATCGAGGATGTCAGGCACAGACAGGCGGAAC  317
           ||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db  19130  CGCACGGCCCCATCCATCCATGCAGGTAACCATCGAGGATGTCAGGCACAGACAGGCGGAAC  19189

Qy    318  GGCCCAATTCGAGGCTATCATTGAGGGCGACCCAGCCCTCGGTGACCTGGTACAAGGA  377
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  19190  GGCCCAATTCGAGGCTATCATTGAGGGCGACCCAGCCCTCGGTGACCTGGTACAAGGA  19249

Qy    378  CAGGGTCCAGCTGGTGGACAGCACCGGCTTAGCAGCAAGAAGGCACCACATACTC  437
           |||||||||||||||| ||||||||||||||||| |||||||||||||||||||||
Db  19250  CAGGGTCCCAGCTGGTGGACAGCACCCGGCTTAGCCAGCAAGAAGGCACCACATACTC  19309

Qy    438  CCTGGTGCTGAGGCATGTGCCTCGAAGGATGCCGGCGTTTACACCTGCCCTGCCCAAAA  497
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db  19310  CCTGGTGCTGAGGCATGTGCCTCGAAGGATGCCGGCGTTTACACCTGCCCTGCCCCAAAA  19369

Qy   4638 ACAGAGCCTCAGCCAGGAGGTGCGCCCTCAGACAAGTTCAAGGACTACCTAGAGAC  4697
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Db   7496 ACAGAGCCTCAGCCAGGAGGTGCGCCCTCAGACAAGTTCAAGGACTACCTAGAGAC  7555

Qy   4698 CATGGCTCCAGAGCTCCTGGAGGGGCCAGGGGCTGTTCCACAGACAGACATCTGGGCCAT  4757
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7556 CATGGCTCCAGAGCTCCTGGAGGGGCTGTTCCACAGACAGACATCTGGGCCAT  7615

Qy   4758 CGGTGTGACAGCCTTCATCATGTCGGCGCCGAGTACCCGGTGAGCAGCGAGGGTGCACG  4817
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7616 CGGTGTGACAGCCTTCATCATGTCGGCGCCGAGTACCCGGTGAGCAGCGAGGGTGCACG  7675

Qy   4818 CGACCTGCAGAGAGAGGACTGCGCCAAGGGGCTGGTCCGGCTGAGCCGGCTACGCGGGGCT  4877
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7676 CGACCTGCAGAGAGAGGACTGCGCCAAGGGGCTGGTCCGGCTGAGCCGGCTACGCGGGGCT  7735

Qy   4878 GTCCGGGGGCCCGTGACCTCCTACCGCACTCGTGCTGCCTGGGCCGCC  4937
           |||||||||||||||||||||||||||||||||||||||||||||||
Db   7736 GTCCGGGGGCCCGTGACCTCCTACCGCACTCGTGCTGCCTGGGCCGCC  7795

Qy   4938 CTGCGCGTCCAGCTGCCGTGCGCAGTGCCCGTGCCTGCTAACAGAGGAGGGCCCCGCCTGTTCGCG  4997
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7796 CTGCGCGTCCAGCTGCCGTGCGCAGTGCCCGTGCCTGCTAACAGAGGAGGGCCCCGGCCTGTTCGCG  7855

Qy   4998 GCCCGCCCCGTGACCTTCCTACCGCGGCGGCGTTCGTGCGCAATCGCGAGAA  5057
           |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   7856 GCCCGCCCCGTGACCTTCCTACCGCGTCGGCGTTCGTGCGCAATCGCGAGAA  7915

Qy   5058 GAGACGGCGCGCTGCTGTACAGAGAGGACACAACCTGCCCAGGTGCGCTGAGGGTGCGCCCCG  5117
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Db   7916 GAGAGGCGCGCGCTGCTGTACAGAGAGGACACAACCTGCCCAGGTGCGCTGAGGGGTCGCCCCG  7975

Qy   5118 GCCACACCCTGGTCTCCCCGCTGGGGGTGCGCTGCGAGACGCGCCAATAAAACGCACAGC  5177
           ||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db   7976 GCCACACCCTTGGTCTCCCCGCTGGGGGTGCTGCTGCGAGACCGCGCCAATAAAAACCCCCAGC  8035

Qy   5178 CGGGCGAGAAAAAAAAAAAAAAAAAAAAAAA  5207
           |||||||||||||||||||||||||||||||
Db   8036 CGGGCGAGAAAAAAAAAAAAAAAAAAAAAAAAAAA  8065

RESULT 5
ABX11642
ID   ABX11642 standard; cDNA; 24120 BP.
XX
AC   ABX11642;
XX
DT   09-MAY-2003  (first entry)
XX
DE   Human serine/threonine or protein kinase 12599, cDNA.
XX
OS   Homo sapiens.
XX
KW   Human; ss; gene; serine/threonine kinase; protein kinase; 12599;
KW   cardiovascular disease; heart failure; myocardial infarction;
KW   blood vessel disorder; atherosclerosis; Kaposi's sarcoma;
KW   blood platelet disorder; thrombocytopaenia; leukaemia; Hodgkin's disease;
KW   haemolytic anaemia; cellular proliferative disorder; cancer;
KW   protein kinase disorder; autoimmune disorder; diabetes mellitus;
KW   psoriasis; inflammatory bowel disease; rheumatoid arthritis;
KW   multiple sclerosis.
XX
FH   Key             Location/Qualifiers
FT   5'UTR           1..71
FT                   /*tag= a
FT   CDS             72..23978
FT                   /*tag= b
FT                   /product= "Kinase 12599"
FT                   /note= "This CDS is specifically claimed in claim 2"
FT   3'UTR           23979..24120
FT                   /*tag= c
XX

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Qy    498  CACTGGTGGCCAGGTGCTCTGCAAGGCAGAGCTGCTGGTGCTTGGGGGGACAATGAGCC   557
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  19370  CACTGGTGGCCAGGTGCTCTGCAAGGCAGAGCTGCTGGTGCTTGGGGGGGACAATGAGCC  19429

Qy    558  GGACTCAGAGAAGCAAAGCACCGGAGGAAGCTGCACTCCTTCTATGAGGTCAAGAGGA   617
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  19430  GGACTCAGAGAAGCAAAGCACCGGAGGAAGCTGCACTCCTTCTATGAGGTCAAGAGAGA  19489

Qy    618  GATTGGAAGGGGCGTGTTTGCTTGTAAAAAGAGCTGCAGCACAAGGAAACAAGATCTT   677
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  19490  GATTGGAAGGGGCGTGTTTGCTTCGTAAAAAGAGCTGCAGCACAAAGGAAACAAGATCTT  19549

Qy    678  GTGCGCTGCCAAGTTCATCCCCTACGGAGCAGAACTCGGCGCCAGGCATACACGGGAGCG   737
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  19550  GTGCGCTGCCAAGTTCATCCCCTACGGAGCAGAACTCGGCGCCAGGCATACACGGGAGCG  19609

Qy    738  AGACATCCTGCCCGGCTGAGCCACCCGCTGGTCACGGAGCTGCTGACCAGTTTGAGAC   797
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  19610  AGACATCCTGCCCGGCTGAGCCACCCGCTGGTCACGGGAGCTGCTGACCAGTTTGAGAC  19669

Qy    798  CCGCAAGACCCTCATCCTCATCTCGGAGCTGTGCTCATCCGAGGAGCTGCTGACCGGCT   857
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  19670  CCGCAAGACCCTCATCCTCATCTCGGAGCTGTGCTCATCCGAGGAGCTGCTGACCGGCT  19729

Qy    858  GTACAGGAAGGGCGTGGTGACGAGCCGGAGGCCCAGGTCTACATCCAGCAGTGGTGGA   917
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  19730  GTACAGGAAGGGCGTGGTGACGAGCCGGAGGCCCAGGTCTACATCCAGCAGTGGTGGA  19789

Qy    918  GGGGCTGCACTACCTGCACAGCCATGGCGTTCTTCCACCTGGACATAAAATCTGCCTAACAT   977
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  19790  GGGGCTGCACTACCTGCACAGCCATGGCGTTCTTCCACCTGGACATAAAGCCCTCTAACAT  19849

Qy    978  CCTGATGGTGCATCCTGCCGCGGGAAGACATTAAAAATCTGCAGCTTGGCTTTGCCCAGAA  1037
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  19850  CCTGATGGTCATCCTGCCCGGGAAGACATTAAAAATCTGCAGCTTTGGCTTTGCCCAGAA  19909

Qy   1038  CATCACCCCACCAGAGCTGCAGTTCAGCCAGTACGGCTCCCCTGAGTTCGTCTCCCCCGA  1097
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  19910  CATCACCCCACCAGAGCTGCAGTTCAGCCAGTACGGCTCCCCTGAGTTCGTCTCCCCCGA  19969

Qy   1098  GATCATCCACCAGCAGAACCCTGTGAGCGAAGCCTCCCACATTTGGGCCATGGGTGTCATCTC  1157
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  19970  GATCATCCACCAGCAGAACCCTGTGAGCGAAGCCTCCGACATTTGGGCCATGGGTGTCATCTC  20029

Qy   1158  CTACCTCAGCGTGACCTGCTCATCCCCATTTGCCGGCGAGAGTGACCGTGCCCACCCTCCT  1217
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  20030  CTACCTCAGCGTGACCTGCTCATCCCCATTTGCCGGCGAGAGTGACCGTGCCCACCCTCCT  20089

Qy   1218  GAACGTCCTGAGAGGGCGCGTGTCATGGAGCAGCCCATGGCTGCCACCTCAGCGAAGA  1277
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  20090  GAACGTCCTGAGAGGGCGCGTGTCATGGAGCAGCCCATGGCTGCCACCTCAGCGAAGA  20149

Qy   1278  CGCCAAAGACTTCATCAAGGCTACGCTGCAGAGAGCCCTCAGGCCCGGCCTAGTGCGGC  1337
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  20150  CGCCAAAGACTTCATCAAGGCTACGCTGCAGAGAGCCCTCAGGCCCGGCCTAGTGCGGC  20209

Qy   1338  CCAGTGCCTCTCCACCCCTGGTTCCTGAAATCCATGGCGTGCGGAGAGGCCCACTTCAT  1397
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  20210  CCAGTGCCTCTCCACCCCTGGTTCCTGAAATCCATGGCGTGCGGAGAGGCCCACTTCAT  20269

Qy   1398  CAACACCAAGCAGCAGCTCAAGTTCCTCCTGGCCGGAAGTCGCTGGAGGCCGTTCCCTGATGAG  1457
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  20270  CAACACCAAGCAGCTTCAAGTTCCTCTGGCCGGAAGTCGCTGGAGGCCGTTCCCTGATGAG  20329

Qy   1458  CTACAAGTCCATCCTGGTGATGGCCTCCATCCCTGAGCTGCTGCGGGGGCCACCCGACAG  1517
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  20330  CTACAAGTCCATCCTGGTGATGGCCTCCATCCCTGAGCTGCTGCGGGGGCCACCCGACAG  20389

Qy   1518  CCCCTCCCTGCGGGTAGCCCGGCCACCTGTCAGGGACACTGGTTGGCTCCTCCCAGTTCCTC  1577
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  20390  CCCCTCCCTGCGGGTAGCCCGGCCACCTGTCAGGGACACTGGTTGGCTCCTCCCAGTTCCTC  20449

Qy   1578  CTCCTCCTCTGACAACGAGCTCGCCCCATTTGCCCGGCGTAAGTCACTGCCCACCCTCCCC  1637
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Db  20450  CTCCTCCTCTGACAACGAGCTCGCCCCATTTGCCCGGGGCTTCGTGGCCCTGGCCAGCTCCCC  20509
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1638  GGTGACACTCACCACTGCTGCCACCTGCTGCCCGGGCTTCCTGTGGGCCCTGGCCAGCTGCC   1697

Db  20510  GGTGACACTCACCACTGCTGCCACCTGCTGCCCGGGCTTCCTGTGGGCCCTGGCCAGCTGCC  20569
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1698  TGAGGAAGCCGAGGCCAGTGAGCCTCCACCGAGGCCTCCACCAGTCTCGGCTGCATCCGGA   1757

Db  20570  TGAGGAAGCCGAGGCCAGTGAGCCTCCACCGAGGCCTCCACCGAGTCTCGGCTGCATCCGGA  20629
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1758  GGGTGCCGGGCCACCGGCCGCCCAGGGGTGCGTGCCCCGGCACAGCGTCATCCGCAGCCT   1817

Db  20630  GGGTGCCGGGCCACCGGCCGCCCAGGGGTGCGTGCCCCGGCACAGCGTCATCCGCAGCCT  20689
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1818  GTTCTACCACCAGGCGGGTGAGAGCCCTGAGCACAGGGGCCCTGGCCCGGGGAGCAGGCG   1877

Db  20690  GTTCTACCACCAGGCGGGTGAGAGCCCTGAGCACAGGGGCCCTGGCCCGGGGAGCAGGCG  20749
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1878  GCACCCGGCCGGGGCGGCCACTGCTGAGGCGGCGGCTACATTGCGGGGCCGCTGCCAGG   1937

Db  20750  GCACCCGGCCGGGGCGGCCACTGCTGAAGGCGGCGGTACATTGCGGGGCCGCTGCCAGG  20809
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1938  CCTGCGGAGCCACTGATGGAGCACCCGGTGCTGGAGGAGGCCGCCAGGGAGGAGACA   1997

Db  20810  CCTGGCGGAGCCACTGATGGAGCACCGGTGCTGGAGGAGGCCGCCAGGGAGGAGCA  20869
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Qy   1998  GGCCACCCTCCTGGCCAAAGCCCCTGCCTCATTCGAGACTGCCCTCCGGTGCCTTCTGG   2057

Db  20870  GGCCACCCTTGGCCCCTGGCCAAAGCCCCTCATTCCGGCGTGCCCTGCCTGCCCTCTGG  20929
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   2058  CACCCACTTGGCCCCTGGCCACATGACATCCTCCTGGGAACATGACTCTCCGAGCACCCCCCG   2117

Db  20930  CACCCACTTGGCCCCTGGCCACATGACACTGCCTCCTGGAACATGACTCTCCGAGCACCCCCCC  20989
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   2118  CCCCTCCTCGGAGGCCTGCGGTGAGGCCACTGCTCCTGCCCTCAGCCCTCAGCCCCTCCGGGGGGC   2177

Db  20990  CCCCTCCTCGGAGGCCTGCGGTGAGGCACAGCTGCCTCAGCCCTCAGCCCCTCCGGGGGGGC  21049
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   2178  CCCTATCAGGGACATGGGGCACCCTGCAGGGGCTCCAAGCAGCTTCCATCCACTGGTGTGGCCA   2237

Db  21050  CCCTATCAGGGACATGGGGCACCCTGCAGGGGCTCCAAGCAGCTTCCATCCACTGGTGTGCCA  21109
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   2238  CCCAGGCACTGCTGCTCAGCCAGAGGCCATCCCCGGACAGCAGCCCTTGGGGGCAGCCAGCCCC   2297

Db  21110  CCCAGGCACTGCTGCTCAGCCAGAGGCCATCCCCGGACAGCAGCCCTTGGGGGCAGCCAGCCCC  21169
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Qy   2298  TTTCTGCCACCCCAAGCACAGGGTTCTGCCCCCCAAGCCCCCACCCAGGGTCAGCCCCCACCAGCAGT   2357

Db  21170  TTTCTGCCACCCCAAGCACAGGGTTCTGCCCCCCAAGCCCCCACCAGGGTCAGCCCCCACCAGCAGT  21229
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   2358  TGCCCCATGCCCTTCCTTCCTGCTCCTTCCCTCCGCAAGAGGCCCCCTTAGTACC   2417

Db  21230  TGCCCCATGCCCTTCCTTCCTGCTCCTTCCCTCCGCAAAGAGGCCCCCTTAGTACC  21289
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   2418  CTCAAGCCCCTTCTTGGGACAGCCCCAGGAGGGGCTGCCAAAGCAAGCCCCCC   2477

Db  21290  CTCAAGCCCCTTCTTGGGACAGCCCCAGGAGCACCCCCCTGCCAAAGCAAGCCCCCC  21349
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   2478  ATTGGACTCTAAGATGGGGCCTGGACCATCTCTTCTTCCTCGGGAGGCCAAAACCCGGCCC   2537

Db  21350  ATTGGACTCTAAGATGGGGCCTGGAGACATCTCTTCTTCCTGGGAGGCCAAAACCCGGCCC  21409
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   2538  CTGCAGTTCCCCAGGGTCAGCCTTCCCCAGGCCTCCCGAGCTCTTCCCAAGTGAGCTCCCTCAGGGT   2597

Db  21410  CTGCAGTTCCCCAGGGTCAGCCTTCCCCAGGCCTCCCGAGCTCTTCCCAAGTGAGCTCCTCCAGGGT  21469
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   2598  GGCTCCTCCCAGGTGGGCACCAGAGCCTGGGCCCCTCCGATGCCGGAGGGCTGGACCCA   2657

Db  21470  GGGCTCCTCCCCAGGTGGGCACCAGAGCCTGGGCCCCTCCGATGCCGGAGGGCTGGACCCA  21529
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   2658  GGAGGCTGAGGGATCTGTCCGACTCCGACCCACCTTGCTCGAGCGGCCTCAGGAACAGGTGAC   2717
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Db  21530  GGAGGCTGAGGATCGTCCGACTCCACCCGACCCTTGCAGCGGCCTCAGGAACAGGCGAC  21589
Qy   2718  CATGCGCAAGTTCTCCCTGGGGTGCGGGGGCTACGCAGCGGTGCTGGCTATGGCAC      2777
           |||||||||||||||||||||||||||||||||||||||||||||||
Db  21590  CATGCGCAAGTTCTCCCTGGGGTGCGGGGGCTACGCAGCGGTGCTGGCTATGGCAC      21649

Qy   2778  CTTTGCCTTGGTGAGATGCAGGGGGCATGCTGGGCGCAGGGGCCCATGTGGCCCAGGAT   2837
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  21650  CTTTGCCTTGGTGGAGATGCAGGGGCAGGGGCCCATGTGGGCCCAGGAT             21709

Qy   2838  AGCCTGGGCGTGTCTGTCCCAGTGAGGAGGAGGAGGAGCAGGCCAGGCGAGTGAGTCCA    2897
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  21710  AGCCTGGGCGTGTCTGTCCCAGTGGAGGAGGAGGAGCAGGCCAGGGCCGAGTGAGTCCCA  21769

Qy   2898  GTCGGAGGAGCAGCAGGAGGCCAGGGCTGAGAGCCACTGCCCCAGGTCAGTGCAAGGCC   2957
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  21770  GTCGGAGGAGCAGCAGGAGGCCAGGGCTGAGAGCCACTGCCCCAGGTCAGTGCAAGGCC   21829

Qy   2958  TGTGCCTGAGGTCGGCAGGGCTTCCCACCAGAGCTCCAGAGAGCCCATGGGAGGA       3017
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  21830  TGTGCCTGAGGTCGGCAGGGCTCCCACCAGAGCTCCAGAGAGCCCATGGGAGGA        21889

Qy   3018  CATCGGGCAGGTCTCCCTGGTGCAGATCCGGGACCTGTCAGTGATGCCGAGGCGGCCGA   3077
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  21890  CATCGGGCAGGTCTCCCTGGTGCAGATCCGGGACCTGTCAGTGATGCCGAGGCGGCCGA   21949

Qy   3078  CACAATATCCCTGGACATTTCCGAGGTGGACCCCCGCCTCACCTCAGACCTGTA        3137
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  21950  CACAATATCCCTGGACATTTCCGAGGTGGACCCCCGCCTACCTCAACCTTCAGACCTGTA  22009

Qy   3138  CGATATCAAGTACCTCCCATTCGAGTTTATGATCTTCAGGAAAGTCCCCAAGTCCGGCCA  3197
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  22010  CGATATCAAGTACCTCCCATTCGAGTTTATGATCTTCAGGAAAGTCCCCAAGTCCGGCTCA 22069

Qy   3198  GCCAGAGCCGCCCTCCCCCATGGCTGAGGAGGCTGGCCAGCGAGGAGTCACAGAGGA     3257
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  22070  GCCAGAGCCGCCCTCCCCCATGGCTGAGGAGGCTGGCCAGCGAGGAGTCACAGAGGA     22129

Qy   3258  GCCCTGGCCAGGTGAACTGGGGCGTGTTGGCAGGAAGCGCAAGTGGTCCTCGCCGTC     3317
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  22130  GCCCTGGCCAGGTGAACTGGGGCGTGTTGGCAGGAAGCGCAAGTGGTCCTCGCCGTC     22189

Qy   3318  TGTGGACGGCGTCGTGCTGGCAGAGGCTGGGGAGGCTCCGGGCACCTGGGGACTGGG     3377
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  22190  TGTGGACGGCGTCGTGCTGGCAGAGGCTGGGGAGGCTCCGGGCACCTGGGGACTGGG     22249

Qy   3378  ACGGCAGCCTCTTCCACTTCCCGGGAGGCACCTGCGCTGGATGAGCGCTGCAGAGCTGGG  3437
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  22250  ACGGCAGCCTCTTCCACTTCCCGGGAGGCACCTGCGCTGGATGAGCGCTGCAGAGCTGGG  22309

Qy   3438  GCTGCGTGAGAGAGTGAAGGCCTCCGTGAGCACACTCTCCCGGATCCTGAAAGGGCAGGCC 3497
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  22310  GCTGGGTGAGAGAGTGAAGGCCTCCGTGAGCACACTCTCCCGGATCCTGAAAGGGCAGGCC 22369

Qy   3498  GGAAGGTCTGAAGAGTGGAGACGGGGCCCCCAGGAAGAGCCAGGCCTTGCTTCCTTCCGGCT 3557
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  22370  GGAAGG TCTGAAGAGTGGAGAAGAGGGGCCCCCAGGAAGAGCCAGGCCTTGCTTCCTTCCGGCT 22429

Qy   3558  CTCAGTTCGAAGAGCTCGGACACTGGGCTGAGCGCCGACCAGCCAGCCAGCTGCCCA     3617
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Db  22430  CTCAGTTCGAAGAGCTCGGACACTGGGCTGAGCGCCGACCAGCCAGCCAGCTGCCCA     22489

Qy   3618  TGTGGTCCTGGGCCAGTCAGTGACACTGGCCTGTCAGCCCAGCGTCCTCATCTCTCTGC   3677
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  22490  TGTGGTCCTGGGCCAGTCAGTGACACTGGCCTGTCAGCCCAGCGTCCTCATCTCTCTGC   22549

Qy   3678  GGCCACCTGAGCGCAAAGACGGAGCGGAGCCCCCTGGAGAGCAGCAGCCGTGTCCTCATCTTCTGC 3737
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  22550  GGCCACCTGAGCGCAAAGACGGAGCGGAGCCCCCTGGAGAGCAGCAGCCGTGTCCTCATCTTCTGC 22609

Qy   3738  CACCCTCAAGAGACTTCCAGCTTCTGACCATCCTGTGGTGGTGGCTAGGACCTGGGTGT   3797
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  22610  CACCCTCAAGAGACTTCCAGCTTCTGACCATCCTGTGGTGGTGGCTGAGGACCTGGGTGT  22669


Qy   3798  GTACCCTGAGCGCTGAGAATCGCTGGGACAGTGACCACCAGCGGCGTCCTCCGAA       3857
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Db  22670  GTACACCTGCAGCGGTGAGCAATGCTGGGACAGTGACCACCACGGGGGTCCTCCGAA     22729

Qy   3858  GGCAGAGCGGCCCTCATCTTCGCCCATGCCGGATATGCCGGAGGGTGTACGCGATGGGGT   3917
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Db  22730  GGCGAGCGCGCCCCTCATCTTCGCCATGCCGGATATCGGGGAGGTGTGCGGATGGGCGGGT  22789

Qy   3918  GCTGCTGGTCTGGAAGCCCGTGGAATCTACGGCCCGTGACCTACAATTGTCGAGTGCAG   3977
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Db  22790  GCTGCTGGTCTGGAAGCCCGTGGAATCCTACGGCCCTGACCTACAATTGTCAGTGCAG     22849

Qy   3978  CCTAGAAGGGGGCAGCTGACCACCACTGCCTCCGACATCTTGACTGCTGCTACCTGAC    4037
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Db  22850  CCTAGAAGGGGGCAGCTGACCACCACTGCCTCCGACATCTTTGACTGCTGCTACCTGAC   22909

Qy   4038  CAGCAAGCTCTCCCGGGGTTGGCACCTACCACCTTCCGCACGGCATGTGTCAGCAAGGCAGG 4097
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Db  22910  CAGCAAGCTCTCCCGGGGTTGGCACCTACCACCTTCCGCACGGCATGTGTCAGCAAGGCAGG 22969

Qy   4098  AATGGGTCCCTACAGCAGCCCCTCGGAGCAAGTCCTCTCCTGGGAGGGGCCCAGCCACTTGGC 4157
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  22970  AATGGGTCCCTACAGCAGCCCCTCGGAGCAAGTCCTCTCCTGGGAGGGGCCCAGCCACTTGGC 23029

Qy   4158  CTCTGAGGAGGAGAGCCAGGAGCCGTCAGCCCAACCCCTGCCCAGCACCAAAGACCTTCGC  4217
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Db  23030  CTCTGAGGAGGAGAGCCAGGAGCCGTCAGCCCAACCCCTGCCCAGCACCAAAGACCTTCGC  23089

Qy   4218  ATTCCAGACACACAGATCCAGAGGGGCCGCTTCAGCGTGGTGCGCCAATGCTGGGGAGAAGGC 4277
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  23090  ATTCCAGACACAGATCCAGAGGGGCCGCTTCAGCGTGGTGCGCCAATGCTGGGGAGAAGGC   23149

Qy   4278  CAGCGGCGGGCGCTGGCCCAAGATCATCCCCTACACCCCAAGACAAGACAGCAGT       4337
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  23150  CAGCGGCGGGCGCTGGCCCAAGATCATCCCCTACACCCCAAGACAAGACAGCAGT       23209

Qy   4338  GCTGCGGAATACGAGGGCCCCGGAGAGGGCTGCCACCTGCCCAGCTGCACGC          4397
           ||||||||||||||||||||||||||||||||||||||||||||||||
Db  23210  GCTGCGGAATACGAGGGCCCCGGAGAGGGCTGCCACCTGCCCAGCTGCACGC          23269

Qy   4398  AGCCTACCTGGCAGAGGCTGCTCTCATCTTGGTGTCTCTGGGCCCCAGCT            4457
           |||||||||||||||||||||||||||||||||||||||||||||
Db  23270  AGCCTACCTGGCAGAGGCTGCTCTCATCTTGGAGTCTCTGGGCCCCCAGCT          23329

Qy   4458  GCTCCCTGCCTGCCGGAGGAGGGCCTCTCCTACTCAGAATCTGAGGTGAAGGACTACCTGTG 4517
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  23330  GCTCCCTGCCTGCCGGAGAGGGCCTCTCCTACTCAGAATCTGAGGTGAAGGACTACCTGTG  23389

Qy   4518  GCAGATGTTGAGTGCCACCCAGTACCTGCACAACCAGCACATCCTGCACCTGGACCTGAG   4577
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  23390  GCAGATGTTGAGTGCCACCCAGTACCTGCACAACCAGCACATCCTGCACCTGGACCTGAG   23449

Qy   4578  GTCCGAGGACAGCATGATCATCACCGAATACAACCTGCTCAAGGTTCGTGGACCTGGGCAATGC 4637
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  23450  GTCCGAGGACAGCATGATCATCACCGAATACAACCTGCTCAAGGTCGTGGACCTGGGCAATGC 23509

Qy   4638  ACAGAGCCTCAGCGACAGGAAGTGCTGCCAGGAGGGCCCAGGGCGGCTCGTGTTCCACAGAGAC 4697
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  23510  ACAGAGCCTCAGCGACAGGAAGTGCTGCCAGGAGGGCCCAGGGGGGCTCGTGTTCCACAGAGAC 23569

Qy   4698  CATGGCTCCAGAGCTCCTGGAGGGGCCCAGGGGGGCTCGTGTTCCACAGAGCCAGCTGCCCA   4757
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  23570  CATGGCTCCAGAGCTCCTGGAGGGGCCCAGGGGGGCTGTGTTCCACAGAGCCAGCTGCCCA    23629

Qy   4758  CGGTGTGACAGCCTTCATCATGGTCAGTACCCGTGAGCGCGTGAGCAGGGTGCACG       4817
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  23630  CGGTGTGACAGCCTTCATCATGGTCAGTACCCGTGAGCGCGTGAGCAGGGTGCACG       23689

Qy   4818  CGACCTGCAGAGGACTGCGCAAGGGGCTCGTGCTCGAGCCGTGTCGACCTGGGTGT       4877
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  23690  CGACCTGCAGAGGACTGCGCAAGGGGCTCGTGCTCGAGCCGCGCCGCTCACGCGGGGGT    23749
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The H19G5 transcript is expressed in the heart. H19G5 polypeptides and
polynucleotides are useful for preventing or treating a cardiac disease,
such as congestive heart failure, dilated congestive cardiomyopathy,
hypertrophic cardiomyopathy, restrictive cardiomyopathy, mitral valve
disease, aortic valve disease or tricuspid valve disease, angina
pectoris, myocardial infarction, cardiac arrhythmia, pulmonary, arterial
or rhenovascular hypertension, arteriosclerosis, atherosclerosis and
cardiac tumours in humans. The polypeptide is also useful for detecting
the expression of a protein capable of regulating signal transduction or
the expression of a protein capable of acting as a donor or acceptor
molecule of a phosphate group. The monoclonal antibodies can be used as
probes for detecting discrete antigens expressed by tissue or cell
samples, and therefore used in humans for localization and monitoring of
microbial infection

SQ   Sequence 5007 BP; 946 A; 1722 C; 1541 G; 798 T; 0 U; 0 Other;

Query Match   94.4%;  Score 4915.8;  DB 5;  Length 5007;
Best Local Similarity  99.9%;  Pred. No. 0;
Matches 4920;  Conservative  0;  Mismatches  7;  Indels  0;  Gaps  0;

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Qy    258 CCCAGGGCCCCATCCATGCAGTAACCATCGAGGATGTGCAGGCACAGACAGGCCGAAC 317
          | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     81 CGCACGGGCCCCATCCATGCAGTAACCATCGAGGATGTGCAGGCACAGACAGGCCGAAC 140

Qy    318 GGGCCCAATTCGAGGCTATCATTGAGGGCAGCAGCCCAGCCCTCGGTGACCTGGTACAAGGA 377
          | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    141 GGGCCCAATTCGAGGCTATCATTGAGGGCAGCAGCCCAGCCCTCGGTGACCTGGTACAAGGA 200

Qy    378 CAGCGTCCAGCTGCTGGACAGCACCCGGCTTAGCCAGCAGCAGGAGGCACCACATACTC 437
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    201 CAGCGTCCAGCTGCTGGACAGCACCCGGCTTAGCCAGCAGCAGGAGGCACCACATACTC 260

Qy    438 CCTGGTGCTGGAGGCATGGCCTCGAAGGATGCCGGCGTTTACACCTGCTGGCCCAAA 497
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    261 CCTGTGTGCTGGAGGCATGGCCTCGAAGGATGCCGGCGTTTACACCTGCTGGCCCAAA 320

Qy    498 CACTGGTGGCCAGGTGCTGCTGCAAGCAGAGCTGGTGGTTGGGGGGACAATGAGCC 557
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    321 CACTGGTGGCCAGGTGCTGCTGCAAGCAGAGCTGGTGGTTGGGGGGACAATGAGCC 380

Qy    558 GGACTCAGAGAAGCAAAGCCACCGAGGAGAAGCTGCACTCCTTCTATGAGGTCAAGGAGGA 617
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    381 GGACTCAGAGAAGCAAAGCCACCGAGGAGAAGCTGCACTCCTTCTATGAGGTCAAGGAGGA 440

Qy    618 GATTGGAAGGGGCGTGTTGGCTTCGTAAAAAGAGTGCAGCACAAAGGAAACAAGATCTT 677
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    441 GATTGGAAGGGGCGTGTTTGGCTTCGTAAAAAGAGTGCAGCACAAAGGAAACAAGATCTT 500

Qy    678 GTGGCGTGCCAAGTTCATCCCCTACGGAGCAGAACTCGGGCCCAGGCATACAGGGAGCG 737
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    501 GTGGCGTGCCAAGTTCATCCCCTACGGAGCAGAACTCGGGCCCAGGCATACAGGGAGCG 560

Qy    738 AGACATCCTGGCCGCGCTGAGCCACCCGTCGTGTCACGGGGTGCTGGACCAGTTTGAGAC 797
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    561 AGACATCCTGGCCGCGCTGAGCCACCCGTCGTGTCACGGGGTGCTGGACCAGTTTGAGAC 620

Qy    798 CCGCAAGACCCTCATCCTCATCCTGGAGCCTGCTGCTCATCCGAGGAGCTGCTGGACCGCCT 857
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    621 CCGCAAGACCCTCATCCTCATCCTGGAGCCTGCTGCTCATCCGAGGAGCTGCTGGACCGCCT 680

Qy    858 GTACAGGAAGGGCGTGGTGGTTGACGGGCCGAGTCAAGGTCTACATCCAGCAGCTGGTGGA 917
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    681 GTACAGGAAGGGCGTGGTGGTTGACGGGCCGAGTCAAGGTCTACATCCAGCAGCTGGTGGA 740

Qy    918 GGGGGCTGCACTACCTGCACAGCCATGCCGTTCCACCTGGACATAAAGCCCTCAACAT 977
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    741 GGGGCTGCACTACCTGCACAGCCATGCCGTTCCACCTGGACATAAAGCCCTCTAACAT 800

Qy    978 CCTGATGTGCATCCTGCCCGGGAAGACATTAAATTCTGGGACTTTGGCTTTGCCCAGAA 1037
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    801 CCTGATGTGCATCCTGCCCGGGAAGACATTAAATTCTGGGACTTTGGCTTTGCCCAGAA 860
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Qy   4878 GTCCGGGGGCGCCGGTGGCCTTCGCGCAGCACTCTGTGCGCCAGCCCTGGGCGCGGCC 4937
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Db  23750 GTCCGGGGGGCGCCGGTGGCCCTTCCTGCGCAGCACTCTGTGCGCCAGCCCTGGGCGCGGCC 23809

Qy   4938 CTGCGCGTCCAGCTGCCTGCAGTGCCGTGGCTAACAGAGGAGGAGGCGCCGGCCTGTTCGCG 4997
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  23810 CTGCGCGTCCAGCTGCCTGCAGTGCCGTGGCTAACAGAGGAGGAGGCGCCGGCCTGTTCGCG 23869

Qy   4998 GCCCGCGCCGTGACCTTCCTACCGCGGCGGCGTGCGGCCTCTTCGTGCGCGAGAA 5057
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  23870 GCCCGCGCCCGTGACCTTCCTACCGCGGCGGCGTCGCGGCTCTTCGTGCGCGAGAA 23929

Qy   5058 GAGAGGCGGCCTGCTGTACAAGAGGCCACAACCTGGCCCAGTGCGCTGCAGGGTCGCCCCG 5117
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  23930 GAGAGGCGCCTGCTGTACAAGAGGCCACAACCTGGCCCAGTGCGCTGCAGGGTCGCCCCG 23989

Qy   5118 GCCACACCCTTGGTCTCCCCGCTCGGGGGTCGCTGCAGACGCGGCCAATAAAAACGCACAGC 5177
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  23990 GCCACACCCTTGGTCTCCCCGCTCGGGGGTCGCTGCAGACGCGGCCAATAAAAACGCCCAGC 24049

Qy   5178 CGGGGCGAGAAGAAAAAAAAAAAAAAAAAAAAAAAAA 5207
          |||||||||||||||||||||||||||||||||||||
Db  24050 CGGGGCGAGAAGAAAAAAAAAAAAAAAAAAAAAAAAA 24079

RESULT 6
AAC62286
ID   AAC62286 standard; cDNA; 5007 BP.
XX
AC   AAC62286;
XX
DT   19-MAR-2001  (first entry)
XX
DE   cDNA encoding a full length human signal transduction polypeptide.
XX
KW   Signal transduction; H19G5; kinase; cardiac disease; angina pectoris;
KW   congestive heart failure; dilated congestive cardiomyopathy;
KW   hypertrophic cardiomyopathy; restrictive cardiomyopathy; hypertension;
KW   mitral valve disease; aortic valve disease; tricuspid valve disease;
KW   myocardial infarction; cardiac arrhythmia; arteriosclerosis;
KW   atherosclerosis; cardiac tumour; microbial infection; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             97..4929
FT                   /*tag= a
FT                   /product= "signal transduction polypeptide H19G5"
XX
PN   WO200063381-A1.
XX
PD   26-OCT-2000.
XX
PF   11-APR-2000; 2000WO-US009488.
XX
PR   16-APR-1999; 99US-0129553P.
XX
PA   (SCIO-) SCIOS INC.
XX
PI   Zeng W, Stanton L, Kong H;
XX
DR   WPI; 2001-007013/01.
DR   P-PSDB; AAB30568.
XX
PT   Novel h19G5 polypeptides capable of regulating signal transduction and
PT   exhibiting kinase activity useful for identifying antibodies to treat
PT   cardiac diseases, and additional mediators of signal transduction.
XX
PS   Claim 4; Page 59-61; 81pp; English.
XX
CC   The present sequence encodes a human protein with putative function in
CC   signal transduction. The polypeptide is designated H19G5. The protein is
CC   capable of regulating signal transduction and exhibits kinase activity.

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Qy   1038  CATCACCCCAGCAGAGCTGCAGTTCAGCCAGTACGGCTCCCCTGAGTTCGTCTCCCCCGA  1097
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    861  CATCACCCCAGCAGAGCTGCAGTTCAGCCAGTACGGCTCCCCTGAGTTCGTCTCCCCCGA   920

Qy   1098  GATCATCCAGCAGAACCCTGTGAGCGAAGCCTTCGACATTTGGCCATGGGTGTCATCTC   1157
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    921  GATCATCCAGCAGAACCCTGTGAGCGAAGCCTTCGACATTTGGCCATGGGTGTCATCTC    980

Qy   1158  CTACCTCAGCCTGACCTGCTCATCCCCATTTGCCGGCGAGAGTGACCGTGCCACCCTCCT   1217
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    981  CTACCTCAGCCTGACCTGCTCATCCCCATTTGCCGGCGAGAGTGACCGTGCCACCCTCCT   1040

Qy   1218  GAACGTCTGGAGGGCGCGTGTCATGGAGCAGCCCATGGCTGCCACCTCAGCGAAGA   1277
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1041  GAACGTCTGGAGGGCGCGTGTCATGGAGCAGCCCATGGCTGCCACCTCAGCGAAGA   1100

Qy   1278  CGCCAAAGACTTCATCAAGGCTACGCTGCAGAGAGCCCTCAGGGCCCGGCCTAGTGCGGC   1337
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1101  CGCCAAAGACTTCATCAAGGCTACGCTGCAGAGAGCCCTCAGGGCCCGGCCTAGTGCGGC   1160

Qy   1338  CCAGTGCCTCTCCCACCCCTGGTTCCTGAAATCCATGCCTCGCGGAGGGCCCACTTCAT   1397
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1161  CCAGTGCCTCTCCCACCCCTGGTTCCTGAAATCCATGCCTCGCGGAGGGCCCACTTCAT   1220

Qy   1398  CAACACCAAGCAGCTCAAGCTCCTCGGCCCGGAAGTCGGCTGGCAGCGTTCCCTGATGAG   1457
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1221  CAACACCAAGCAGCTCAAGCTCCTCGGCCCGGAAGTCGGCTGGCAGCGTTCCCTGATGAG   1280

Qy   1458  CTACAAGTCCATCCTGGTGATGGCGTCCATCCTGAGCCTGAGCTGCTCGCGGGGCCACCCGACAG   1517
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1281  CTACAAGTCCATCCTGGTGATGGCGTCCATCCTGAGCCTGAGCTGCTCGCGGGGCCACCCGACAG   1340

Qy   1518  CCCCTCCCTCGGGGTAGCCCGGCACCTGCGCCCCATTTGCCCCGGGGCTTCCCAGTTCCTC   1577
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1341  CCCCTCCCTCGGGGTAGCCCGGCACCTGCGCCCCATTTGCCCCGGGGCTTCCCAGTTCCTC   1400

Qy   1578  CTCTCCTCCTGACACAGCAGCTTGCTGCGCCCCATTTGCCCCGGGGCTAAGTCACTGCCACCCTCCCC   1637
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1401  CTCTCCTCCTGACACAGCAGCTCGCTGCCCCCATTTGCCCCGGGGCTAAGTCACTGCCACCCTCCCC   1460

Qy   1638  GGTGACACACTCACCACTGCTGCACCCCTCGGCCCTTCCTGCGGCCCTCGGCCCAGCCTGCC   1697
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1461  GGTGACACACTCACCACTGCTGCACCCCTCGGCCCTTCCTGCGGCCCTCGGCCCAGCCTGCC   1520

Qy   1698  TGAGGAAGCCGAGGCCAGTGAGCCTCACCGGCCTCGTGCCCCAGCCTCCACGGCCTGCATCTCCCCA   1757
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1521  TGAGGAAGCCGAGGCCAGTGAGCCTGCGTGCCCCAGCTCGTGCCCCAGCTCCGCATCTCCCGA   1580

Qy   1756  GGGTGCCCGGCCACCGGCCGCCCAGGGCTGCCTGCCCGGCACAGCGTCATCCCGCAGCCT   1817
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1581  GGGTGCCCGGCCACCGGCCGCCCAGGGCTGCCTGCCCGGCACAGCGTCATCCCGCAGCCT   1640

Qy   1818  GTTCTACCACCAGGCGGGTGAGAGCCGCACTGCTGAAGGGGCCCTACATTGCGGGGGCGTGCCAGG   1877
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1641  GTTCTACCACCAGGCGGGTGAGAGCGGCACACGGCCCTACATTGCGGGGGCGCAGGCAGGCG   1700

Qy   1878  GCACCACCCCTCGCCCAAGCCCCTCATTGGACACCGGGCCGCCAGGGAGGACCGCTGCCAGG   1937
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1701  GCACCCGCCCGCCGGCGGGTGAGGCGCACCTGGCTACATTGGCGGGAGGGGGCGCCAGGAGGAGCA   1760

Qy   1938  GGCACCCTTGGCCCTCGGCCCCTCATTGAGACTGCCCTCCGGCTGCCTGCCTCCTGG   1997
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1761  CCTTGCGCGAGCCACTGGACACCGGGCTCCCGCACCTCCTGGACTTCCGGCTGCCTGCCTCCTGG   1820

Qy   1998  GGCACCCCCTGCCCAAAGCCCCTCATTGGACAAGCCCCCTCTCCGAGCACCCCCG   2057
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1821  GGCACCCCCTGCCCAAAGCCCCTCATTGGACAAGCCCCTCTCCGAGCACCCCCG   1880

Qy   2058  CACCCACTTGGCCCCTGCCCCCTGCCCCAGCCACTCCCTGGAACATGACTCTCCGAGCACCCCCG   2117
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1881  CACCCACTTGGCCCCTGCCCCCTGCCCCAGCCACTCCCTGGAACATGACTCTCCGAGCACCCCCG   1940

Qy   2118  CCCCTCCTCCTGGGAGGCGCTTGCGTGGGGTGAGGCCACCAGCGCGACTGCAGCAGGCCGCTGCCCTTCAGCCCCTCCGGGGGGC   2177
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Db          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1941  CCCCTCCTCCTCGGAGGCGCTTGCGTGGGGTGAGGCCACCAGCGCGACTGCTGCCTTCAGCCCCTCCGGGGGGGC   2000

Qy   2178  CCCTATCAGGGACATGGGGCACCCTCAGGGCTCCAAGCAGCTTCCATCCACTGGTGCCA   2237
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2001  CCCTATCAGGGACATGGGGCACCCTCAGGGCTCCAAGCAGCTTCCATCCACTGGTGCCA   2060

Qy   2238  CCCAGGGCACTGCTCAGCCAGAGAGGCCATCCCGGACAGCCTTGGGGGGCAGCCAGCCCC   2297
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2061  CCCAGGGCACTGCTCAGCCAGAGAGGCCATCCCGGACAGCCCTTGGGGGGCAGCCAGCCCC   2120

Qy   2298  TTTCTGCCACCCCAAGCAGGGTTCTGCCCCCAGGAGGGCTGCAGCCCCACCCCAGCAGT   2357
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2121  TTTCTGCCACCCCAAGCAGGGTTCTGCCCCCAGGAGGGCTGCAGCCCCACCCCAGCAGT   2180

Qy   2358  TGCCCCATGCCCTCCTGGCTCCTTCCTCCTTCCTCGGATCTTGCAAAGAGAGCCCCTTAGTACC   2417
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2181  TGCCCCATGCCCTCCTGGCTCCTTCCTCCTTCCTCCAGGATCTTGCAAAGAGAGCCCCTTAGTACC   2240

Qy   2418  CTCAAGCCCCTTCTTGGACAGCCCCAGGCACCCCCCTGCCCCTGCCAAAGCAAGCCCCCC   2477
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2241  CTCAAGCCCCTTCTTGGACAGCCCCAGGCACCCCCCTGCCCCTGCCAAAGCAAGCCCCCC   2300

Qy   2478  ATTGGACTCTAAGATGGGGCCTGGAGACATCTCTCTTCCTCGGAGGCCAAAACCCGGCGC   2537
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2301  ATTGGACTCTAAGATGGGGCCTGGAGACATCTCTCTTCCTCGGAGGCCAAAACCCGGCCC   2360

Qy   2538  CTGCAGTTCCCCAGGGTCAGCCTCCCAGGCGAGCTCTTCCCAGTGAGCTCCCTCAGGGT   2597
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2361  CTGCAGTTCCCCAGGGTCAGCCTCCCAGGCGAGCTCTTCCCAACTGAGCTCCCTCAGGGT   2420

Qy   2598  GGGCTCCTCCCAGGTGGGCACAGAGCCTGCCCCCCTCCCACCTTGCGAGCCGCCTCAGGGAACAGGTGAC   2657
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2421  GGGCTCCTCCCAGGTGGGCACAGAGCCTGCCCCCCTCCCACCCACCTTGCAGCCGCCTCAGGGAACAGGGAC   2480

Qy   2658  GGAGGCTGAGGATCTGTCTGCCAGTCCCACCACCTTGCGAGCGCTGGCCAGCAGGCGGTCATGGCAC   2717
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2481  GGAGGCTGAGGATCTGTCCGACTCCACCACCACCTTGCAGCCGCTGGCCAGCAGGCGGAC   2540

Qy   2718  CATGGCCAAGTTCTCCCTGGGTGGTGCGCGGGGCATGTGGGGCGGCCCATGTGGGCTGCCAGGAT   2777
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2541  CATGGCCAAGTTCTCCCTGGGTGGTGCGCGGGGCATGTGGGGCGGCCCATGTGGGCTGCCAGGAT   2600

Qy   2778  CTTTGCCTTTGGTGGAGATGCAGGGGCATGTGGGGAGCAGGAGCAGGAGGCTGAGTCCCA   2837
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2601  CTTTGCCTTTGGTGGAGATGCAGGGGCATGTGGGGAGCAGGAGCAGGAGGCTGAGTCCCA   2660

Qy   2838  AGCCTGGGCTGTGTCCCAGTGGGGCACAGCGTCATCCCGCAGCCTCAGTGCAAGGCC   2897
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2661  AGCCTGGGCTGTGTCCCAGTGGGGCACAGCGTCATCCCGCAGCCTCAGTGCAAGGCC   2720

Qy   2898  GTCGGAGGAGCAGCAGGAGGCTGAGAGCCCACTGCCCCAGGTCAGTGCAAGGCC   2957
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2721  GTCGGAGGAGCAGCAGGAGGCTGAGAGCCCACTGCCCCAGGTCAGTGCAAGGCC   2780

Qy   2958  TGTGCCTGAGGTCGGCAGGGCTCCCACCAGGAGCTCTCCAGAGCCCAGAGCCCCATGGGGAGGA   3017
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2781  TGTGCCTGAGGTCGGCAGGGCTCCCACCAGGAGCTCTCCAGAGCCCACCCCATGGGGAGGA   2840

Qy   3018  CATCGGCGCAGTCTCCTGTGTCGACATTTCCCGAGGTGCAGATCCGGACCCCGCCTACCTCAGACCTGTA   3077
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2841  CATCGGCGCAGTCTCCTGTGTCGACATTTCCCGAGGTGCAGATCCGGACCCCGCCTACCTCAGACCTGTA   2900

Qy   3078  CGATATCAAGTACCTCCCATTCCAGTTTATGATCTTCAGGAAGTCCCCAAGTCCGCTCA   3137
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2901  CGATATCAAGTACCTCCCATTCCAGTTTATGATCTTCAGGAAAGTCCCCAAGTCCGCTCA   2960

Qy   3138  CACCCACTTGGCCCCCTGCCCCAGCCACTCCCTGGAACATGACTCTCCGAGCACCCCCG   3197
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2961  CACCCACTTGGCCCCCTGCCCAGCCACTCCCTGGAACATGACTCTCCGAGCACCCCCG   3020

Qy   3198  GCCAGAGCCGCCCTCCCCATGGCTGAGGAGAAGTGGCCCGAGTTCCCGGAGCCCACGTG   3257
```

Db  3021 GCCAGAGCCGCCTCCCCATGGCTGAGGAGGAGCTGGCCGAGTTCCCGGAGCCCACCTG 3080
Qy  3258 GCCCTGGCCAGGTGAACTGGCCCCCACCAGGCCTGAGATCACAGAGGAGTCAGAGGA 3317
Db  3081 GCCCTGGCCAGTGAACTGGCCCCCACCAGGCCTGGAGATCACAGAGGAGTCAGAGGA 3140
Qy  3318 TGTGGACGCGCTGCTGGCCAGGAGACGCAAGTGTCCTCGCCGTC 3377
Db  3141 TGTGGACGCGCTGCTGGCAGGAGGCGCAAGTGGTCCGTCCGCCGTC 3200
Qy  3378 ACGCAGCCTCTTCCACTTCCCTGGAGGCACCTGCCGTGGATGAGCCTGCAGAGTGGG 3437
Db  3201 ACGCAGCCTCTTCCACTTCCCTGGGAGGCACCTGGCGCTGGATGAGCCTGCAGAGTGGG 3260
Qy  3438 GCTGCCTGAGAGAGTGAAGGCCTCCGTGGAGCACATCTCCGGATCCTGAAGGGCAGGCC 3497
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Qy  3558 CTCAGGTCTGAAGAGCTGGGACCTGGGACACCGGCCGACATTCCTAAGGGAGCTCTCAGATGAGAC 3617
Db  3381 CTCAGGTCTGAAGAGCTGGGACCTGGGACACCGGCCGACATTCCTAAGGGAGCTCTCAGATGAGAC 3440
Qy  3618 TGTGGTCCTGGGCCAGTCAGTGACACTGGCCTGCCAGGTGTCAGCCCAGCTGCCCA 3677
Db  3441 TGTGGTCCTGGGCCAGTCAGTGACACTGGCCTGCCAGGTGTCAGCCCAGCTGCCCA 3500
Qy  3678 GGCCACCTGGAGCAAAGACGGAGCCCCCCTGGAGCAGCAGCCGTGTCCTCATCTCTGC 3737
Db  3501 GGCCACCTGGAGCAAAGACGGAGCCCCCCTGGAGCAGCAGCCGTGTCCTCATCTCTGC 3560
Qy  3738 CACCCTCAAGAACTTCCAGCTTCCACCATCCTGTGTGCTGAGGACCTGGGTGT 3797
Db  3561 CACCCTCAAGAACTTCCAGCTTCCACCATCCTGTGTGGTGCTGAGGACCTGGGTGT 3620
Qy  3798 GTACACCTGCAGCGTGAGCAATGCGCTGGGGACAGTGACCACCACGGCGTCCTCCGGAA 3857
Db  3621 GTACACCTGCAGCGTGAGCAATGCGCTGGGGACAGTGACCACCACGGCGTCCTCCGGAA 3680
Qy  3858 GGCAGAGCGCGCCCCTCATCTTCGCCCATGCCCGGATATCGGGGAGGTGTACGCGGATGGGGT 3917
Db  3681 GGCAGAGCGCGCCCCTCATCTTCGCCCATGCCCGGATATCGGGGAGGTGTACGCGGATGGGGT 3740
Qy  3918 GCTGCTTGGTCTGGAAGCCGGGCCTGGAATCCTTACGGCCCCTGACCTACATTGTGCAGTGCAG 3977
Db  3741 GCTGCTTGGTCTGGAAGCCGGGCCTGGAATCCTTACGGCCCCTGTGACCTACATTGTGCAGTGCAG 3800
Qy  3978 CCTAGAAGGGCGGCAGCTGACCACCACACTGGCCTCCGACATCTTTGACTGCTGCTACCTGAC 4037
Db  3801 CCTAGAAGGGCGGCAGCTGACCACCACACTGGCCTCCGACATCTTTGACTGCTGCTACCTGAC 3860
Qy  4038 CAGCAAGCTCTCCCCGGGGTGCACCTGCACCTACACCTTCCGCACGACGCGCAGGCAGG 4097
Db  3861 CAGCAAGCTCTCCCCGGGGTGGCACCTGCACCTACACCTTCCGCACGCACGAGAGGCAGG 3920
Qy  4098 AATGGGTCCCTACACAGCAGCCCTCCTCGGAGCAAGTCCTCCTGGAGGGGCCCAGCCACCTGGC 4157
Db  3921 AATGGGTCCCTACACAGCAGCCCTCCTCGGAGCAAGTCCTCCTGGAGGCGCCCAGCCACCTGGC 3980
Qy  4158 CTCTGAGGAGGAGGAGCCAGGGCGGTCAGCCGAGCCCAACCCCTGCCCAGCACAAAGACCTTCGC 4217
Db  3981 CTCTGAGGAGGAGGAGCCAGGGCGGTCAGCCGAGCCCAACCCCTGCCCCAGCCACACAAAGACCTTCGC 4040
Qy  4218 ATTCCAGACACAGATCCAGAGAGGGGCCGCTTCAGCGGTGCGGCAATGCTGGGAGAAGGC 4277
Db  4041 ATTCCAGACACAGATCCAGAGGGGGCCGCTTCAGCGTGCGGCAATGCTGGGAGAGGC 4100
Qy  4278 CAGCGGGCGGCGGCTGCCGCCCAAGCATCATCCCCTACCACCCCCAAGGACAAGACAGCAGT 4337
Db  4101 CAGCGGGCGGCGGCTGCCGCCCAAGATCATCCCCTACCACCCCCAAGGACAAGACAGACAGCAGT 4160

Qy  4338 GCTGCGCGAATACGAGGCCCTCAAGGGCCTGCCCACCTGGCCACGC 4397
Db  4161 GCTGCGCGAATACGAGGCCCTCAAGGGCCTGGGCCACCTGGCCCAGCTGCCACGC 4220
Qy  4398 AGCCTACCTCAGCCCCGGCACCTGGTGCTCATCTTGGAGCTGTGTCTCTGGGCCCGAGCT 4457
Db  4221 AGCCTACCTCAGCCCCGGCACCTGGTGCTCATCTTGGAGCTGTGTCTCTGGGCCCGAGCT 4280
Qy  4458 GCTCCCCTGCCTGCCGAGAGGGCCTCCTACTCCTACTCAGAATCTGAGGTGAAGGACTACCTGTG 4517
Db  4281 GCTCCCCTGCCTGCCGAGAGGGCCTCCTACTCCTACTCAGAATCCAGAGGTGAAGGACTACCTGTG 4340
Qy  4518 GCAGATGTTGAGTGCCACCCAGTACCTGCACAACCAGCACATCCTGCACCTGGACCTGAG 4577
Db  4341 GCAGATGTTGAGTGCCACCCAGTACCTGCACAACCAGCACATCCTGCACCTGGACCTGAG 4400
Qy  4578 GTCCGAGAACATGATCATCACCGAATACAACCTGCTCAAGGTCGTGACCTGGCAATGC 4637
Db  4401 GTCCGAGAACATGATCATCACCGAATACAACCTGCTCAAGGTCGTGGACCTGGCAATGC 4460
Qy  4638 ACAGAGCCTCAGCCAGGAGAAGTGTCGCCCTCAGACAAGTTCAAGGACTACCTAGAGAC 4697
Db  4461 ACAGAGCCTCAGCCAGGAGAAGGTGCTGCCCCTCAGACAAGTTCAAGGACTACCTAGAGAC 4520
Qy  4698 CATGGCTCCAGAGCTCCTGGAGGGCCAGGGGGTGTTCCACAGACAGACATCTGGGCCAT 4757
Db  4521 CATGGCTCCAGAGCTCCTGGAGGGCCAGGGGGTGTTCCACAGACAGACATCTGGGCCAT 4580
Qy  4758 CGGTGTGACAGCCTTCATCATGCTGAGCGCCAGTACCCGGTGAGCAGGTGAGGGTGCACG 4817
Db  4581 CGGTGTGACAGCCTTCATCATGCTGAGCGCCGGTGAGCAGGTGAGGGTGCACG 4640
Qy  4818 CGACCTGCAGAGAGGACTGGCGCAAGGAGGCTGGTCCGGCCGCTGCTACGCGGGGGCT 4877
Db  4641 CGACCTGCAGAGAGGACTGCGCAAGGAGGCTGCTACGCGGGGGCT 4700
Qy  4878 GTCCGGGGGCGCCGTGGCCTTCGTCGTGCGCCGCACTCGTGTGCGCGCCCTGGGGGCCGGCCG 4937
Db  4701 GTCCGGGGGCGCCGTGGCCTTCGTCGTGCGCCGCACTCGTGTGCGCGCCCTGGGGGCCGGCCG 4760
Qy  4938 CTGGCGCGTCCAGTGCCTGCAGTGCCCGGTGGCTAACAGAGAGGGGCCCGGCCTGTTCGCG 4997
Db  4761 CTGGCGCGTCCAGTGCCTGCAGTGCCCGGTGGCTAACAGAGAGGGGCCCGGCCTGTTCGCG 4820
Qy  4998 GCCCCGCCCGTGACTTCCTCCACGCGGCGGCTCGTGTGCGCGAGAA 5057
Db  4821 GCCCCGCCCGTGACTTCCTCCACGCGGCGGCTCGTGTGCGCGAGAA 4880
Qy  5058 GAGACGCGCGGCGTGTGTCAGAGGCACAACCTGGCCCAGGTGCGTGAGGGTCGCCCCG 5117
Db  4881 GAGACGCGCGGCGGCCCGTGCGTACAGAGAGCACAACCTGGCCCAGGTGCGTGAGGGTCGCCCCG 4940
Qy  5118 GCCACCCCTGGTCTCCCCGCTGGGGGTCGCTGCAGACGCGGCCAATAAAAACGCACAGC 5177
Db  4941 GCCACCACCCTTGGTCTCCCCGCTGGGGGTCGCTGCAGACGCGGCCAATAAAAACGCACAGC 5000
Qy  5178 CGGGCGA 5184
Db  5001 CGGGGCGA 5007

RESULT 7
AAC62287
ID   AAC62287 standard; cDNA; 7928 BP.
XX
AC   AAC62287;
XX
DT   19-MAR-2001  (first entry)
XX
DE   cDNA encoding a splice variant of a signal transduction polypeptide.
XX
KW   Signal transduction; H19G5; kinase; cardiac disease; angina pectoris;

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KW   congestive heart failure; dilated congestive cardiomyopathy;
KW   hypertrophic cardiomyopathy; restrictive cardiomyopathy; hypertension;
KW   mitral valve disease; aortic valve disease; tricuspid valve disease;
KW   myocardial infarction; cardiac arrhythmia; arteriosclerosis;
KW   atherosclerosis; cardiac tumour; microbial infection; splice variant; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             60..7850
FT                   /*tag= a
FT                   /product= "signal transduction polypeptide H19G5 splice
FT                   variant"
XX
PN   WO200063381-A1.
XX
PD   26-OCT-2000.
XX
PF   11-APR-2000; 2000WO-US009488.
XX
PR   16-APR-1999; 99US-0129553P.
XX
PA   (SCIO-) SCIOS INC.
XX
PI   Zeng W, Stanton L, Kong H;
XX
DR   WPI; 2001-007013/01.
DR   P-PSDB; AAB30569.
XX
PT   Novel h19G5 polypeptides capable of regulating signal transduction and
PT   exhibiting kinase activity useful for identifying antibodies to treat
PT   cardiac diseases, and additional mediators of signal transduction.
XX
PS   Claim 4; Page 65-68; 81pp; English.
XX
CC   The present sequence encodes a splice variant of human in signal
CC   transduction polypeptide. The polypeptide is designated H19G5. The
CC   protein is capable of regulating signal transduction and exhibits kinase
CC   activity. The H19G5 transcript is expressed in the heart. H19G5
CC   polypeptides and polynucleotides are useful for preventing or treating a
CC   cardiac disease, such as congestive heart failure, dilated congestive
CC   cardiomyopathy, hypertrophic cardiomyopathy, restrictive cardiomyopathy,
CC   mitral valve disease, aortic valve disease or tricuspid valve disease,
CC   angina pectoris, myocardial infarction, cardiac arrhythmia, pulmonary,
CC   arterial or rhenovascular hypertension, arteriosclerosis, atherosclerosis
CC   and cardiac tumours in humans. The polypeptide is also useful for
CC   detecting the expression of a protein capable of regulating signal
CC   transduction or the expression of a protein capable of acting as a donor
CC   or acceptor molecule of a phosphate group. The monoclonal antibodies can
CC   be used as probes for detecting discrete antigens expressed by tissue or
CC   cell samples, and therefore used in humans for localization and
CC   monitoring of microbial infection
XX
SQ   Sequence 7928 BP; 1535 A; 2644 C; 2488 G; 1261 T; 0 U; 0 Other;

Query Match             94.4%;  Score 4915.8;  DB 5;  Length 7928;
Best Local Similarity   99.9%;  Pred. No. 0;
Matches 4920;  Conservative   0;  Mismatches   7;  Indels   0;  Gaps   0;

Qy    258 CCCAGGGCCCCATCCATGGAGGTAACCATCGAGGATGTGCAGGCACAGACAGGCGAAC 317
          |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db   3002 CGCACGGCGCCCCATCCATGCAGGTAACCATCGAGGATGTGCAGGCACAGACAGGCGGAAC 3061

Qy    318 GGCCAATTCGAGGCTATCATTGAGGGCGACACCCCAGACCCTCGGTGACCTGGTACAAGGA 377
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3062 GGCCAATTCGAGGCTATCATTGAGGGCGACACCCCAGACCCTCGGTGACCTGGTACAAGGA 3121

Qy    378 CAGCGTCCAGCTGGTGACAGCAGCAGCACCCCGGCGCTTAGCCAGCAGCAAGAAGGCACCACATACTC 437
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3122 CAGCGTCCAGCTGGTGACAGCAGCAGCACCCCGGCGCTTAGCCAGCAGCAAGAAGGCACCACATACTC 3181

Qy    438 CCTGGTGCTGAGGCATGTGGCCTCGAAGGATGCCGGCGTTTACACCTGCTGCCCCAAAA 497
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3182 CCTGGTGCTGAGGCATGTGGCCTCGAAGGATGCCGGCGTTTACACCTGCTGCCCCAAAA 3241

Qy    498 CACTGTGGCCAGGTGCTCTGCAAGGCAGAGCTCTGGTGCTTGGGGGGGACAATGAGCC 557
          ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3242 CACTGCGTGGCCAGGTGCTCTGCAAGGCAGAGCTCTGGTGCTTGGGGGGGACAATGAGCC 3301

Qy    558 GGACTCAGAGAAGCAAAGCCACCGAGGAAGCTGCACTCCTTCTATGAGGTCAAGGACGA 617
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3302 GGACTCAGAGAGCAAAGCCACCGAGGAAGCTGCACTCCTTCTATGAGGTCAAGGACGGA 3361

Qy    618 GATTGGAAGGGGCGTGTTGGCTTCGTAAAAAGAGTGCAGCACAAAGGAAACAAGATCTT 677
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3362 GATTGGAAGGGGCGTGTTGGCTTCGTAAAAAGAGTGCAGCACAAAGGAAACAAGATCTT 3421

Qy    678 GTGCCTGCCAAGTTCATCCCCCTACGGAGCAGAACTCGGGCCCAGGCATACAGGGAGCG 737
          ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3422 GTGCCGTGCCAAGTTCATCCCCCTACGGAGCAGAACTCGGGCCCAGGCATACAGGGAGCG 3481

Qy    738 AGACATCCTGGCCGCGCTGAGCCACCCGCTGGTCACGGGCGTCTGCTGACCAGTTTGAGAC 797
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3482 AGACATCCTGGCCGCGCTGAGCCACCCGCTGGTCACGGGCGTCTGCTGACCAGTTTGAGAC 3541

Qy    798 CCGCAAGACCCTCATCCTCATCCTGGAGCTGTGCTCATCCGGAGGAGCTGCTGACCGGCCT 857
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3542 CCGCAAGACCCTCATCCTCATCCTGGAGCTGTGCTCATCCGGAGGAGCTGCTGACCGGCCT 3601

Qy    858 GTACAGGAAGGGCGTGGTGACGGAGGCCCGAGTCAAGGTCTCACATCCAGCAGCTGGTGA 917
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3602 GTACAGGAAGGGCGTGGTGACGGAGGCCCGAGTCAAGGTCTCACATCCAGCAGCTGGTGA 3661

Qy    918 GGGGCTGCACTACCTGCACAGCCATGGCGGTCTCCCACCTGGACATAAAGCCCTCTAACAT 977
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3662 GGGGCTGCACTACCTGCACAGCCATGGCGGTCTCCCACCTGGACATAAAGCCCCTAACAT 3721

Qy    978 CCTGATGGTGCATCCTGCCCGGGAAGACATTAAAATCTGCGACTTTGGCTTTGCCCCAGAA 1037
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3722 CCTGATGGTGCATCCTGCCCGGGAAGACATTAAAATCTGCGACTTTGGCTTTGCCCCAGAA 3781

Qy   1038 CATCACCCCAGCAGAGCTGCAGTTCAGCCAGTACGGCTCCCCGAGTTCGTCTCCCCCGA 1097
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3782 CATCACCCCAGCAGAGCTGCAGTTCAGCCAGTACGGCTCCCCGAGTTCGTCTCCCCCGA 3841

Qy   1098 GATCATCCAGCAGAACCCTGTGAGCGAAGCCTCCGACATTTGGGCCATGGGTGTCATCTC 1157
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3842 GATCATCCAGCAGAACCCTGTGAGCGAAGCCTCCGACATTTGGGCCATGGGTGTCATCTC 3901

Qy   1158 CTACCTCAGCTGACCTGCTCATCCCCATTGCCGGCGAGAGTGACCGTGCCACCCTCCT 1217
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Db   3902 CTACTTCAGCTGACCTGCTCATCCCCATTGCCGGCGAGAGTGACCGTGCCACCCTCCT 3961

Qy   1218 GAACGTCCTGGAGGGGCGGCGGTGTCATGGAGCAGCCCATGGCGTGCCCACCTCAGCGGAAGA 1277
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Db   3962 GAACGTCCTGGAGGGGCGGCGGTGTCATGGAGCAGCCCATGGCGTGCCCACCTCAGCGGAAGA 4021

Qy   1278 CGCCAAAGAGACTTCATCAAGCTAGCGTCGCAGAGAGCCCCTCAGGCCCCGGCCAGTGCGGGC 1337
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4022 CGCCAAAGAGACTTCATCAAGCTAGCGTCGCAGAGAGCCCCTCAGGCCCCGGCCAGTGCGGGC 4081

Qy   1338 CCAGTGCCTCTCCCCACCCCTGGTTCCTGGAAATCCATGCCTGCCGGAGGAGGCCCACTTCAT 1397
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4082 CCAGTGCCTCTCCCCACCCCTGGTTCCTGGAAATCCATGCCTGCCGGAGGAGGCCCACTTCAT 4141

Qy   1398 CAACACCAAGCAGCTCAAGTTCCTCCTGGCCCGGCCCGAAGTCGCTGGCAGCGTTCCCTGATGAG 1457
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4142 CAACACCAAGCAGCTCAAGTTCCTCCTGGCCCGGCCCGAAGTCGCTGGCAGCGTTCCCTGATGAG 4201

Qy   1458 CTACAAGTCCATCCTGGTGATGCGCTCCATCCTGGAGGGCTGCTCGCGGGGCCACCCGACAG 1517
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Db   4202 CTACAAGTCCATCCTGGTGATGCGCTCCATCCTGGAGGGCTGCTCGCGGGGCCCACCCGACAG 4261

Qy   1518 CCCCTCCCTCGGCGTAGCCCGGCACCTTGCAGGGACACTCGGTGCTCCTCCAGTTCCTC 1577
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4262 CCCCTCCCTCGGCGTAGCCCGGCACCTTGCAGGGACACTCGGTGCTCCTCCAGTTCCTC 4321
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Qy  1578  CTCCTCCTCTGACAAGAGTCTCGCCCCATTTGCCGGGCTAAGTCACTGCCACCCTCCCC  1637
          ||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db  4322  CTCCTCCTCTGACAACGAGCTCGCCCCATTTGCCGGGCTAAGTCACTGCCACCCTCCCC  4381

Qy  1638  GGTGACACACTCACCACTGCTGCACCCCGGGCTTCCTGCGGCCTCGGCCAGCCTGCC    1697
          |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4382  GGTGACAACTCACCACTGCTGCACCCCGGGCTTCCTGCGGCCTCGGCCAGCCTGCC    4441

Qy  1698  TGAGGAAGCCGAGGCCAGTGAGCGCTCACCGAGCGTCCGCCTGCATCTCCCGA      1757
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Db  4442  TGAGGAAGCCGAGGCCAGTGAGCGCTCACCGAGCGTCCGCCTGCATCTCCCGA      4501

Qy  1758  GGGTGCCGGGCCACCGGCCGCCCAGGGCTGCGTGCCCGGCACAGCGTCATCCGCAGCCT  1817
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Db  4502  GGGTGCCGGGCCACCGGCCGCCCAGGGCTGCGTGCCCGGCACAGCGTCATCCGCAGCCT  4561

Qy  1818  GTTCTACCACCAGGGCGGGTGAGAGCCTGAGCACGGGGCCCTGCCCCGGGGACAGGGCG  1877
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4562  GTTCTACCACCAGGGCGGGTGAGAGCCTGAGCACGGGGCCCTGCCCCGGGGACAGGGCG  4621

Qy  1878  GCACCCGGCCCGGGCGGCGGCACCTGTCTGAAGGGCGGCTACATTGCGGGGGCGCTGCAGG  1937
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4622  GCACCCGGCCCGGGCGGCGGCACCTGTCTGAAGGGCGGGTACATTGCGGGGGCGCTGCAGG  4681

Qy  1938  CCTGGCGCGAGCCACTGATGGAGCACCCGCTGCTGGAGGAGGAGGGCGCGCCAGGGAGAGCA  1997
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4682  CCTGGCGCGAGCCACTGATGGAGCACCCGCTGCTGGAGGAGGAGGGCGCGCCAGGGAGAGCA  4741

Qy  1998  GGCCACCCTCCTGGCCACCCCCTCATTCGAGACTGCCCTCCGGCTGCCTCCGGCCGCCTCTGG  2057
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4742  GGCCACCCTCCTGGCCACCCCCTCATTCGAGACTGCCCTCCGGCTGCCTCCGGCCGCCTCTGG  4801

Qy  2058  CACCCACTTGCCCCTGGCCACAGCCACTCCCTGGAACATGACTCTCCGAGCACCCCCCC     2117
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4802  CACCCACTTGCCCCTGGCCACAGCCACTCCCTGGAACATGACTCTCCGAGCACCCCCCG     4861

Qy  2118  CCCCTCCTCGGAGGGCTGCCGTGAGGCACAGCGACTGCCTTCAGCCCCCTCCGGGGGGG    2177
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4862  CCCCTCCTCGGAGGGCTGCCGTGAGGCACAGCGACTGCCTTCAGCCCCCTCCGGGGGGGC   4921

Qy  2178  CCCTATCAGGGACATGGGGCACCCTCAGGGCTCCAAGCAGCTTCCATCCACTGGTGCCA   2237
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4922  CCCTATCAGGGACATGGGGCACCCTCAGGGCTCCAAGCAGCTTCCATCCACTGGTGCCA   4981

Qy  2238  CCCAGGCACTGCTCACCCAGAGAGCCCATCCCCAGACACAGCCCTTGGGGGGCAGCAGCCC  2297
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4982  CCCAGGCACTGCTCAGCCAGAGAGCCCATCCCCAGACAGCCCTTGGGGGGCAGCAGCCCC  5041

Qy  2298  TTTCTGCCACCCAGCAGGGTTCTGCCCCCAGGAGGGCTGCAGCCCCACCCAGCAGT      2357
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5042  TTTCTGCCACCCAGCAGGGTTCTGCCCCCAGGAGGGCTGCAGCCCCACCCAGCAGT      5101

Qy  2358  TGCCCCATGCCCTCCTGGCTCCTTCCCTCCAGGATCTTGCAAAGAGGCCCCCTTAGTACC  2417
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5102  TGCCCCATGCCCTCCTGGCTCCTTCCCTCCAGGATCTTCCAAAGAGGCCCCCTTAGTACC  5161

Qy  2418  CTCAAGCCCCTTCTTGGGACAGCCCCCTGCCCCTGCCCCAAAGCAAGCCCCCC        2477
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Db  5162  CTCAAGCCCCTTCTTGGGACAGCCCCCTGCCCCTGCCCCAAAGCAAGCCCCCC        5221

Qy  2478  ATTGGACTCTAAGATGGGGGCTGAGACATCTCTTCCTCCTGGAGGCCAAAACCCGGCCC   2537
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5222  ATTGGACTCTAAGATGGGGGCTGAGACATCTCTTCCTCCTGGAGGCCAAAACCCGGCCC   5281

Qy  2538  CTGCAGTTCCCCAGGTCAGCCTTCCCTGGCTTCCTCCGCGAGCTCTTCCAAGTGAGCTCCCTCAGGGT  2597
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5282  CTGCAGTTCCCCAGGTCAGCCTTCCCTGGCTTCCTCCGCGAGCTCTTCCAAGTGAGCTCCCTCAGGGT  5341

Qy  2598  GGGCTCCTCCTCCCCCAGGTGGGCACCAGAGACCTGGCCGGAGGGCTGGACCCCA       2657
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5342  GGGCTCCTCCTCCCCCAGGTGGGCACCAGAGACCTGGCCGGAGGGCTGGACCCCA       5401
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Qy  2658  GGAGGCTGAGGATCTGTCCGACTCCACACCCACCTTGCAGCGGCCTCAGGAACAGTGAC  2717
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5402  GGAGGCTGAGGATCTGTCCGACTCGTCCACACCCACCTTGCAGCGGCCTCAGGAACAGCAGGGAC  5461

Qy  2718  CATGCGGCAAGTTCTCCCTGGGTGGTCGCGGGGGCTACGCAGCGGGCTTGGCTATGGCAC  2777
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5462  CATGCGGCAAGTTCTCCCTGGGTGGTCGCGGGGGCTACGCAGCGGGCTTGGCTATGGCAC  5521

Qy  2778  CTTTGCCTTGGTGGAGATGCAGGGGGCATGCTGGGGCGCAGGGGGCCCATGTGGGCCAGGAT  2837
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5522  CTTTGCCTTTGGTGGGACGATGCAGGGGGCATGCTGGGGCGCAGGGGGCCCATGTGGGCCAGGAT  5581

Qy  2838  AGCCTGGGGCTGTGTCCCAGTCGAGGAGGAGGAGGGCCAGGGCTGAGTCCCA          2897
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5582  AGCCTGGGGCTGTGTCCCAGTCGAGGAGGAGGAGGGCCAGGGCTGAGTCCCA          5641

Qy  2898  GTCGGAGGAGCAGCAGGGCCAGGGCTGAGAGCCCACTGCCCCAGTGCAGTCAAGGCC     2957
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5642  GTCGGAGGAGCAGCAGGGCCAGGGCTGAGAGCCCACTGCCCCAGTGCAGTCAAGGCC     5701

Qy  2958  TGTGCCTGAGGTCGGCAGGGGCTCCCACCAGGAGGTCTCCAGAGCCCACCCCATGGGAGGA  3017
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5702  TGTGCCTGAGGTCGGCAGGGCTCCCACCAGGAGCTCCCAGAGCCCACCCCATGGGAGGA   5761

Qy  3018  CATCGGGCAGGTCTCCTGGTGCAGATCCGGGACTGTCAGTGATGCCGGAGGCGGCCGA    3077
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5762  CATCGGGCAGGTCTCCTGGTCGGTCGAGATCCGGGACCTGTCAGTGATGCCGGAGGCGGCCGA  5821

Qy  3078  CACAATATCCCTGGACATTTCCGAGGTGGACCCCGGCTCACCTCAACCCTCAGACCTGTA  3137
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5822  CACAATATCCCTGGACATTTCCGAGGTGGACCCCGGCTCACCTCAACCTCTCAGACCTGTA  5881

Qy  3138  CGATATCAAGTACCTCCCATTCCGAGTTTATGATCTTCAGGAAAGTCCCCAAGTCGCGCTCA  3197
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5882  CGTGGACCGCGTCGCTGCTGCGAGAGGCGTCGCCGTGGGCAGGAAGCCAAGTGGTCCTGCCGTC  5941

Qy  3198  GCCAGAGCCGCCCTCCCCATGGCTGGAGGAGGAGGCTGGCCGAGTTCCCGGAGCCCACGTG  3257
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5942  GCCAGAGCCGCCCTCCCCATGGCTGGAGGAGGCTGGCCGAGTTCCCGGAGCCCACGTG    6001

Qy  3258  GCCCTGGCCAGGTGAACTGGGCCCCACGAGGGCCCAGGGAGATCACAGAGGAGTCAGAGGA  3317
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  6002  GCCCTGGCCAGGTGAACTGGGCCCCACGAGGGCCCAGGGAGATCACAGAGGAGTCAGAGGA  6061

Qy  3318  TGTGGAGCGCTGCTGGCAGGAGGGCTGTGCCGTGGCCGTGGCGGTCCTCGGCCGTC     3377
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  6062  TGTGGAGCGCTGCTGGCAGGAGGGCTGCGTGGCCGTGGCGGTCCTCGGCCGTC     6121

Qy  3378  ACGCAGCCTCCTTCCACTTCCCACTTCCCGGAGGCACTGCCGCTGATGAGCCTGCAGAGCTCGGG  3437
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  6122  ACGCAGCCTCCTTCCACTTCCCACTTCCCGGAGGCACTGCCGCTGGATGAGCCTGCAGAGCTCGGG  6181

Qy  3438  GCTGCGTGAGAGAGTGAAGGCTGAAGGCCTGGAGGCACATCTCCGGATCCTGAAGGGGCAGCGCC  3497
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  6182  GCTGCGTGAGAGAGTGAAGGCTGAAGGCCTGGAGGCACATCTCCGGATCCTGAAGGGGCAGCGCC  6241

Qy  3498  GGAAGGTTCTGGAGAAGGGGAAGGGGCCCCCCGAGCGGCCAGAGAAGAGCCAGGCCTTGCTTCCTTCCGGCT  3557
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  6242  GGAAGGTTCTGGAGAAGGGGAAGGGGCCCCCCGAGCGGCCAGAGAAGAGCCAGGCCTTGCTTCCTTCCGGCT  6301

Qy  3558  CTCAGGTCTGAAGAGTGGGGACCTGGAGGCGCCGAGCGCCGACATTCCTAAGGGAGTCTCAGATGAGAC  3617
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  6302  CTCAGGTCTGAAGAGTGGGGACCTGGAGGCGCCGAGCGCCGACATTCCTAAGGGAGTCTCAGATGAGAC  6361

Qy  3618  TGTGGTCCTGGGCCAGTCAGTGACACTGGCCTGCAGCGTGTCAGCCGAGCCAGCCTGCCA  3677
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  6362  TGTGGTCCTGGGCCAGTCAGTGACACTGGCCTGCAGCGTGTCAGCCGAGCCAGCTGCCCA  6421

Qy  3678  GGCCACCTGAGCAAAGACGAGCCCCCTGCCCGTGGAGACGCAGCAGCAGCCGTGTCCTCATCTCTGC  3737
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  6422  GGCCACCTGAGCAAAGACGAGCCCCCTGGAGAGACGCAGCAGCAGCCGTGTCCTCATCTCTGC  6481

Qy  3738  CACCCTCAAGAACTTCTCAGCTTCTGACATCCTGGTGGTGGTGCGCTGGTGACCTGGGTGT  3797
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  6482  (continued)
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Db  6482  CACCCTCAAGAACTTCAGCTTCTGACCATCCTGGTGGTGGCTGAGGACCTGGGTGT  6541
Qy  3798  GTACACCTGCAGCGTGAGCAATGCGCTGGGGACAGTGACCACCACGGCGGTCCTCCGGAA  3857
Db  6542  GTACACCTGCAGCGTGAGCAATGCGCTGGGGACAGTGACCACCACGGCGGTCCTCCGGAA  6601
Qy  3858  GGCAGAGCGCCCCTCATCTCTGCCATGCCCGGATATCGGGGAGTGTACGCGGATGGGGT  3917
Db  6602  GGCAGAGCGCCCCTCATCTTCGCCATGCCCGGATATCGGGGAGGTGTACGCGGATGGGGT  6661
Qy  3918  GCTGCTGGTCTGGAAGCCCGTGGAATCCTGACCTCCTGTGACCTGGCAGTGCAGTGCAG  3977
Db  6662  GCTGCTGGTCTGGAAGCCCGTGGAATCCTGACCCCTGTGACCTACATTGTGCAGTGCAG  6721
Qy  3978  CCTAGAAGGCGGCAGTGACCACCACTGGCCTCCGACATCTTTGACTGCTGCTACCTGAC  4037
Db  6722  CCTAGAAGGCGGCAGTGACCACCACTGGCCTCCGACATCTTTGACTGTGCTACCTGAC  6781
Qy  4038  CAGCAAGTCTCCCGGGGTGGCACTTACACCTTCCGCACGGCATGTGTCAGCAAGGCAGG  4097
Db  6782  CAGCAAGTCTCCCGGGGTGGCACTTACACCTTCCGCACGGCATGTGTCAGCAAGGCAGG  6841
Qy  4098  AATGGGTCCTACAGCAGCACCCCTCGGAGCAGCCCCTCCTGGGGAGGGCCCAGCCACCTGGC  4157
Db  6842  AATGGGTCCTACAGCAGCACCCCTCGGAGCAGCCCCTCCTGGGGAGGGCCCAGCCACCTGGC  6901
Qy  4158  CTCTGAGGAGGAGCCAGGGCCGGTCAGCCCAACCCCTGCCCAGCACACAAAGACCTTCGC  4217
Db  6902  CTCTGAGGAGGAGCCAGGGCCGGTCAGCCCAACCCCTGCCCAGCACACAAAGACCTTCGC  6961
Qy  4218  ATTCCAGACACAGATCCAGAGGGCGCCGCTTCAGCGTGGTCGGCAATGTGGGAGAAGGC  4277
Db  6962  ATTCCAGACACAGATCCAGAGGGCGCCGCTTCAGCGTGGTCGGCAATGTGGGAGAAGGC  7021
Qy  4278  CAGCGGCGGGCGGGCTGCCGCCAAGATCATCCCCTACCACCCCCAAGGACAAGACAGCAGT  4337
Db  7022  CAGCGGCGGGCGGGCTGCCGCCAAGATCATCCCCTACCACCCCCAAGGACAAGACAGCAGT  7081
Qy  4338  GCTGCGGCGAATACGGACGCCCTCAAGGGCGTGCGCCACCGCCAGCTGCACGC  4397
Db  7082  GCTGCGCCAATACGGACGCCCTCAAGGGCCCTGCGCCACCGCCAGCTGCACGC  7141
Qy  4398  AGCCTACCTCAGCCCCGGACCTGTGCTCATCTTGAGCTGTCCTGGGCCCGAGCT  4457
Db  7142  AGCCTACCTCAGCCCCGGACCCCCGGCCACCTGGTCGCTCATCTTGGACGTGCTCTCGGGCCCCGACT  7201
Qy  4458  GCTCCCCTGCCCTGGCCGGAGAGGCGCCCCTACTCAGAATCTGAGGTGAAGGACTACCTGTG  4517
Db  7202  GCTCCCCTGCCCTGGCCGGAGAGGCCCTCCTACTCAGAATCCGAGGTGAAGGACTACCTGTG  7261
Qy  4518  GCAGATGTTGAGTGCCACCCAGTACCTGCACAACCAGCACATCCTGACCTGACCTGAG  4577
Db  7262  GCAGATGTGAGTGCCACCCAGTACCTGCACAACCAGCACATCCTGCACCTGACCTGAG  7321
Qy  4578  GTCCGAGAACATGATCATCACCGAATACAACCTGCTCAAGGTCGTGCAATGC  4637
Db  7322  GTCCGAGAACATGATCATCACCGAATACAACCTGCTCAAGGTCGTGCAATGC  7381
Qy  4638  ACAGAGCCTCAGCCAGCAGGAGAAGGTGCTGCCCTCAGACAAGTTCAAGACTACCTAGAGAC  4697
Db  7382  ACAGAGCCTCAGCCAGCAGGAGAAGGTGCTGCCCTCAGACAAGTTCAAGGACTACCTAGAGAC  7441
Qy  4698  CATGGCTCCAGAGCTCCTGGACGGGCCAGGGGCGCTGTTCCACAGACAGCATCTGGGCCAT  4757
Db  7442  CATGGCTCCAGAGCTCCTGGACGGGCCAGGGGCGCTGTTCCACAGCAGCACAGCATCTGGGCCAT  7501
Qy  4758  CGGTGTGACAGCCTTCATCATGCTGAGCGCCGAGTACCCGGTGAGCGAGCGGAGGGTGCACG  4817
Db  7502  CGGTGTGACAGCCTTCATCATGCTGAGCGCCGAGTACCCGGTGAGCGAGCAGGTGCCACG  7561
Qy  4818  CGACCTGCAGAGGACTGCGCAAGGGCTGGTCCGGCTGAGCCGCTGCTACGCGCGGGGCT  4877

Db  7562  CGACCTGCAGAGGACTGCGCAAGGGCTGGTCCGGCTGAGCCGCTGCTACGCGGGGCT  7621
Qy  4878  GTCCGGCGGGCGCCCGTGGGCCTTCGTGCGCGAGCACTCTGTGCGGCCGGCCCGGGCCCGGCC  4937
Db  7622  GTCCGGGGGGCGCCCGTGGCCTTCCTGCGCGAGCACTCTGTGCGGCCGGCCCGGGCCCGGCC  7681
Qy  4938  CTGCGCGTCCAGTGCCTCGAGTGCCCGGCCTAACAGAGGAGGGCCGCCTGTTCGCG  4997
Db  7682  CTGCGCGTCCAGTGCCTGCGCAGTGCCCGGCCTAACAGAGGAGGGCCCGGCCTGTTCGCG  7741
Qy  4998  GCCCGGCCCGTGACCTTCCCTACCGCGGCGGCGTGCGCGGGCTGCGGGTCTTCGTGCGGCAATCGCGAGAA  5057
Db  7742  GCCCCGGCCCGTGACCTTCCCTACCGCGGCGGCGTGCGCGGGCTGCGGGTCTTCGTGCGGCAATCGCGAGAA  7801
Qy  5058  GAGACGCGGCGCTGCGTACAGAGAGCCACAACCTGGCCCAGGTGCGCGTGAGGGTCGCCCCG  5117
Db  7802  GAGACGCGGCGCTGCTGTACAAGAGGCAACCTGGCCCAGGTGCGCGTGAGGGTCGCCCCG  7861
Qy  5118  GCCACACCCTTGGTCTCCCCGCTGGGGTCGCTGCAGACGCGGCGCCAATAAAACGCACAGC  5177
Db  7862  GCCACACCCCTTGGTCTCCCCGCTGGGGGTCGCTGCAGACGCGGCGCCAATAAAAACGCACAGC  7921
Qy  5178  CGGGCGA  5184
Db  7922  CGGGCGA  7928

RESULT 8
AAH46904
ID  AAH46904 standard; cDNA; 4936 BP.
XX
AC  AAH46904;
XX
DT  25-SEP-2001  (first entry)
XX
DE  cDNA encoding human protein kinase SGK145.
XX
KW  Protein kinase; enzyme; cytostatic; nootropic; neuroprotective; human;
KW  antiparkinsonian; virucide; antibacterial; antifungal; antimigraine;
KW  analgesic; hypotensive; hypertensive; immunosuppressive; antiallergic;
KW  antipsoriatic; antirheumatic; antiarthritic; ophthalmological; anorectic;
KW  osteopathic; thrombolytic; antiarteriosclerotic; antiasthmatic;
KW  vasotropic; antidiabetic; gene therapy; ss.
XX
OS  Homo sapiens.
XX
FH  Key           Location/Qualifiers
FT  CDS           1..4851
FT                /*tag= a
XX
PN  WO200155356-A2.
XX
PD  02-AUG-2001.
XX
PF  25-JAN-2001; 2001WO-US002337.
XX
PR  25-JAN-2000; 2000US-0178078P.
PR  31-JAN-2000; 2000US-0179364P.
PR  17-FEB-2000; 2000US-0183173P.
PR  17-MAR-2000; 2000US-0190162P.
PR  29-MAR-2000; 2000US-0193404P.
PR  13-NOV-2000; 2000US-0247013P.
XX
PA  (SUGE-) SUGEN INC.
XX
PI  Plowman G, Whyte D, Manning G, Sudarsanam S, Martinez R;
XX
DR  WPI; 2001-476202/51.
DR  P-PSDB; AAB85504.
XX
PT  Kinase polypeptides useful for treating cancers, Alzheimer's disease,
PT  viral infections, diabetes, obesity, organ transplant rejection and
PT  rheumatoid arthritis.

```
XX
PS  Example 1: Page 204-205; 218pp; English.
XX
CC  The invention provides human protein kinases and protein kinase-like
CC  enzymes and polynucleotides encoding the polypeptides. The kinase
CC  polypeptides and their modulators are useful for treating a disease or
CC  disorder such as cancer, immune-related diseases, cardiovascular disease,
CC  brain or neuronal-associated disease and metabolic disorders, including
CC  cancers of tissues, cancers of hematopoietic origin, diseases of the
CC  central nervous system, diseases of the peripheral nervous system,
CC  Alzheimer's disease, Parkinson's disease, multiple sclerosis, amyotrophic
CC  lateral sclerosis, viral infections, infections caused by prions,
CC  bacteria and fungi, ocular diseases, migraines, pain, sexual dysfunction,
CC  mood disorders, attention disorders, cognition disorders, hypotension,
CC  hypertension, psychotic disorders, neurological disorders, dyskinesias,
CC  metabolic disorders, and organ transplant rejection. They are also useful
CC  for treating rhinitis, autoimmunity, atherosclerosis, psoriasis,
CC  osteoarthritis, asthma, chronic inflammatory pelvic disease, chronic
CC  inflammatory bowel disease, rheumatoid arthritis, metabolic disorders
CC  such as diabetes, obesity, cardiovascular diseases such as reperfusion
CC  injury, coronary thrombosis, clotting disorders and atherosclerosis,
CC  ocular diseases such as glaucoma, retinopathy and macular degeneration,
CC  psychiatric and neurological disorders such as anxiety, schizophrenia,
CC  dementia, manic depression, etc. The polynucleotides are useful in gene
CC  therapy techniques to treat the above mentioned disorders. Sequences
CC  AAH46891-46922 represent human protein kinases encoding cDNA molecules
XX
SQ  Sequence 4936 BP; 923 A; 1695 C; 1524 G; 794 T; 0 U; 0 Other;

Query Match         93.8%;   Score 4885.2;   DB 4;   Length 4935;
Best Local Similarity    99.6%;   Pred. No. 0;
Matches 4915;   Conservative  0;  Mismatches  0; Indels 18; Gaps  1;

Qy   268 CCATCCATGCAGAGTAACCATCGAGGATGTGCAGGCACAGACAGGCGAACGGCCAATTC 327
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 CCATCCATGCAGAGTAACCATCGAGGATGTGCAGGCACAGACAGGCGAACGGCCAATTC 60

Qy   328 GAGGCTATCATTGAGGGCGACCACCAGCCCTCGGTGACCTGGTACAAGGACAGCGTCCAG 387
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 GAGGCTATCATTGAGGGCGACCACCAGCCCTCGGTGACCTGGTACAAGGACAGCGTCCAG 120

Qy   388 CTGGTGACAGCACCCGGCTTAGCCAGCAGCAAGAAGGCACCACCATACTCCCTGGTGCTG 447
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 CTGGTGACAGCACCCGGCTTAGCCAGCAGCAAGAAGGCACCACCATACTCCCTGGTGCTG 180

Qy   448 AGGCATGTGGCCTCGAAGGATGCGGGCGTTTACACCTGGTCGGCCAAAACACTGGTGGC 507
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 AGGCATGTGGCCTCGAAGGATGCGGGCGTTTACACCTGGTCGGCCAAAACACTGGTGGC 240

Qy   508 CAGGTGCTCTGCAAGGCAGAGCTGCTGGTGCTTGGG-----------GGGGAC 549
         ||||||||||||||||||||||||||||||||||||            ||||||
Db   241 CAGGTGCTCTGCAAGGCAGAGCTGCTGGTGGTCTTGGGGCTTGGGCCGCTTCCACTCCTTAGGGGAC 300

Qy   550 AATGAGCCGGACTCAGAGAGCAAAGCCACCGGAGGAAGCTGCACTCCTTCTTATGAGGTC 609
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 AATGAGCCGGACTCAGAGAGCAAAGCCACCGGAGGAAGCTGCACTCCTTCTTATGAGGTC 360

Qy   610 AAGGAGGAGATTGGAAGGGGCGTGTTTGGCTTCGTAAAAAGAGTGCAGCACAAAGGAAAC 669
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 AAGGAGGAGATTGGAAGGGGCGTGTTTGGCTTCGTAAAAAGAGTGCAGCACAAAGGAAAC 420

Qy   670 AAGATCTTGTGCGCCTGCCAAGTTCATCCCCTACGGAGCAGAACTCGGGCCCAGGCATAC 729
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 AAGATCTTGTGCGCCTGCCAAGTTCATCCCCTACGGAGCAGAACTCGGGCCCAGGCATAC 480

Qy   730 AGGGAGCGAGACATCCTGGCCACCCGCTGGTCACGGGGGCTGCTGGACCAG 789
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 AGGGAGCGAGACATCCTGGCCACCCGCTGGTCACGGGGGCTGCTGGACCAG 540

Qy   790 TTTGAGACCCCGCAAGACCCTCATCCTCATCCTCGAGACCTGTGCTCATCCGAGGAGCTGCTG 849
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 TTTGAGACCCCGCAAGACCCTCATCCTCATCCTCGAGACCTGTGCTCATCCGAGGAGCTGCTG 600

Qy   850 GACCGGCCTGTACAGGAAGGGCGGTGGTGGTGACGGAGGCCCGAGGTCAGGTCAAGGTCTACATCCAGCAG 909
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 GACCGGCCTGTACAGGAAGGGCGGTGGTGGTGACGGAGGCCCGAGGTCAGGTCAAGGTCTACATCCAGCAG 660

Qy   910 CTGGTGGAGGGCTGCACTACCTGCACAGCCATGGCGTTCTCCACCTGGACATAAAGCCC 969
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 CTGGTGGAGGGCTGCACTACCTGCACAGCCATGGCGTTCTCCACCTGGACATAAAGCCC 720

Qy   970 TCTAACATCCTGATGGTGCATCCTGCCCGGAAGACATTAAAATCTGCGACTTTGGCTTT 1029
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 TCTAACATCCTGATGGTGCATCCTGCCCGGAAGACATTAAAATCTGCGACTTTGGCTTT 780

Qy  1030 GCCCAGAACATCACCCAGCAGAGCTGCAGTTCAGCCAGTACGGCTCCCTGAGTTCGTC 1089
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 GCCCAGAACATCACCCAGCAGAGCTGCAGTTCAGCCAGTACGGCTCCCTGAGTTCGTC 840

Qy  1090 TCCCCGATCATCCAGCAGAACCCTGAGCGAAGCCTCCGACATTGGGCATGGT 1149
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 TCCCCGAGATCATCCAGCAGAACCCTGAGCGAAGCCTCCGACACATTGGGCCATGGT 900

Qy  1150 GTCATCTCCTACCTGCTCATCCCCATTGCGGGAGAGTGACCGTGCC 1209
         |||||||||||||||||||||||||||||||||||||||||||||
Db   901 GTCATCTCCTACCTGCTCATCCCCATTGCCGGCGAGAGTGACCGTGCC 960

Qy  1210 ACCCTCCTGAACGTCCTGGAGGGGCGCGTGTCATGGAGCAGCCCATGGCTGCCCACCTC 1269
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 ACCCTTCTGAACGTCCTGGAGGGGCGCGTGTCATGGAGCAGCCCATGGCTGCCCACCTC 1020

Qy  1270 AGCGAAGAGCGCCAAAGACTTCATCAAGGTAGGCTGCAGAGAGCCCGCTCAGGCCCGCCT 1329
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021 AGCGAAGAGCGCCAAAGACTTCATCAAGGTAGGCTGCAGAGAGCCCGCTCAGGCCCGCCT 1080

Qy  1330 AGTGGCGGCCCAGTGCCTCTCCCACCCTGGTTCCTGGAAATCCATGCTGCCGGAGGAGGCC 1389
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1081 AGTGGCGGCCCAGTGCCTCTCCCACCCTGGTTCCTGAAATCCATGCTGCCGGAGGAGGCC 1140

Qy  1390 CACTTCATCAACACCAAGAGCTCAAGTTCCTCCTGCTCGCTGGCAGCGTTCC 1449
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1141 CACTTCATCAACACCAAGAGCTCAAGTTCCTCCTGCTCGCTGGCAGCGTTCC 1200

Qy  1450 CTGATGAGCTACAAGTCCATCCTGGTGATGCCCGGCTCCATCCCTGGTGCTCGCGGGGCCCA 1509
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1201 CTGATGAGCTACAAGTCCATCCTGGTGATGCCCGGCTCCATCCCTGAGTCTCGCGGGGCCCA 1260

Qy  1510 CCCGACAGCCCCTCCCTCCGCGTAGCCCGGCCACCTCTGCAGGGACACTGGTGGCTCCTCC 1569
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1261 CCCGACAGCCCCTCCCTCCGCGTAGCCCGGCCACCTCTGCAGGGACACTGGTGGCTCCTCC 1320

Qy  1570 AGTTCCTCCTCCTCTGACACACTCACCACTGTGCCCGGGCTAAGTCACTGCCA 1629
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1321 AGTTCCTCCTCCTCTGACACACTCACCACTGTGCCCGGGCTAAGTCACTGCCA 1380

Qy  1630 CCCTCCCCGTGCACACTCACCACTGTGCCCGGGCTTCCTGCGCGGCCCTCGGCC 1689
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1381 CCCTCCCCGGTGACACACTTCACCACTGTGCCCGGGCTTCCTGCGCGGCCCTCGCGC 1440

Qy  1690 AGCGTGCTGAGGAAGCCGAGGCCAGTGAGCCGGCAGTGAGCGTCCGCCTCCGGCCCTGCA 1749
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1441 AGCGTGCTGAGGAAGCCGAGGCCAGTGAGCCGGCAGTGAGCGTCCGCCTCCGGCCCTGCA 1500

Qy  1750 TCTCCCGAGGGTGCCGGGCTCCACCGGGGGTGAGGCGTGCGTGCCCGGCACAGCCGTCATC 1809
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1501 TCTCCCGAGGGTGCCGGGCTCCACCGGGGGTGAGGCGTGCGTGCCCGGCACAGCCGTCATC 1560

Qy  1810 CGCAGCCTGTTCTCACCACCCGGGCCCTGAGGGTGAGCTGCTGGACCAG 1869
         |||||||||||||||||||||||||||||||||||||||||||||||||
Db  1561 CGCAGCCTGTTCTCACCACCCGGGCCCTGAGCGGTGAGCTGCTGGACCAG 1620

Qy  1870 AGCAGGCGGCACCCGGCCCCGGCGGCGCGGGCTACATTGCGGGGGCG 1929
         |||||||||||||||||||||||||||||||||||||||||||||||
Db  1621 AGCAGGCGGCACCCGGCCCCGGCGGCGGTACATTGCGGGGGCG 1680

Qy  1930 CTGCCAGGGCTGCCGAGCCACTGATGGAGCACCGCGTGCTGCTGGAGGAGGCCGGCCGCCAGG 1989
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Db  2761 TGGGAGGACATCGGGCAGGTCTCCCTGGTGCAGATCCGGCACCTGTCAGTGATGCGGAG 2820
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3070 GCGGCGACCACAATATCCCTGGACAATTCCGAGTGGACCCCGCTCACCTCAACCTCTCA 3129
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2821 GCGGCGACACACAATATCCCTGGACAATTCCGAGTGGACCCCGCTCACCTCAACCTCTCA 2880
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3130 GACCTGTACGATATCAAGTACCTCCATTCCGAGTTTATGATCTTCAGGAAAGTCCCCAAG 3189
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2881 GACCTGTACGATATCAAGTACCTCCATTCCGAGTTTATGATCTTCAGGAAAGTCCCCAAG 2940
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3190 TCCGCTCAGCCAGACGCCGCCCTCCCCCATGGCTGAGGAGGACGTTGGCCGAGTTCCCGGAG 3249
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2941 TCCGCTCAGCCAGACGCCGCCCTCCCCCATGGCTGAGGAGGACGTTGGCCGAGTTCCCGGAG 3000
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3250 CCCACGTGGCCCTGGCCAGGTGAACTGGGCCCCACGCAGGCCTGGAGATCACAGAGGAG 3309
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3001 CCCACGTGGCCCTGGCCAGGTGAACTGGGCCCCACGCAGGCCTGGAGATCACAGAGGAG 3060
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3310 TCAGAGGATGTTGGACGCGCTGCTGGCAGAGGCTGCCGTGGGCAGGAGCGCAAGTGGTCC 3369
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3061 TCAGAGGATGTGGACGGCGTGCTGGCAGAGGCTGCCGTGGGCAGGAGCGCAAGTGGTCC 3120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3370 TCGCCGTCAGCGAGCTCTTCCACTTCCCTGGGAGGCACCTGCGCTGATGAGCCTGCA 3429
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3121 TCGCCGTCACGCAGCCTCTTCCACTTCCCTGGGAGGCACCTGCGCTGATGAGCCTGCA 3180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3430 GAGCTGGGGCTGCGTGGAGAGTGAAGGCTCCGTGGAGCACATCTCCCGGATCCTGAAG 3489
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3181 GAGCTGGGGCTGCGTGAGAGAGTGAAGGCTCCGTGGAGCACATCTCCCGGATCCTGAAG 3240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3490 GGCAGGCCGAAGGTCTGAGAAGAGAGGGCCCCCAGGAAGAAGAGCCAGGCCTTGCTTCC 3549
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3241 GGCAGGCCGAAGGTCTGAGAAGAGAGGGCCCCCAGGAAGAAGAGCCAGGCCTTGCTTCC 3300
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3550 TTCGGCTCTCAGGTCTGAAGAGTCCTGGGACACCGGACGAGCGCCCGACATTCCTAAGGAGCTCTCA 3609
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3301 TTCCGGCTCTCAGGTCTGAAGAGTCCTGGGACACCGGACGAGCGCCGACACATTCCTAAGGAGCTCTCA 3360
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3610 GATGAGACTGTGGTCCTGGGCCAGTCAGTGACTCGACACTGGCCTGCCCTGTGTCCTC 3669
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3361 GATGAGACTGTGGTCCTGGGCCAGTCAGTGACTCGACACTGGCCTGCCCTGTGTCCTC 3420
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3670 GCTGCCCAGGCCACCTGGAGAAGACGGAGCCCCCCTCGGAGAGCAGCAGCCCGTGTCCTC 3729
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3421 GCTGCCCAGGCCACCTGGAGAAAGACGGAGCCCCCCTCGGAGAGCAGCAGCCCGTGTCCTC 3480
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3730 ATCTTCTGCCACCCTCAAGAGACTTCCAGCTTCTGACCATCCTGGTGGTGGCTGAGGAC 3789
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3481 ATCTTCTGCCACCCTCAAGAGACTTCCAGCTTCTGACCATCCTGGTGGTGGCTGAGGAC 3540
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3790 CTGGGTGTGTACACCTGCAGCGTGAGCAATGCGCTGGGACAGTGACCACCGGGCGTC 3849
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3541 CTGGGTGTGTACACCTGCAGCGTGAGCAATGCGCTGGGACAGTGACCACCGGGCGTC 3600
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3850 CTCCGAAGGCAGAGCGCCCTCATCTTCGCCATGCCCGGATATCGGGGAGTGTACGCG 3909
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3910 GATGGGGTGCTGCTTGGAAGTCTCACGGCCCGTGGAATCCTACGGCCTACCACTGTG 3969
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3661 GATGGGGTGCTGCTGGTCTGGAAGCCCGTGGAATCCTACGGCCTACCACTGTG 3720
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3970 CAGTGCAGCCTAGAAGGCGGCAGCTGGACCACACTGGACTGCTGC 4029
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3721 CAGTGCAGCCTAGAAGGCGGCAGCTGGACCACACTGGACTGCTGC 3780
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4030 TACCTGACCAGCAGCAAGCTCTTCCCGGGTGCACCTTCGCACGGCATGTGTCAGC 4089
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3781 TACCTGACCAGCAGCAAGCTCTTCACACCTTCGCACGGCATGTGTCAGC 3840
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  4090 AAGGCAGGAATGGGTCCCATACAGCACCCCGGAGCAAGTCTTCCTGGGAGGGCCCCAGC 4149
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3841 AAGGCAGGAATGGGTCCCATACAGCACCCCGGAGCAAGTCTTCCTGGGAGGGCCCCAGC 3900
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Db  1681 CTGCCAGGCCTGCGCGAGCCACTGGAGCACCGCGTGCTGAGGAGGAGGCCGCCAGG 1740
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1990 GAGGAGCAGGCCACCCTCCTGCCCAAAGCCCCTCATTCGAGACTGCCCTCCGGCTGCCT 2049
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1741 GAGGAGCAGGCCACCCTCCTGCCCAAAGCCCCTCATTCGAGACTGCCCTCCGGCTGCCT 1800
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2050 GCCTCTGCACCCACTTGGCCCCTGGCCACAGCCACTCCCTGGAACATGGACTTCCGGAGC 2109
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1801 GCCTCTGCACCCACTTGGCCCCTGGCCACAGCCACTCCCTGGAACATGACTCTCCGGAC 1860
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2110 ACCCCCGCCCCTCCTCGGAGGCTGCGGTGAGGACAGCGACTGCCTTCAGCCCCCTCC 2169
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1861 ACCCCCGCCCCTCCTCGGAGGCTGCGGTGAGGACAGCGACTGCCTTCAGCCCCCTCC 1920
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2170 GGGGGGCCCTATCAGGGACATGGGGCTCCAGGGCTTCAAGCAGCTTCATCACT 2229
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1921 GGGGGGCCCTATCAGGGACATGGGGCTCCAGGGCTTCAAGCAGCTTCATCCACT 1980
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2230 GGTGGCCACCCGACTGCTCAGCAGAGGCCATCCCGGACGCCCTTGGGGGAG 2289
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1981 GGTGGCCACCCGACTGCTCAGCAGAGGCCATCCCGGACAGCCCTTGGGGGCAG 2040
         |||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2290 CCAGCCCCTTTCTGCACCCCAAGCAGGGTTCTGCCCCCCAGGAGGGGCTGCAGCCCCAC 2349
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2041 CCAGCCCCTTTCTGCACCCCAAGCAGGGTTCTGCCCCCCAGGAGGGGCTGCAGCCCCCAC 2100
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2350 CCAGCAGTTGCCCATGCCCTGCCTCCTCCCTGGATCTTGCAAAGAGGCCCCC 2409
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2101 CCAGCAGTTGCCCCATGCCCTGCCTCCTCCCTGGATCTTGCAAAGAGGCCCCC 2160
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2410 TTAGTACCCTCAAGCCCCTTCTTGGGACAGCCCAGGCACCCCCTGCCCAAAGCA 2469
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2161 TTAGTACCCTCAAGCCCCTTCTTGGGACAGCCCAGGCACCCCCTGCCCAAAGCA 2220
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2470 AGCCCCCCATTGGACTCTAAGATGGGCCTGGAGACATCTCTTCCTCCTGGGAGGCCAAAA 2529
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2221 AGCCCCCCATTGGACTCTAAGATGGGCCTGGAGACATCTCTTCCTCCTGGGAGGCCAAAA 2280
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2530 CCCGGCCCCTGCAGTTCCCCCAGGGTCAGCCTCAGCGAGCTCTTCCCAAGTGAGCTCC 2589
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2281 CCCGGCCCCTGCAGTTCCCCCAGGGTCAGCCTCAGCGAGCTCTTCCCAAGTGAGCTCC 2340
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2590 CTCAGGTGGGGCTCCTCCCAGGTGGGCACAGAGCCTGGGGCCCCTGGCCCTGGCGATGCGGAGGGC 2649
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2341 CTCAGGGTGGGGCTCCTCCCAGGTGGGCACAGAGCCTGGGGCCCCTGGCCCTGGCGATGCGGAGGGC 2400
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2650 TGGACCCAGGAGGCTGGAGGATCGTCCGACTCCACACCCACCTTGCAGGGCCTCAGGAA 2709
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2401 TGGACCCAGGAGGCTGAGGATCGTCCGACTCCACACCCACCTTGCAGGGCCTCAGGAA 2460
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2710 CAGTGACCATGCGCAAGTTCTCCCTGGGTGGTCGCGGGGGCTACGCAGGCGTGGCTCGC 2769
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2461 CAGGCGACCATGCGCAAGTTCTCCCTGGGTGGTCGCGGGGGCTACGCAGGCGTGGCTGC 2520
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2770 TATGGCACCTTTGCCTTTGGTGGAGATGCAGGGGGCATGCTGGGGGCAGGGGCCATGTGG 2829
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2521 TATGGCACCTTTGCCTTTGGTGGAGATGCAGGGGGCATGCTGGGGGCAGGGGCCCATGTGG 2580
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2830 GCCAGGATAGCCTGGGCTGTGTCCCAGTCGGAGGAGGAGGAGGAGAGGCCAGGGCT 2889
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2581 GCCAGGATAGCCTGGGCTGTGTCCCAGTCGGAGGAGGAGCAGGAGGAGGAGGCCAGGGCT 2640
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2890 GAGTCCCAGTCGGAGGAGCAGGAGGCCAGGGCTGAGAGCCCACTGCCCCAGGTCAGT 2949
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2641 GAGTCCCAGTCGGAGGAGCAGGAGGCCAGGGCTGAGAGCCCACTGCCCCAGGTCAGT 2700
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  2950 GCAAGGCCGTGCTGCTCGGGTCGGCCAGGTCTCGGCCAGGAGCTCTTCCAGAGCCCACCCA 3009
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2701 GCAAGGCCGTGCTGCTCGGGTCGGCCAGGTCTCCCAGGAGCTCTTCCAGAGCCCACCCCA 2760
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  3010 TGGGAGGACATCGGGCAGGTCTCCCTGGTGCAGATCCGGCACCTGTCAGTGATGCGGAG 3069
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

RESULT 9
AAC62285
ID   AAC62285 standard; cDNA; 4175 BP.
XX
AC   AAC62285;
XX
DT   19-MAR-2001  (first entry)
XX
DE   cDNA encoding a human signal transduction polypeptide.
XX
KW   Signal transduction; H19G5; kinase; cardiac disease; angina pectoris;
KW   congestive heart failure; dilated congestive cardiomyopathy;
KW   hypertrophic cardiomyopathy; restrictive cardiomyopathy; hypertension;
KW   mitral valve disease; aortic valve disease; tricuspid valve disease;
KW   myocardial infarction; cardiac arrhythmia; arteriosclerosis;
KW   atherosclerosis; cardiac tumour; microbial infection; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..4056
FT                   /tag= a
FT                   /product= "signal transduction polypeptide H19G5"
XX
PN   WO20006381-A1.
XX
PD   26-OCT-2000.
XX
PF   11-APR-2000; 2000WO-US009488.
XX
PR   16-APR-1999;  99US-0129553P.
XX
PA   (SCIO-) SCIOS INC.
XX
PI   Zeng W,  Stanton L,  Kong H;
XX
DR   WPI; 2001-007013/01.
DR   P-PSDB; AAB30567.
XX
PT   Novel h19G5 polypeptides capable of regulating signal transduction and
PT   exhibiting kinase activity useful for identifying antibodies to treat
PT   cardiac diseases, and additional mediators of signal transduction.
XX
PS   Claim 4; Page 57-59; 81pp; English.
XX
CC   The present sequence encodes a human protein with putative function in
CC   signal transduction. The polypeptide is designated H19G5. The protein is
CC   capable of regulating signal transduction and exhibits kinase activity.
CC   The H19G5 transcript is expressed in the heart. H19G5 polypeptides and
CC   polynucleotides are useful for preventing or treating a cardiac disease,
CC   such as congestive heart failure, dilated congestive cardiomyopathy,
CC   hypertrophic cardiomyopathy, restrictive cardiomyopathy, mitral valve
CC   disease, aortic valve disease or tricuspid valve disease, angina
CC   pectoris, myocardial infarction, cardiac arrhythmia, pulmonary, arterial
CC   or rhenovascular hypertension, arteriosclerosis, atherosclerosis and
CC   cardiac tumours in humans. The polypeptide is also useful for detecting
CC   the expression of a protein capable of regulating signal transduction or
CC   the expression of a protein capable of acting as a donor or acceptor
CC   molecule of a phosphate group. The monoclonal antibodies can be used as
CC   probes for detecting discrete antigens expressed by tissue or cell
CC   samples, and therefore used in humans for localization and monitoring of
CC   microbial infection
XX
SQ   Sequence 4175 BP; 778 A; 1459 C; 1283 G; 655 T; 0 U; 0 Other;

Query Match             79.6%;  Score 4146.6;  DB 5;  Length 4175;
Best Local Similarity   99.9%;  Pred. No. 0;
Matches 4149;  Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy    1055 TGCAGTTCAGCCAGTACGGCTCCCCCGAGTTCGTCTCCCCCGAGATCATCCAGCAGAACC 1114
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5 TGCAGTTCAGCCAGTACGGCTCCCCCGAGTTCGTCTCCCCCGAGATCATCCAGCAGAACC 64

Qy    4150 CACCCTGCCCTCTGAGGAGGAGGAGGCCCAGGGGCGGTCAGCCCAGCACCCCTGCCCAGCACAAAG 4209
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3901 CACCCTGGCCCTCTGAGGAGGAGGAGGCCCAGGGGCGGTCAGCCCAGCACCCCTGCCCAGCACAAAG 3960

Qy    4210 ACCTTCGCATTCCAGACACAGATCCAGAGGGGCCGCTTCAGCCGTGGTGCGGCAATGCTGG 4269
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3961 ACCTTCGCATTCCAGACACAGATCCAGAGGGGCCGCTTCAGCCGTGGTGCGGCAATGCTGG 4020

Qy    4270 GAGAAGGCCAGCGGCGGCGGCGGCGGCTGCCGCCAAGATCATCCCTACCACCCCAAGGACAAG 4329
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4021 GAGAAGGCCAGCGGCGGCGGCGGCGGCTGCCGCCAAGATCATCCCTACCACCCCAAGGACAAG 4080

Qy    4330 ACAGCAGTGCTGCGGAATACGAGGCCCTCAAGGGCCTGGCCACCCGCACCTGGCCCAG 4389
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4081 ACAGCAGTGCTGCGGAATACGAGGCCCTCAAGGGCCTGGCCACCCGCACCTGGCCCAG 4140

Qy    4390 CTGCACGCAGCTACCTCAGCCCCCGGCACCTGGTGCTCATCTTGGAGCTGTGCTCTGGG 4449
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4141 CTGCACGCAGCTACCTCAGCCCCCGGCACCTGGTGCTCATCTTGGAGCTGTGCTCTGGG 4200

Qy    4450 CCCGAGCTGCTCCCCCTGCCTGGCCGAGAGGGCCTTCCTACTTCAGAATCTGAGTGAAGGAC 4509
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4201 CCCGAGCTGCTCCCCCTGCCTGGCCGAGAGGGCCTTCCTACTTCAGAATCCGAGTGAAGGAC 4260

Qy    4510 TACCTGTGGCAGATGTTGAGTGCCACCCAGTACCTGACAACCAGCACATCCTGCGACCTG 4569
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4261 TACCTGTGGCAGATGTTGAGTGCCACCCAGTACCTGACAACCAGCACATCCTGCGACCTG 4320

Qy    4570 GACCTGAGGTCCGAGAACATGATCATCACCGAATACACCTGCTCAAGGTCGTGGACCTG 4629
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4321 GACCTGAGGTCCGAGAACATGATCATCACCGAATACACCTGCTCAAGGTCGTGGACCTG 4380

Qy    4630 GGCAATGCACAGAGCCTCAGCCAGGAGAAGGTGCTGCCCTCAGACAAGTTCAAGGACTAC 4689
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4381 GGCAATGCACAGAGCCTCAGCCAGGAGAAGGTGCTGCCCTCAGACAAGTTCAAGGACTAC 4440

Qy    4690 CTAGAGACCATGGCTCCCAGAGCTTCCAGAGCTCCTGAGGGGCTGTTCCACAGACAGACATC 4749
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4441 CTAGAGACCATGGCTCCCAGAGCTTCCAGAGCTCCTGAGGGGCTGTTCCACAGACAGACATC 4500

Qy    4750 TGGGCCATCGGTGTGACAGCCTTCATCATGTCTGAGCGCCGAGTACCCGGTGAGCAGGCGAG 4809
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4501 TGGGCCATCGGTGTGACAGCCTTCATCATGTCTGAGCGCCGAGTACCCGGTGAGCAGGCGAG 4560

Qy    4810 GGTGCAGCGCGACCTGCAGAGAGACTGCCAAGGGGCTGGTCCGGCTGAGCCGTGCTCTAC 4869
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4561 GGTGCAGCGCGACCTGCAGAGAGACTGCCAAGGGGCTGGTCCGGCTGAGCCGTGCTCTAC 4620

Qy    4870 GCGGGGCTGTCCGGGGGGCGCGCGTGGCCTTCCTGCGCACTCGTGTCGCGCCCCTGG 4929
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4621 GCGGGGCTGTCCGGGGGGCGCGCGTGGCCTTCCTGCGCACTCGTGTCGCGCCCCTGG 4680

Qy    4930 GGCCCGGCCCTGCGCGTCCAGCTGCCTGCAGTGCCCGTGGCTAACAGAGGAGGGCCCGGCC 4989
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4681 GGCCCGGCCCTGCGCGTCCAGCTGCCTGCAGTGCCCGTGGCTAACAGAGGAGGGCCCGGCC 4740

Qy    4990 TGTTCGGCGGCCGGCCCGTGACCTTCCCTACCGGCGGCGTCTTCGTGCCGCAAT 5049
            |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4741 TGTTCCGGCGCCCCGGCCCGTGACCTTCCCTACCGGCGGCGTCTTCGTGCCGCAAT 4800

Qy    5050 CGCGAGAAGAGACGCGGCGGCGTGCTTGCTGTACAAGAGGCACAACCTGGCCCAGGTGCGCTGAGGG 5109
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4801 CGCGAGAAGAGACGCGGCGGCGTGCTTGCTGTACAAGAGGCACAACCTGGCCCAGGTGCGCTGAGGG 4860

Qy    5110 TCGCCCCGGCCACACCCTTGGTCTCCCCCGCTGGGGTGCTCGCAGACGCGGCCAATAAAAG 5169
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4861 TCGCCCCGGCCACACCCTTGGTCTCCCCCGCTGGGGTGCTCGCAGACGCGGCCAATAAAAA 4920

Qy    5170 CGCACAGCCGGGCGAG 5185
            ||||||||||||||||
Db    4921 CGCACAGCCGGGCGAG 4936

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Qy  1115  CTGTGAGCGAAGCCTCCGACATTTGGCCATGGGTGTCATCTCCTACCTCAGCCTGACCT  1174
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    65  CTGTGAGCGAAGCCTCCGACATTTGGCCATGGGTGTCATCTCCTACCTCAGCCTGACCT   124

Qy  1175  GCTCATCCCATTGCCGGCGAGAGTGACCGTGCCACCTCCTGAACGTCCTGGAGGGGC  1234
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   125  GCTCATCCCATTGCCGGCGAGAGTGACCGTGCCACCTCCTGAACGTCCTGGAGGGGC   184

Qy  1235  GGGTGTCATGGAGCAGCCCATGGCCGGCTGCCCACCTCAGCGAAGACGCCAAAGACTTCATCA  1294
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   185  GGGTGTCATGGAGCAGCCCATGGCCGGCTGCCCACCTCAGCGAAGACGCCAAAGACTTCATCA   244

Qy  1295  AGGCTACGCTGCAGAGAGCCCCTCAGGCCCGGCTAGTGCGGCCCAGTGCCTCTCCCACC  1354
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   245  AGGCTAGCTGCAGAGAGCCCCTCAGGCCCGGCTAGTGCGGCCCAGTGCCTCTCCCACC   304

Qy  1355  CCTGGGTTCCTGAAATCCATGGCTGCGGGAGGAGGCCACTTCATCAAACCAAGCAGTCA  1414
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   305  CCTGGGTTCCTGAAATCCATGGCTGCGGGAGGAGGCCACTTCATCAAACCAAGCAGTCA   364

Qy  1415  AGTTCCTCCTGGCCCGAAGTCGCTGGCAGCGTTCCTGATGAGCTACAAGTCCATCCTGG  1474
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   365  AGTTCCTCCTGGCCCGAAGTCGCTGGCAGCGTTCCTGATGAGCTACAAGTCCATCCTGG   424

Qy  1475  TGAATGGCCTCCATCCCTGAGCTGCTGCGGGGCTGCGGGGCCCACCCGACAGCCCCTCCCTGGGCCCTAG  1534
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   425  TGATGGCCTCCATCCCTGAGCTGCTGCGGGGCTGCGGGGCCCACCCGACAGCCCCTCCCTGGGCCGTAG   484

Qy  1535  CCCGGCACCTCTGCAGGACACTGGTGGCTCTCCCAGTTCCTCCTCCTCCTCTGACAACG  1594
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   485  CCCGGCACCTCTGCAGGACACTGGTGGCTCTCCCAGTTCCTCCTCCTCCTCTGACAACG   544

Qy  1595  AGCTCGCCCATTGCCGGGGCTTCTGCCGGGCTAGTCACTGCACCCTCCCGGTGACACTCACCAC  1654
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   545  AGCTCGCCCATTGCCGGGGCTTCTGCCGGGCTAGTCACTGCACCCTCCCGGTGACACTCACCAC   604

Qy  1655  TGCTGCACCCCGGGGTTCTCTGCCGGGCCCTTCGGCCTGCCCAGCTGCCTCCCGAGGAAGCCGAGGCCA  1714
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   605  TGCTGCACCCCGGGGTTCTCTGCCGGGCTTCTGGCCTGCCCAGCTGCCTCCCGAGGAAGCCGAGGCCA   664

Qy  1715  GTGAGCCTCCACCGAGGCCCCAGCTTCCCGCCTTCGGCATCTCCCGAGGGGTGCCCGGGCCCACCGG  1774
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   665  GTGAGCCTCCACCGAGGCCCCAGCTTCCCGCCTCCGCATCTCCCGAGGGGTGCCGGGGCCCACCGG   724

Qy  1775  CCGCCCAGGGCTGCGTGCCCGCCCCGGCACAGCCGTCATCCTGTTCTCACCAGGCGG  1834
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   725  CCGCCCAGGGCTGCGTGCCCGCCCCGGCACAGCCGTCATCCTGTTCTCACCAGGCGG   784

Qy  1835  GTGAGAGCCCTGAGACGGGGCGGCGGGGCCCTTGCCGGGCCGCACCCGCCGGGGCGGC  1894
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   785  GTGAGAGCCCTGAGACGGGGCGGCGGGGCCCTTGCCGGGCCGCACCCGCCGGGGCGGC   844

Qy  1895  GGCACCTGCTGAAGGGCGCGGTACATTGCCCTCCGGCGGCGCTGCCAGGCCTGCGGGAGCCCACTGA  1954
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   845  GGCACCTGCTGAAGGGCGCGGTACATTGCCCTCCGGCGGCGCTGCCAGGCCTGCGGGAGCCCACTGA   904

Qy  1955  TGGAGCACCCGCGTGCTGGAGGAGGCGGCCCAGGGAGGAGCCCCCAGGGGGGCGCACCCCACTTGGCCCCTG  2014
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   905  TGGAGCACCCGCGTGCTGGAGGAGGCGGCCCAGGGAGGAGCCCCCAGGGGGGCGCACCCCACTTGGCCCCTG   964

Qy  2015  AAGCCCCCTCATTCGAGACTCCTGGAACATGCCCTCGGCACCCCCCGGGGGGCCCTTGGCCCCTG  2074
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   965  AAGCCCCCTCATTCGAGACTCCTGGAACATGCCCTCGGCACCCCCCGGGGGGCCCTTGGCCCCTG  1024

Qy  2075  GCCACAGCCACTCCCTGGAACATGAGTCTTCCGAGCACCCCCGGGGGGCCCTTATCAGGGACATGG  2134
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1025  GCCACAGCCACTCCCTGGAACATGAGTCTTCCGAGCACCCCCGGGGGGCCCTATCAGGGACATGG  1084

Qy  2135  GCGGTGAGCCACAGCGGACGTGGCCAGCGACTGCCTTCAGCCCCTTCAGCCCCCTTCAGGGGCTCGGCACCCCTTCAGGGACATGG  2194
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1085  GCGGTGAGCCACAGCCACAGCGGACGTGGCCAGCGACTGCCTTCAGCCCCTTCAGGGGCTCGGCACCCCTATCAGGGACATGG  1144
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Qy  2195  GGCACCCTCAGGGTTCCAAGCAGCACTTCATCCACTGGTGGCCACCCAGGCACTGCTTCAGC  2254
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1145  GGCACCCTCAGGGTTCCAAGCAGCACTTCCATCCACTGGTGGCCACCCAGGCACTGCTTCAGC  1204

Qy  2255  CAGAGAGGCCATCCCGGCACAGCCCTTGGGGCAGCCGCCCTTTCTGCCACCCCAAGC  2314
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1205  CAGAGAGGCCATCCCGGACGACAGCAGCCCTTGGGGCAGCCGCCCTTTCTGCCACCCCAAGC  1264

Qy  2315  AGGGTTCTGCCCCGCCAGGAGGGTGCAGCCCACCCAGCAGTTGCCCGTGCCCATGCCTCCTG  2374
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1265  AGGGTTCTGCCCCGCCAGGAGGGTGCAGCCCACCCAGCAGTTGCCCATGCCCTCCTG  1324

Qy  2375  GCTCCTTCCTCGCAGGATCTTGCAAAGAGGGCCCCTTAGTACCCTCAGCCCCTTCTTGG  2434
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1325  GCTCCTTCCCTCGCAGGATCTTGCAAAGAGGGCCCCTTAGTACCCTCAGCCCCTTCTTGG  1384

Qy  2435  GACAGCCCCAGGCACCCCCTGCCCTGCCAAAGCAAGCCCCCCATTGGACTCTAAGATGG  2494
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1385  GACAGCCCCAGGCACCCCCTGCCCTGCCAAAGCAAGCCCCCATTGGACTCTAAGATGG  1444

Qy  2495  GGCCTGGAGACATCTCTCTTCCTGGGAGGCCAAAACCCGGCCCGCCCTGCCAGTTCCCCAGGGT  2554
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1445  GGCCTGGAGACATCTCTCTTCCTGGGAGGCCAAAACCCGGCCCGCCCTGCCAGTTCCCCAGGGT  1504

Qy  2555  CAGCTCCCAGGGGAGCTCTTCCCAAGTGAGCTCCTCAGGGTGGGCTCCTCCCAGGTGG  2614
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1505  CAGCTCCCCAGGGGAGCTCTTCCCAAGTGAGCTCCCTCAGGTGGGGCTCCTCCCAGGTGG  1564

Qy  2615  GCACAGAGCCTGGCCCCTCCCCTTGGATGCCGGCCTCAGGAACAGTGACCAAGTTCTCCC  2674
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1565  GCACAGAGCCTGGCCCCTCCCCTTGGATGCCGGCCTCAGGAACAGGACGAAGTTCTCCC  1624

Qy  2675  CCGACTCCACACCCACCTTGAGCGCGGCCTCAGGAACAGTGCAAGTTCTCCC  2734
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1625  CCGACTCCACACCCACCTTGAGCGCGGCCTCAGGAACAGGACGAAGTTCTCCC  1684

Qy  2735  TGGGTGGTGCGCGGGGCTACGCAGGCGTGGCTTATGGGCCATGTGGGCCAGGATAGCGCAAGTTCCC  2794
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1685  TGGGTGGTTGCGCGGGGCTACGCAGGCGTGGCTTATGGGCCATGTGGGCCAGGATAGCGCAAGTTCCC  1744

Qy  2795  ATGCAGGGGGCATGCTGGGGCAGCAGGAGGCCCATGTGGGCAGGATAGCGCTGGGCTGTGTCCC  2854
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1745  ATGCAGGGGGCATGCTGGGGCAGCAGGAGGCCCATGTGGGCCAGGATAGCGCTGGGCTGTGTCCC  1804

Qy  2855  AGTCGGAGGAGGAGGAGGAGGAGGCCAGGGCTGAGTCCCAGTTCGGAGGAGCAGCAGG  2914
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1805  AGTCAGAGGAGGAGGAGGAGGAGGAGGCCAGGGCTGAGTCCCAGTTCGGAGGAGCAGCAGG  1864

Qy  2915  AGGCCAGGGCTGAGAGCCCACTGCCCCCAGGTCAGTGCAAGCCTGTGCCTGTGCTCGAGGTCGGCA  2974
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1865  AGGCCAGGGCTGAGAGCCCACTGCCCCCAGGTCAGTGCAAGCCTGTGCCTGTGCTCGAGGTCGGCA  1924

Qy  2975  GGGCTCCACCAGGAGTCTTCCAGAGCCCACCCCATGGGAGGACATCGGGCAGGTCTCCC  3034
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1925  GGGCTCCCACCAGGAGTCTTCCAGAGCCCACCCCATGGGAGGACATCGGGCAGGTCTCCC  1984

Qy  3035  TGGTGCAGATCCGGGACTCGGGTGCAGGTGATGCGGAGGCGGCCGCACAAATATCCCTGGACA  3094
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1985  TGGTGCAGATCCGGGACTCGGGTGCAGGTGATGCGGAGGCGGCCGCACAAATATCCCTGGACA  2044

Qy  3095  TTTCCGAGGTGGACCCCGCCCTCAACCTCTCGACGATATCAAGTACCTCC  3154
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2045  TTTCCGAGGTTGGACCCCGCCCTCAACCTCTCGACGATATCAAGTACCTCC  2104

Qy  3155  CATTCGAGTTTATGATCTTCAGGAAAGTCCCCAAGTCGCGCTCAGCCAGAGCCGCCCTCCC  3214
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2105  CATTCGAGTTTATGATCTTCAGGAAAGTCCCCAAGTCGCGCTCAGCGAGCCGCCCTCCC  2164

Qy  3215  CCATGGCTGGAGGAGGCTGGCCGAGTTGGCCGACCTCCGGACCCCGAGGCTGCCAGTGAAC  3274
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2165  CCATGGCTGGAGGAGGCTGGCCGAGTTGGCCGACCTCCGGACCCCGAGGCTGCCAGTGAAC  2224

Qy  3275  TGGGGCCCCACGCAGCCGCAGGATCACAGAGAGTCAGGAGTCAGGGATGTGGACGGCGGCTGG  3334
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Db    3305  CCCTCAGGGGCCTGGCCGCCACCCGCACCTGGCCCAGCTGCACGCAGCCTACCTCAGCCCCC  3364

Qy    4415  GGGACCTGGTGCTCATCTTGGAGCTGT  4474
            |||||||||||||||||||||||||||
Db    3365  GGCACCTGGTGCTCATCTTGGAGCTGT  3424

Qy    4475  AGAGGGCCTCTTACTCAGAATCTGA  4534
            |||||||||||||||||||||||||
Db    3425  AGAGGGCCTCCTACTCAGAATCCGA  3484

Qy    4535  CCCAGTACCTGCACAACCAGCACATCC  4594
            |||||||||||||||||||||||||||
Db    3485  CCCAGTACCTGCACAACCAGCACATCC  3544

Qy    4595  TCACCGAATACAACCTGCTCAGGTGTGA  4654
            ||||||||||||||||||||||||||||
Db    3545  TCACCGAATACAACCTGCTCAGGTCGTGA  3604

Qy    4655  AGAAGGTGCTGCCCTCAGACAAGTTCA  4714
            |||||||||||||||||||||||||||
Db    3605  AGAAGGTGCTGCCCTCAGACAAGTTCA  3664

Qy    4715  TGGAGGGCCAGGGGTGTTCCACAGACA  4774
            |||||||||||||||||||||||||||
Db    3665  TGGAGGGCCAGGGGTGTTCCACAGACA  3724

Qy    4775  TCATGTGAGCGGCCGAGTACCCGTGA  4834
            ||||||||||||||||||||||||||
Db    3725  TCATGCTGAGCGGCCGAGTACCCGTGA  3784

Qy    4835  TGCGCAAGGGGCTGGTCCGGCTGGA  4894
            |||||||||||||||||||||||||
Db    3785  TGCGCAAGGGGCTGGTCCGGCTGGA  3844

Qy    4895  CCTTCCTGCGCAGCACTCTGTGCG  4954
            ||||||||||||||||||||||||
Db    3845  CCTTCCTGCGCAGCACTCTGTGCG  3904

Qy    4955  TGCAGTGCCGTGGCTAACAGAGGA  5014
            ||||||||||||||||||||||||
Db    3905  TGCAGTGCCCGTGGCTAACAGAGGA  3964

Qy    5015  TCCCTACCGCGGCGGCTCGTCGCC  5074
            ||||||||||||||||||||||||
Db    3965  TCCCTACCGCGGCGGCTCGTCGCC  4024

Qy    5075  ACAAGAGGCACAACCTGCCAGTGCG  5134
            |||||||||||||||||||||||||
Db    4025  ACAAGAGGCACAACCTGCCAGTGCG  4084

Qy    5135  CCCGCTGGGGGGTCGCTGCAGACGCG  5194
            ||||||||||||||||||||||||||
Db    4085  CCCCTGGGGGGTCGCTGCAGACGCG  4144

Qy    5195  AAAAAAAAAAA  5207
            ||||||||||
Db    4145  AAAAAAAAAAA  4157

Db    2225  TGGGCCCCACGCAGCAGGCCTGGAGATCACAGAGAGTCAGAGAGGATGGACGGCGCTGCTGG  2284

Qy    3335  CAGAGGCTGCCGTGGGGCAGGAAGCGCAAGTGGT  3394
            ||||||||||||||||||||||||||||||||||
Db    2285  CAGAGGCTGCCGTGGGGCAGGAAGCGCAAGTGGT  2344

Qy    3395  TCCCTGGGAGGCACCTGCCGCTGGATGAGCGGTG  3454
            ||||||||||||||||||||||||||||||||||
Db    2345  TCCCTGGGAGGCACCTGCCGCTGGATGAGCGGTG  2404

Qy    3455  AGGGCTTCGTGGAGCACATCTCCGGATCCTGAAGG  3514
            |||||||||||||||||||||||||||||||||||
Db    2405  AGGGCTTCGTGGAGCACATCTCCGGATCCTGAAGG  2464

Qy    3515  AGGGGCCCCCAGGAAGAGCCAGGCCTTG  3574
            ||||||||||||||||||||||||||||
Db    2465  AGGGGCCCCCAGGAAGAGCCAGGCCTTG  2524

Qy    3575  GGGACCGAGCGCCGACATTCCTAAGGGAGA  3634
            ||||||||||||||||||||||||||||||
Db    2525  GGGACCGAGCGCCGACATTCCTAAGGGAGA  2584

Qy    3635  CAGTGACACTGGCCTGCCAGGTGTCAGCCCA  3694
            |||||||||||||||||||||||||||||||
Db    2585  CAGTGACACTGGCCTGCCAGGTGTCAGCCCA  2644

Qy    3695  ACGGAGCCCCCTGAGAGCAGCAGC  3754
            ||||||||||||||||||||||||
Db    2645  ACGGAGCCCCCTGAGAGCAGCAGC  2704

Qy    3755  AGCTTCTGACCATCCTGGTGTGGTG  3814
            |||||||||||||||||||||||||
Db    2705  AGCTTCTGACCATCCTGGTGTGGTG  2764

Qy    3815  GCAATGCGCTGGGGACAGTGACCAC  3874
            |||||||||||||||||||||||||
Db    2765  GCAATGCGCTGGGGACAGTGACCAC  2824

Qy    3875  CTTGCCATGCCCGGATATCGGGGAGG  3934
            |||||||||||||||||||||||||
Db    2825  CTTCGCCATGCCCGGATATCGGGGAGG  2884

Qy    3935  CCGGTGAATCCTACGGCCCTGTGACCAT  3994
            ||||||||||||||||||||||||||||
Db    2885  CCGGTGAATCCTACGGCCCTGTGACCAT  2944

Qy    3995  GGACCACACTGGCCTCCGACATCTTTGA  4054
            ||||||||||||||||||||||||||||
Db    2945  GGACCACACTGGCCTCCGACATCTTTGA  3004

Qy    4055  GTGGCACTTACACCTTCCCGAGCAAGTC  4114
            ||||||||||||||||||||||||||||
Db    3005  GTGGCACTTACACCTTCCCGACACGGCAAGTC  3064

Qy    4115  GCCCCTCGGAGCAAGTCCTCCTGGGAGGG  4174
            |||||||||||||||||||||||||||||
Db    3065  GCCCCTCGGAGCAAGTCCTCCTGGGAGGG  3124

Qy    4175  AGAGGGCGGTCAGCCCCAACCCTGCCCAG  4234
            |||||||||||||||||||||||||||||
Db    3125  AGGGGGCGGTCAGCCCCAACCCCTGCCCAG  3184

Qy    4235  AGAGGGGCCCGTTCAGCGTGTGCGCAATG  4294
            |||||||||||||||||||||||||||||
Db    3185  AGAGGGGCCCGCTTCAGCGTGTGCGCAATG  3244

Qy    4295  CCGCAAGATCATCCCCTACCACCCCAAGGA  4354
            ||||||||||||||||||||||||||||||
Db    3245  CCGCCAAGATCATCCCCTACCACCCCAAGGA  3304

Qy    4355  CCCTCAAGGGGCTGCGCACCCGACCTGCCC  4414
            ||||||||||||||||||||||||||||||
Db    3305  CCCTCAAGGGGCTGCGCACCCGACCTGCCC

Query Match      61.4%;   Score 3197.8;   DB 6;   Length 3225;

Best Local Similarity  99.9%;     Pred. No. 0;
Matches 3210;  Conservative  0;  Mismatches  0;  Indels  2;  Indels  1;  Gaps  1;

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Qy   1979  AGGCGGCCAGGGAGGAGGAGCAGGCAGGCCACCCTCCTGGCCAAAGCCCCTCCATTCGAGACTGCCC  2038
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     13  AGGCGGCCAGGGAGGAGGAGCAGGCAGGCCACCCTCCTGGCCAAAGCCCCTCCATTCGAGACTGCCC  72

Qy   2039  TCCGGCTGCCTGCCTCTGGCACCCACTTGGCCCCTGGCCACAGCCACTCCCTGGAACATG  2098
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     73  TCCGGCTGCCTGCCTCTGGCACCCACTTGGCCCCTGGCCACAGCCACTCCCTGGAACATG  132

Qy   2099  ACTTCCGAGACACCCCCGCCCTCCTCGGAGGCCTGCGGTGAGGCCACAGCGACTGCCTT  2158
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    133  ACTCTCCGAGCACACCCCCCGCCCTCCTCGGAGGCCTGCGGTGAGGCACAGCGACTGCCTT  192

Qy   2159  CAGCCCCTCCGGGGGGGCCCTATCAGGGACACATGGGCACCCTCAGGGCTCCAAGCAGC  2218
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    193  CAGCCCCTCCGGGGGGGCCCTATCAGGGACACATGGGCACCCTCAGGGCTCCAAGCAGC  252

Qy   2219  TTCCATCCACTGTGGCCACCCAGGCACTGCTCAGCCAGGAGAGGCCATCCCCGGACAGCC  2278
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    253  TTCCATCCACTGTGGCCACCCAGGCACTGCTCAGCCAGGAGAGGCCATCCCCGGACAGCC  312

Qy   2279  CTTGGGGCCAGCCAGCCCTTTCTGCCACCCCAAGCAGGGTTCTGCCCCCCAGGAGGGCT  2338
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    313  CTTGGGGCCAGCCAGCCCTTTCTGCCACCCCAAGCAGAGGTTCTGCCCCCCAGGAGGGCT  372

Qy   2339  GCAGCCCCACCCAGCAGTGCCCATGCCCTCCTCTGGCTCCTCCCTCCTCCTCCAGGATCTTGCA  2398
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    373  GCAGCCCCACCCAGCAGTGCCCATGCCCTCCTCTGGCTCCTCCCTCCTCCTCCAGGATCTTGCA  432

Qy   2399  AAGAGGCCCCTTAGTACCCTCAAGCCCCTTCTT-GGGACAGCCCAGGCACCCCTGCC  2457
            ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db    433  AAGAGGCCCCTTAGTACCCTCAAGCCCCTTTCTTCTGGGGACAGCCCAGGCACCCCCTGCC  492

Qy   2458  CCTGCCAAAGCAAGCCCCCATTGGACTCTAAGATGGGGCCTGGAGACATCTCTTCCT  2517
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    493  CCTGCCAAAGCAAGCCCCCATTGGACTCTAAGATGGGGCCTGGAGACATCTCTTCCT  552

Qy   2518  GGGAGGCCAAAACCCGGCCCTGCAGTTCCCAGGTCAGCCTCCCAGGCGAGCTCTTCC  2577
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    553  GGGAGGCCAAAACCCGGCCCTGCAGTTCCCAGGTCAGCCTCCCAGGCGAGCTCTTCC  612

Qy   2578  CAAGTGAGCTCCCTCAGGGTGGGCTCCTCCCAGGTGGGCACAGAGCCTGGCCCCTCCCTG  2637
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    613  CAAGTGAGCTCCCTCAGGGTGGGCTCCTCCCAGGTGGGCACAGAGCCTGGCCCCTCCCTG  672

Qy   2638  GATGCCGAGGGCTGACCCAGGAGGCTGAGGATCGTCCGACTCCACCACCCACCTTGCAG  2697
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    673  GATGCCGAGGGCTGACCCAGGAGGCTGAGGATCGTCCGACTCCACCACCCACCTTGCAG  732

Qy   2698  CGGCCTCAGGAACAGGTGACCATGCGCAAGTTCTCCCTGGGTGGTCGCGGGGGCTACGCA  2757
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    733  CGGCCTCAGGAACAGGTGACCATGCGCAAGTTCTCCCTGGGTGGTCGCGGGGGCTACGCA  792

Qy   2758  GGCGTGGCTGCCTATGGCACCTTTGGCCATTTGGGTGGAGATGCAGGGGGCATGCTGGGGCAG  2817
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    793  GGCGTGGCTGCCTATGGCACCTTTGGCCACTTTGGCCATTTGGTGGAGATGCAGGGGGCATGCTGGGGCAG  852

Qy   2818  GGGCCCATGTGGGCCAGGATAGCCCAGTGCGTGCTCCCAGTGCAGGAGGAGGAGCAGGAG  2877
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    853  GGGCCCATGTGGGCCAGGATAGCCTGGGCTGTCCAGTGCGTGCTCCCAGTGCAGGAGGAGGAGCAGGAG  912

Qy   2878  GAGGCCAGGGCTGAGTCCCAGTCGGAGGAGCAGGAGGGCCAGGGCTGAGAGCCCACTG  2937
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    913  GAGGCCAGGGCTGAGTCCCAGTCGGAGGAGCAGGAGGGCCAGGGCTGAGAGCCCACTG  972

Qy   2938  CCCCAGGTCAGTGCAAGGCCTGCAAGGCCTCGGCAGGGTCGGCAGGCTCCCACCAGAGCTCCA  2997
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    973  CCCCAGGTCAGTGCAAGGCCTGCAAGGCCTGCAAGGCCTCGGCAGGGTCGGCAGGCTCCCACCAGAGCTCCA  1032

Qy   2998  GAGCCCACCCATGGAGGAGGACATCCGGCCAGGTCTTCCCTGGTGCAGATCCGGGACCGTCA  3057
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Db  1033 GAGCCCACCCCATGGAGGACATCGGGACGTCTCCCTGTGTGCAGAATCGGGACCTGTCA 1092

Qy  3058 GGTGATGGGAGAGGCGGCCGACACAATATCCCTGGACATTCCCGAGGTGACCCCGCCTAC 3117
         ||||||||||||||  |||||||||||||||||||||||||| |||||||||||||||||
Db  1093 GGTGATGCGGAGGCGGCCGACACAATATCCCTGGACATTTCCGAGGTGACCCCGCCTAC 1152

Qy  3118 CTCAACCTCTGAGACCTGTACGATATCAAGTACCTTCCCATTCGAGTTTATGATCTTCAGG 3177
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1153 CTCAACCTCTGAGACCTGTACGATATCAAGTACCTTCCCATTCGAGTTTATGATCTTCAGG 1212

Qy  3178 AAAGTCCCAAGTCCGCTCAGCAGAGCCGCCTCCCCATGGCTGAGGAGAGCTGGCC 3237
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1213 AAAGTCCCAAGTCCGCTCAGCCAGAGCCGCCTCCCCATGGCTGAGGAGAGCTGGCC 1272

Qy  3238 GAGTTCCGGAGCCACGTGGCCCTGGCCAGGTGAACTGGCCCCCACGCAGGCCTGGAG 3297
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1273 GAGTTCCCGGAGCCACGTGGCCCTGGCCAGGTGAACTGGCCCCCACGCAGGCCTGGAG 1332

Qy  3298 ATCACAGAGGAGTCAGAGGATGTGGACGCGCTGCTGGCGAGAGCTGCCGTGGGCAGGAAG 3357
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Db  1333 ATCACAGAGGAGTCAGAGGATGTGGACGCGCTGCTGGCGAGAGCTGCCGTGGGCAGGAAG 1392

Qy  3358 CGCAAGTGGTCCTCGCCGTCACGCAGCCTCTTCACTTCCCTGGGAGGCCACCTGCCGCTG 3417
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Db  1393 CGCAAGTGGTCCTCGCCGTCACGCAGCCTCTTCACTTCCCTGGGAGGCCACCTGCCGTG 1452

Qy  3418 GATGAGCCTGCAGCGAGCCTGCCTGCGTGAGAGTGAAGGCCTTCCGTGCAGCACATCTCC 3477
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1453 GACGAGCCTGCAGCGAGCCTGCCTGCGTGAGAGTGAAGGCCTTCCGTGCAGCACATCTCC 1512

Qy  3478 CGGATCCTGAAGGGCAGGCCCGGAAGTCTCTGGAGAAGGGAGGCCCCCAGGAAGAAGGCCA 3537
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1513 CGGATCCTGAAGGGCAGGCCCGGAAGTCTCTGGAGAAGGGAGGGCCCCCAGGAAGAAGGCCA 1572

Qy  3538 GGGCCTTGCTTCCTTCGGGCTTCAGGTCTCAGGTCTTGAAGAGCTGGAGCTCGGCTGGACCGACCGACAATTCCTA 3597
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Db  1573 GGGCCTTGCTTCCTTCGGGCTTCAGGTCTCAGGTCTTGAAGAGCTGGAGCTCGGGACCGACAATTCCTA 1632

Qy  3598 AGGGAGCTCTCAGATGAGACTGTGGTCCTGGGCCAGTCAGTGACACTGGCCTTCCCAGTTG 3657
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1633 AGGGAGCTCTCAGATGAGACTGTGGTCCTGGGCCAGTCAGTGACACTGGCCTTGCCAGGTG 1692

Qy  3658 TCAGCCCAGCCAGTCGCTGCCCACCTGGGCAGCAAAGACACGGAGCCCCCTGGAGACGCAGC 3717
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1693 TCAGCCCAGCCAGTCGCTGCCCACCTGGGCAGCAAAGACACGGAGCCCCCTGGAGACGCAGC 1752

Qy  3718 AGCCGTGTCCATCTCTGCCACCTCAAGAACTTCAGCTTCTGACCATCCTGGTGGTG 3777
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1753 AGCCGTGTCCATCTCTGCCACCTCAAGAACTTCAGCTTCTGACCATCCTGGTGGTG 1812

Qy  3778 GTGGCTGAGGACCTGGGTGTGTACACACTGGGGACCAATGCGCTGAGCCAGTGACC 3837
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1813 GTGGCTGAGGACCTGGGTGTGTACACCTGGGGACCAATGCGCTGGGGACCAGTGACC 1872

Qy  3838 ACCACGGCGCGTCTCCGGAAGGCAGAGCGCGCCCCTCATCTTCGCCATGCCGGATATCGGG 3897
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1873 ACCACGGGCGGTCCTCCGGAAGGCAGAGCGCGCCCCTCATCTTCGCCATGCCGGATATCGGG 1932

Qy  3898 GAGGTGTACCGGCGATGGGGTTGCTGCTGGTCTGAAGCCCGTTGAAATCCTACGGCCCTGTG 3957
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1933 GAGGTGTACCGGCGATGGGGTTGCTGCTGGTCTGAAGCCCGTTGAAATCCTACGGCCCCTGTG 1992

Qy  3958 ACCTACATTGTGCAGTGCAGCCTAGAAGGCGGCAGCTGGACACCACTGGCCTTCCGGACATC 4017
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Db  1993 ACCTACATTGTGCAGTGCAGCCTAGAAGGCGGCAGCTGGACCACTGGCCTTCCGGACATC 2052

Qy  4018 TTTGACTGCTGCTACCTGACCAGCAAGTCTCCCGGGGTGGCACCTTCCGGCACG 4077
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Db  2053 TTTGACTGCTGCTACCTGACCAGCAAGTCTCCCGGGGTGGCACCTTCCGGCACG 2112

Qy  4078 GCATGTGTCAGCAAGGCAGGAATGGGTCCCTACAGCAGCCCCTACGCAGTCCTCCCTG 4137
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Db  2113 GCATGTGTCAGCAAGGCAGGAATGGGTCGCTGTCTGACGCAGCCCTACGCAGTCCTCCCTG 2172
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Db  4138 GGAGGGCCCAGCCACCTGGCCTCTGAGAGGAGGAGCCAGGGCGCGGTCAGCGACCAACCCTG 4197

Qy  2173 GGAGGGCCCAGCCACCTGGCCTCTGAGGAGGAGGAGCCAGGGCGCGGTCAGCGACCAACCCTG 2232
Db  2173 GGAGGGCCCAGCCACCTGGCCTCTGAGGAGGAGGAGCCAGGGCGCGGTCAGCGACCAACCCTG 2232

Qy  4198 CCCAGCACAAAGACCTTCGCATTCGAGATCCAGACACAGATCCAGAGGGGCCCGCTTCAGCGTGGTG 4257
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Db  2233 CCCAGCACAAAGACCTTCGCATTCGAGATCCAGACACAGATCCAGAGGGGCCCGCTTCAGCGTGGTG 2292

Qy  4258 CGGCAATGCTGGGAGAAGGCCAGCGGGGGCGGGCTGCCGCCGCCAAGATCATCCCTACCAC 4317
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2293 CGGCAATGCTGGGAGAAGGCCAGCGGGGGCGGGCTGCCGCCGCCAAGATCATCCCTACCAC 2352

Qy  4318 CCCAAGGACAAGACAGCAGTGCTGCGCGAATACGAGGCCCTCAAGGGCCTGCGCCACCCG 4377
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Db  2353 CCCAAGGACAAGACAGCAGTGCTGCGCGAATACGAGGCCCTCAAGGGCCTGCGCCACCCG 2412

Qy  4378 CACCTGGCCCAGCTGCACGCAGCCTACCTCAGCCCCGCACCTGGTCTCATCTTGGAG 4437
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Db  2413 CACCTGGCCCAGCTGCACCCAGCCTACCTCAGCCCCGCACCTGGTCTCATCTTCGGAG 2472

Qy  4438 CTGTGCTCTGGGCCCGAGTGCTCCCCTGCGTGGCCGAGAACATGATCATCACCTGCTCAAG 4497
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Db  2473 CTGTGCTCTGGGCCCGAGTGCTCCCCTGCGTGGCCGAGAACATGATCATCATCAGAATCC 2532

Qy  4498 ATCCTGCACCTGGACCTGAGGTCCGAGAACATGATCATCACCGAATACAACCTGCTCAAG 4557
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Db  2533 GTCGTGGACCTGGACCTGGCAATGTCACAGACGTCACCGAGTGTTGAGTGTTGAGTCACAACCAGCAC 2592

Qy  4558 GTCGTGGACCTGGGCAATGCACAGACGCTCAGCTGCACACGAGTGCTGCCCTCAGACAAG 4617
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2593 GTCGTGGACCTGGGCAATGCACAGACGCTCAGCTGCACACGAGTGCTGCCCTCAGACAAG 2652

Qy  4618 TTCAAGGACTACCTAGAGACCATGGCTTCCTCCAGAGCTCCTGAGGGCAGGGGCGTGTTCA 4677
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2653 TTCAAGGACTACCTAGAGACCATGGCTTCCTCCAGAGCTCCTGAGGGCAGGGGCGTGTTCA 2712

Qy  4678 CAGACAGACATCTGGCCATCGGTGTGACAGCCTTCATCATGCTGAGCGGCCGAGTACCGG 4737
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2713 CAGACAGACATCTGGGCCATCGGTGTGACAGCCTTCATCATGCTGAGCGGCCGAGTACCCG 2772

Qy  4738 GTGAGCAGCAGCTGCACGCGACCTGCAGGGTCGTGCTCCAGAGGACTGCGCAAGGCTGTGGTCGGGCTG 4797
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2773 GTGAGCAGCAGCTGCACGCGACCTGCAGGGTGCGCAAGGCTGTGGTCGGGCTG 2832

Qy  4798 AGCCGCTGTACGCGGGGCGTGTCCGGGGGCGGCCGGTGGCCTTCCTGCCGCACTCGTGC 4857
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Db  2833 GTGAGCAGCGAGGGTGCACGCGACCTGCCGCAACCTGCGGCAGGGGTGGTCGGCACTCGTGC 2892

Qy  4858 GCCCAGCCCTGGGGCGCCCGGCTGCGTGCCCAGCGGCCTGCGACTCGTAACAGAG 4917
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Db  2893 GCCCAGCGCCTGGGGCGCCCGGCTGCGTGCCCAGTCGCCTGCGACTCGTGC 2952

Qy  4918 GTGCGGCTGAGGGTCGCCCCGCGTCGGCCGGCCCGCGGCCCCGCGGCCCCGAGAGCTGCGCGTC 4977
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  2953 GCCCAGCCCTGGGGCGCCCGGCTGCGTCCGCGGCCCGCGGCCCCGACCTTCCCTACCGCGGCCTGCGCGTC 3012

Qy  4978 GAGGGCTGAGGGGTCCGGCGGCTCCTGGTCGGAAGCCGTGGAATCCTGCTACGGCCCGTGGTG 5037
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Db  3013 GAGGGCCGGGGGTCCGGCGGTGTCGGCGGCTCCTGGTCGGAAGCCGTGAACTTCCCTACCGCGGCCTGCGCGTC 3072

Qy  5038 TTCGTGCGCAATCGCGAGAAGAGACGCGCGGCTGCTCGTGTACAAGAGACACAAACCTGCCCCAG 5097
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3073 TTCGTGCGCAATCGCGAGAAGAGACGCGCGGCTGCTCGTGTACAAGAGACACAAACCTGCCCCAG 3132

Qy  5098 GTGCGGCTGAGGGTCGCCCCGGCCCACACCCTTGGTCTCCCCGCGGTCGCTGCGACACG 5157
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3133 GTGCGGCTGAGGGTCGCCCCGGCCCACACCCTTGGTCTCCCCGCGGTCGCTGCGACACG 3192

Qy  5158 CGCCAATAAAAACGCACAGCCCGGGCGGAAAAA 5190
         |||||||||||||||||||||||||
Db  3193 CGCCAATAAAAACGCACAGCCCGGGCGGAAAAA 3225
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RESULT 11
ABN79527
ID    ABN79527 standard; cDNA; 382 BP.
XX
AC    ABN79527;
XX
DT    08-JUL-2002  (first entry)
XX
DE    Human kinase-like ORP4474 cDNA, SEQ ID NO:8947.
XX
KW    Human; ORF; open reading frame; ORFX; drug screening; diagnosis;
KW    disease monitoring; cytokine; cell proliferation; cell differentiation;
KW    immune modulation; haematopoiesis regulation; tissue growth;
KW    angiogenesis; activin; inhibin; chemotactic; chemokinetic; haemostatic;
KW    thrombolytic; tumour inhibition; bodily characteristic; fertility;
KW    behaviour; cancer; proliferative disorder; neurological disorder;
KW    cardiovascular disease; immune system disorder; organ transplantation;
KW    tissue growth disorder; tissue regeneration disorder; diabetes mellitus;
KW    hypothyroidism; cholesterol ester storage disease; infection; vulnerary;
KW    vasotropic; antipsoriatic; antidiabetic; cytostatic; nootropic;
KW    neuroprotective; antiatherosclerotic; anticoagulant; thrombolytic;
KW    cardiant; hypotensive; antithyroid; antiinflammatory; immunomodulator;
KW    dermatological; analgesic; virucide; antibacterial; fungicide; gene; ss.
XX
OS    Homo sapiens.
XX
PN    WO200190366-A2.
XX
PD    29-NOV-2001.
XX
PF    24-MAY-2001; 2001WO-US017076.
XX
PR    24-MAY-2000; 2000US-0206690P.
XX
PA    (CURA-) CURAGEN CORP.
XX
PI    Leach MD,  Shimkets RA;
XX
DR    WPI; 2002-106200/14.
DR    P-PSDB; ABP35501.
XX
PT    Novel human polypeptides and polynucleotides useful for diagnosing,
PT    preventing and treating cardiovascular disease, neurodegenerative,
PT    hyperproliferative disorders and disorders related to organ
PT    transplantation.
XX
PS    Claim 1; Page 2478; Page 2478; 2508pp; English.
XX
CC    Sequences ABP31028-ABP35561 represent 4534 novel human proteins
CC    designated ORF (open reading frame) 1-4534, and sequences ABN75054-
CC    ABN79587 represent cDNAs encoding them. The invention also encompasses
CC    polypeptides at least 80% identical to the ORF1-ORF4534 (collectively
CC    referred to as ORFX) proteins, polynucleotides at least 85% identical to
CC    the ORFX nucleic acid sequences, vectors and host cells comprising ORFX
CC    polynucleotides, the recombinant production of ORFX proteins, antibodies
CC    specific for ORFX proteins, methods of detecting ORFX polynucleotides and
CC    polypeptides, methods of screening for modulators of ORFX expression or
CC    activity, and methods of screening individuals for a predisposition to an
CC    ORFX-associated disorder. The ORFX proteins of the invention have a wide
CC    range of biological activities, such as cytokine, cell proliferation,
CC    cell differentiation, immune modulation, haematopoiesis regulation,
CC    tissue growth, angiogenesis, activin or inhibin activity, chemotactic/
CC    chemokinetic activity, haemostatic activity, thrombolytic activity,
CC    receptor/ligand, antiinflammatory activity, tumour inhibition activity,
CC    and antiinfective activity, and may also be involved in the determination
CC    of bodily characteristics, fertility and behaviour. ORFX proteins,
CC    nucleic acids and antibodies may be used in the treatment of cancers,
CC    other proliferative disorders such as psoriasis and benign tumours,
CC    neurological disorders such as epilepsy and Alzheimer's disease,
CC    cardiovascular diseases, immune system disorders, disorders related to
CC    organ transplantation, disorders of tissue growth and regeneration,
CC    diseases such as diabetes mellitus, hypothyroidism, and cholesterol ester

CC    storage disease, and infectious diseases caused by viral, bacterial,
CC    fungal and other pathogens. ORFX nucleic acids may also be used as a
CC    source of primers and probes, in the detection of ORFX genomic sequences
CC    or transcripts, in the identification and cloning of homologous
CC    sequences, in genetic diagnosis, and in forensic biology. The ORFX
CC    nucleic acids may additionally be used to produce transgenic animals
CC    which may be useful for studying the function and/or activity of ORFX
CC    protein, and in drug screening. The ORFX proteins may also be used as
CC    immunogens to generate specific antibodies, which are useful in the
CC    diagnosis, treatment and monitoring of ORFX-associated diseases
XX
SQ    Sequence 382 BP; 86 A; 104 C; 126 G; 65 T; 0 U; 1 Other;

Query Match             6.9%;  Score 358.4; DB 6;  Length 382;
Best Local Similarity  99.7%;  Pred. No. 1.4e-55;
Matches  359;  Conservative   0;  Mismatches   1;  Indels   0;  Gaps   0;

Qy    502 GGTGGCCAGGTGCTCTGCAAGGCAGAGCTGGTGCTTGGGGGGGACAATGAGCCGGAC 561
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     13 GGTGGCCAGGTGCTCTGCAAGGCAGAGCTGCTGGTGCTTGGGGGGGACAATGAGCCGGAC 72

Qy    562 TCAGAGAAGCAAAGCCACCGGAGGAGAGTCGCACTCCTTCTATGAGGTCAAGGAGGAGATT 621
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     73 TCAAAGAAGCAAAGCCACCGGAGGAGAGTGCACTCCTTCTATGAGGTCAAGGAGGAGATT 132

Qy    622 GGAAGGGGCGTTGTTTGGCTTCGTAAAAGAGTGCAGCACAAAGGAAACAAGATCTTGTGC 681
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    133 GGAAGGGGCGTGTTTGGCTTCGTAAAAGAGTGCAGCACAAAGGAAACAAGATCTTGTGC 192

Qy    682 GCTGCCAAGTTCATCCCCCTACGGAGCAGAACTCGGGCCCAGGCATACAGGGAGCGAGAC 741
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    193 GCTGCCAAGTTCATCCCCCTACGGAGCAGAACTCGGGCCCAGGCATACAGGGAGCGAGAC 252

Qy    742 ATCCTGGCCGCGCCGGCTGGAGCCACCCGCTGGTCACGGGGCGTGCTGACCAGTTTGAGACCCCGC 801
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    253 ATCCTGGCCGCGCCGGCTGGAGCCACCCGCTGGTCACGGGGCGTGCTGACCAGTTTGAGACCCCGC 312

Qy    802 AAGACCCTCATCCTCATCCTGGAGCTGTGCTCATCCGAGGAGTGCTCGACCGCCCTGTAC 861
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    313 AAGACCCTCATCCTCATCCTGGAGCTGTGCTCATCCGAGGAGTGCTCGGACCGCCCTGTAC 372

RESULT 12
AAF44662
ID    AAF44662 standard; cDNA; 7710 BP.
XX
AC    AAF44662;
XX
DT    27-MAR-2001  (first entry)
XX
DE    Novel protein kinase cDNA, SEQ ID NO: 42.
XX
KW    Human; mouse; protein kinase; antiarthritic; antisclerotic; osteopathic;
KW    immunosuppressive; cardiant; renal; antiinflammatory; antiasthmatic;
KW    dermatological; antidiabetic; antiinfertility; gene therapy; vaccine;
KW    immune disorder; cardiovascular disease; neurodegenerative disease;
KW    cancer; autoimmune disorder; stroke; inflammatory bowel disease;
KW    inflammatory pelvic disease; multiple sclerosis; psoriasis; ss.
XX
OS    Homo sapiens.
XX
PN    WO20007346H-A2.
XX
PD    07-DEC-2000.
XX
PF    26-MAY-2000; 2000WO-US014842.
XX
PR    28-MAY-1999;  99US-0136503P.
XX
PA    (SUGE-) SUGEN INC.
XX
PI    Plowman GD,  Martinez R,  Whyte D,  Sudersanam S;
XX

```
DR   WPI; 2001-032161/04.
DR   P-PSDB; AAB65635.
XX
PT   Nucleic acids encoding kinase polypeptides, useful for diagnosing and
PT   treating immune-related diseases and disorders, cardiovascular disease,
PT   neurodegenerative diseases and/or cancers.
XX
PS   Example 1; Fig 2; 310pp; English.
XX
CC   The present sequence encodes a novel protein kinase. The nucleic acids
CC   and the protein kinases they encode may be used in the treatment and
CC   diagnosis of diseases associated with inappropriate kinase expression
CC   such as immune-related diseases and disorders, cardiovascular disease,
CC   neurodegenerative diseases and/or cancers. The nucleic acids and
CC   complementary sequences may also be used as DNA probes in diagnostic
CC   assays. The kinase polypeptides may be used as antigens in the production
CC   of antibodies of kinase expression and activity. Anti-kinase antibodies
CC   and kinase antagonists may also be used to down regulate kinase
CC   expression and activity. Diseases related to kinase expression and
CC   activity include rheumatoid arthritis, atherosclerosis, autoimmune
CC   disorders, complications of organ transplantation, myocardial infarction,
CC   immune disorders, cardiomyopathies, strokes, renal failure, oxidative-
CC   stress related disorders, chronic inflammatory bowel disease, chronic
CC   inflammatory pelvic disease, multiple sclerosis, asthma, osteoarthritis,
CC   psoriasis, rhinitis, autoimmunity, diabetes, cancers and reproductive
CC   disorders
XX
SQ   Sequence 7710 BP; 1446 A; 2534 C; 2447 G; 1283 T; 0 U; 0 Other;

Query Match    6.3%;   Score 327.6;  DB 4;  Length 7710;
Best Local Similarity   56.6%;   Pred. No. 8.5e-50;
Matches  725;  Conservative   0;  Mismatches  519;  Indels  36;  Gaps  5;

Qy    256  CTCCCAGGGCCCCCATCCATGCAGGTAACCATGCAGGGATGGTGCAGGCACAGACAGGCGGA   315
Db   1498  CTGGCAGAGGCCCCTCGGTTTGAGTCCATCATGGAGGACGTGAGGTGGGGGGCTTGGGGAA  1557
Qy    316  ACGGCCCAATTCAGAGGCTATCATTGAGGGCGACCCACAGCCTCCGTGACCTGTACAAG    375
Db   1558  ACTGCTCGCTTTGCGGTGGTGTGGTCGAGGGAAAAACCACTGCCGGACATCATGTGGTACAAG  1617
Qy    376  GACAGCGTCCAGCTGGTGGACAGACACCGGGCTTAGCCAGCAGCAAGAAGGCACCACATAC    435
Db   1618  GACCAGGTGCTGCTGACCGAGAGCAGCCATGCAGCCATGTCGTGTACGAGGGAATGAGTGC  1677
Qy    436  TCCCTGGTGCTGAGGGCATGTGGCCTGAAGGATGCCGGCGGTTTACACCGCCTGGCCCAA    495
Db   1678  TCCCTGGTTGGTGCTGCTCAGCACGGCGGGGGGCCCCAGGATGAGGGCGGTCTACACCTGCACCGTCACCGCCCAG  1737
Qy    496  AACACTGGTGGCCCAGGTGCTCTGCAAGGCAGCGAGCTGCTGGTGC----------TT    540
Db   1738  AACCTGGGGGGTGAGGTCTCCGCAAAGCACAGCTGGCTGTGCATTCAGCTCAGACAGCT  1797
Qy    541  GGGGGGACAATGAGCCGGACCAGGAAGCCACCGGAGGAAAGCCAAAGCCAGAGAAGCCACATCCTCCTC  600
Db   1798  ATGGAGGTCGAGGGGGTCGGGAGGGATGAGGACCATCGAGGAAGGAGACTCAGCGACTTT  1857
Qy    601  TATGAGGTCAAGGAGGAGGATTGGAAGGGGCGTGTTTGGCTTCGTPAAAAAGAGTGCAGCAC   660
Db   1858  TATGACATCCACCAGGAGATCGGCAGGGGTGCTTTCTCCTACTTGCGGCGCATAGTGGAG  1917
Qy    661  AAAGGAAACAAGATCTTGTGCCGTGCCAAGTTCATCCCCTACCGGGAGCAGCAGAACTCGGGCC   720
Db   1918  CGTAGCTCGGCCTGGAGTTTGCGGCCAAGTTCATCCCGCCGCAAGGCCAAAGGCA  1977
Qy    721  CAGGCCATACAGGGAGCGAGACCAGACATCCTCGGCCCGCCTGAGCCACCCGCCTGGTCACCGGGGGCTG  780
Db   1978  TCAGCGCGTCGGAGGCGGCCCGCGTGCTGGCCCAGGCTCCAGACGACTGTGTCCTCTACTTC  2037
Qy    781  CTGGACCCAGTTTGAGACCCGCAAGACCCTCATCCTCATCCTTGGAGCTGTTGCTCATCCGAG   840
Db   2038  CATGAGGCCTTCCGAGAGGGCCGCGGGGACTCGGTCATTGTCACCGAGCTCTGCACA--GAG  2094
Qy    841  GAGCTGCTGACCGACCGTCGTACAGGAAGGGGCGTGGTGACGGAGGCCGAGGCCGAGGTCAAGGTCTAC   900
Db   2095  GAGCTGCTGGAGCGGAATCGCCAGGAAACCCACCGTGTGAGTCGTGAGATCCGGGCCCAT  2154
Qy    901  ATCCAGCAGCTGGGTGGGAGGGCTGCACTACCTGCCACAGCCATGCGGTTCTCCACCTGGAC   960
Db   2155  ATGCGGCAGGTGCTCAGAGGGAATACACTACCTGCCACCAGAGCCACGTGCTGCACCTCGAT  2214
Qy    961  ATAAAGCCCTCTAACATCCTGATGGTGCATCCTGCCCGGGAAGACATTAAA-----ATC  1014
Db   2215  GTCAAGCCTGAGAACCTGCGTGGTGGTGTGGGATGGTGCTGCGGGGCAGCAGCAGGTGCGGATC  2274
Qy   1015  TGCGGACTTGGCTTGCCCAGAACATCACCCCGACCAGAGCTGCAGTTCAGCCAGTACGGC  1074
Db   2275  TGTGACTTTGGGAATGCCCAGGAGCTGACTCCAGGAGAGCCCCCAGTACTGCCAGTATGGC  2334
Qy   1075  TCCCTGGAGTTCGTCTCCCCCGGATCATCCAGCAGCAGAACCCTGTGAGCGAGGCCTCCGAC  1134
Db   2335  ACACCCGAGTTGTAGCACCCGAGATTGCAATCAGAGCCCGTGTCAGCGTCACTGAC  2394
Qy   1135  ATTTGGGCCATGGGTCATCTCCTACCTCAGCCTGACCTGGTCATCCTGCTCATCCCCATTGGCCGGC  1194
Db   2395  ATCTGGCCTGTGGGTGTTGCTGCCTTCCTCTGTCTGACAGGAATCTCCCCGTTGTTGGG  2454
Qy   1195  GAGAGTGACCGTGCCACCCTCCTGAACGTCCTGGAGGGGGGCGTGTCATGGAGCAGCCCC  1254
Db   2455  GAAAATGACCGGACACACATTGATGAACATCGAAACTACACACGTGGCCTTCGAGGAGACC  2514
Qy   1255  ATGGCTGCCCACCTCAGCGAAGACGCCAAAGACTTCATCAAGGCTACGCTGCAGAGAGCC  1314
Db   2515  ACATTCCTGAGCCTGAGCAGGGAGGCCCGGGGCTTCCTCATCAAAGTGTTGGTGCAGGAC  2574
Qy   1315  CCTCAGGCCCCGGCCCAGTGCGGCCCCAGTGCCTCCTCCCACCCCTGGTTCCTGAAATCCATG  1374
Db   2575  CGGCCTG---AGACCTACCGCAGAAGAGACCCTAGAACATCCTTGGTT---------CAAA  2622
Qy   1375  CCTGCGGAGGAGGCCCACTTCATCAACACCAACAAGCAGCTCAAGTTCCTCTCGGCCCGAAGT  1434
Db   2623  ACTCAGGCAAAGGGCGCAGAGGTGAGCACGGATCACCTGAAGCTATTCCTCTCCGGCGG  2682
Qy   1435  CGCTGCGACGGTTCCCTGATGAGCTACAAGTCCATCCTGGTGATGGCGCTCATCCCTGAG  1494
Db   2683  AGGTGCAGCGCTCCCAGATCAGCTACAAAATGCCACCTGGTGCTGCGGCCCCATCCCCGAG  2742
Qy   1495  CTGCTGCGGGGGCCACCCGGA  1514
Db   2743  CTGCTGCGGGGGCCCCCCAGA  2762
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PD   31-JAN-2002.
XX
PF   20-JUL-2001; 2001WO-US023092.
XX
PR   21-JUL-2000; 2000US-0220038P.
PR   28-JUL-2000; 2000US-0222112P.
PR   04-AUG-2000; 2000US-0222831P.
PR   11-AUG-2000; 2000US-0224729P.
XX
PA   (INCY-) INCYTE GENOMICS INC.
PA   (THOR/) THORNTON M.
XX
PI   Thornton M, Yue H, Khan FA, Gururajan R, Hafalia AJA, Walia NK;
PI   Patterson C, Ramkumar J, Gandhi AR, Policky JL, Baughn MR;
PI   Triboulev CM, Baandman O, Nguyen DB, Lu Y, Burford N, Lal P, Ding L;
PI   Yao MG, Elliott VS, Recipon SA, Kearney L, Lu DAM, Greenwald SR;
PI   Tang YT, Xu Y, Walsh RT, Gietzen KJ, Yang J, Hillman JL;
XX
DR   WPI; 2002-206083/26.
XX
PT   New human kinase polypeptide, useful in diagnosis, prevention and
PT   treatment of cancer, immune disorder, growth and developmental disorder,
PT   cardiovascular disorder and lipid disorder.
XX
PS   Claim 5; Page 191-193; 196pp; English.
XX
CC   The present invention relates to an isolated human kinase polypeptide
CC   (PKIN) or a biologically active/immunogenic fragment of PKIN. PKIN is
CC   useful for diagnosing, treating and preventing cancer (e.g., leukaemia,
CC   lymphoma, melanoma), an immune disorder (e.g., acquired immunodeficiency
CC   syndrome (AIDS), Addison's disease, allergy, anaemia, asthma, Crohn's
CC   disease, rheumatoid arthritis), a growth and developmental disorder (e.g.
CC   bursitis, cirrhosis, hepatitis, psoriasis, Cushing's syndrome), a
CC   cardiovascular disorder (e.g., atherosclerosis, hypertension, myocardial
CC   infarction), and a lipid disorder (e.g., fatty liver, cholestasis,
CC   Gaucher's disease, Niemann-Pick's disease). PKIN is useful in a number of
CC   drug screening techniques and to analyse the proteome of a tissue or cell
CC   type. PKIN is useful for creating knockin humanised animals or transgenic
CC   animals to model human diseases, in somatic or germline gene therapy, to
CC   generate a transcript image of a tissue or cell type, for detecting
CC   differences in the chromosomal location due to translocation, inversion,
CC   etc., among normal, carrier or affected individuals, and as hybridisation
CC   probes for mapping naturally occurring genomic sequences. PKIN is useful
CC   in southern or northern analysis, dot blot or other membrane-based
CC   technologies, in PCR technologies, in dipstick, pin, multiformat enzyme
CC   linked immunosorbent (ELISA)-like assays and in microarrays utilising
CC   fluids or tissues from patients to detect altered PKIN expression. The
CC   present sequence is human PKIN-18 cDNA. Note: This sequence is said to
CC   encode PKIN-18 referred as SEQ ID NO:18 (AAE19160). However this does not
CC   appear to be the case
XX
SQ   Sequence 7789 BP; 1469 A; 2558 C; 2470 G; 1292 T; 0 U; 0 Other;

Query Match             6.3%;  Score 327.6;  DB 6;  Length 7789;
Best Local Similarity  56.6%;  Pred. No. 8.5e-50;
Matches  725;  Conservative   0;  Mismatches 519;  Indels  36;  Gaps  5;

Qy    256 CTCCCAGGGCGCCCCCATCCATGCAGGTAACCATGGATGTGCAGGCACAGACAGGCGGA 315
                                                                                    
Db   1560 CTGGCAGGAGGCCCTCGGTTTGAGTCCATCATGAGTCCAGGACCGTGGAGGTGGGGGAA 1619

Qy    316 ACGGGCCCAATTCGAGGCTATCATTGAGGGCGACCCACAGCGCCTCGGTGACCTGGTACAAG 375
                                                                                    
Db   1620 ACTCTCGCTTTGCGGTGCGTGGTGTGGACAGCACCCGGCTTAGCCAGCAGCAAGAAGGCACCACATAC 1679

Qy    376 GACAGCGTCCAGTGGTGGTGACAGCACCCGGCTTTAGCCAGCAGCAAGAAGGCACCACATAC 435
                                                                                    
Db   1680 GACGAGGTGCTGCTGACCGCCGAGGCAGCAGCCATGGCGTTCGTGTACGGAGGAATGAGTGC 1739

Qy    436 TCCCTGGTGCTGAGGCATGTGGCCTCCGAAGGATGCCCGGCGTTTACCTGCTCGGCCCCA 495
                                                                                    
Db   1740 TCCCTGGTGGTGCTGCTCAGCCAGGACGCAGCCCGGGGGCCCAGGATGGAGGCGTCTTCACCTCTACACCTGCCACCACCGGCCCAG 1799
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Qy    496 AACACTGGTGCCCAGTGCTCTGCAAGGCAGAGCTGCTGTGC------------TT 540
                                                                                    
Db   1800 AACCTGGCGGGTGAGGTCTTCCTGCAAAGCAGAGTTGGCTGTGTGCATTCAGCTCAGACAGCT 1859

Qy    541 GGGGGGACAATGAGCCGACTCAGAGAAGCAAAGCCACCGGAGGAAGCTGCACTCCTTC 600
                                                                                    
Db   1860 ATGGAGGTCGAGGGGGTCGGGGGAGGATGAGGACCATCGAGGAGGAAGGAGACTCAGCGGACTTT 1919

Qy    601 TATGAGGTCAAGGAGGAGATTGGAGGGGGTGTTGGCGTTCGTAAAAGAGAGTGCAGCAC 660
                                                                                    
Db   1920 TATGACATCCACCAGGAGATCGGCAGGGGGTGCTTCTCCTACTTGCGGCGCATAGTGGAG 1979

Qy    661 AAAGGAAACAAGATCTTGTGCGCTGCCAGTTCATCCCCTACGGAGCGGAGGAGAACTCGGGCC 720
                                                                                    
Db   1980 CGTAGCTCCGGCCTGGAGTTTGCGGCCAAGTTCATCCCCAGCCCAGCCAAGCCAAAGGCA 2039

Qy    721 CAGGCATACAGGGAGGCGAGACATCCTGGGCGCGTGAGCCGCGGCACCCGGGTCACGGGGGCTG 780
                                                                                    
Db   2040 TCAGGCCGTCGGGAGGCCCCCGGTCTGGCCAGGCTCCAGGACGACGACTGTGTCCTCTACTTC 2099

Qy    781 CTGGACCCAGTTGAGACCCGCAAAGACCCTCATCCTCATCCTGAGCTGTGCTCATCCCAG 840
                                                                                    
Db   2100 CATGAGCCTTGCAGGCGCGGGGGACTGGCTCATTGTCACCGAGCTCGCACA----GAG 2156

Qy    841 GAGCTGCTGACCGCCTGTACAGGAAGGGCGTGGTGACGAGGGCCGAGTCAAGGTCTAC 900
                                                                                    
Db   2157 GAGCTGCTGGAGCGAATCGGCCAGGAAAACCCACCGTGTGAGTCTGAGATCCGGGCCTAT 2216

Qy    901 ATCCACCAGCTGGTGGAGGGGCTGCACTACCTGCACAGCCATGGCGTTCCCACCTGGAC 960
                                                                                    
Db   2217 ATGCGGACGGTGCTAGAGGGAATACACTACCTGCACAGCCACGTGCACCTGCACCTCGAT 2276

Qy    961 ATAAAGCCCTCTAACATCTGATGGTGCATCCTGCCCGGGAAGACATTAAA------ATC 1014
                                                                                    
Db   2277 GTCAAGCCTGAGAACCTGTCGTGTGGATGGTGCTGCGGGCCAGCAGGTGCCGGATC 2336

Qy   1015 TGCGACTTGGCTTGTGCCCAGACAATCACCCCAGCGAGCTGCAGTTCAGCCAGTACCGC 1074
                                                                                    
Db   2337 TGTGACTTTGGGAATGCCCAGGACCTGCTGGGACTCCAGGAGCGCCCCAGTACTGGC 2396

Qy   1075 TCCCCTGAGTTCGTCTCCCCCGAGATCATCCAGCAGAACCCTGTGAGCGAAGCCTCCGAC 1134
                                                                                    
Db   2397 ACACCTGAGTTTGTAGCACCCGAGATTGTCAATCAGAGCCCGTGTCGGAGTCACTGAC 2456

Qy   1135 ATTTGGGCCATGGGTGTCATCTCCTACCTCAGCCTGACCTGCTCATCCCCATTTGCCGGC 1194
                                                                                    
Db   2457 ATCTGGCCTGTGGGTGTTGTTGCCTTCCTGTGGATCCTGTGCCAGGAATCTCCCGTTTGTTGGG 2516

Qy   1195 GAGAGTGACCGTGCCACCCTCCTGAACGTCCTGAGGGGCGCGTGTCATGGAGCAGCCCC 1254
                                                                                    
Db   2517 GAAAATGACCGGACAACATTGATGAACATCCGAAACTACAACGTGGCTTCGAGGAGACC 2576

Qy   1255 ATGGCTGCCCACCTCAGCGAGAGCGCCAAAGACTTCATCAAGGCTACGCTGCGAGAGCC 1314
                                                                                    
Db   2577 ACATTCCTGAGCCTGACACAGGGAGGCCCGGGGCTTCCTCATCAAAGTGTTGGTGCAGGAC 2636

Qy   1315 CCTCAGGCTCCGGCGCCTAGTGCGGCCCCAGTGCCTCTCCCACCCCCTGGTTCCTGAAATCCATG 1374
                                                                                    
Db   2637 CGGCTG--AGACCTACCGCGACGAAGAGACACCCTAGAACATCCTTCGTT-------CAAA 2684

Qy   1375 CCTGGCGGAGGCCCCACTTCATCACACCAAGCAGCTCAAGTTCCTCCTGGCCGGAAGT 1434
                                                                                    
Db   2685 ACTCAGCAAGAGGGCGCAGAGGTGAGCACGGATCACCTGAAGGCTATTCCTCTCCCGGCCG 2744

Qy   1435 CGCTGGCAGTGGTGGTGACAGCACCCGGCTTTAGCCAGCAGCAAGAAGGCACCACATAC 1494
                                                                                    
Db   2745 AGGTGGCAGCGGCCTCCCAGATCCCAGCTCACAATGCACCTGTGCTGCCACCATCCCCAG 2804

Qy   1495 CTGCTGCGGGGCCCACCCGA 1514
                                                                                    
Db   2805 CTGCTGCGGGGCCCCCCAGA 2824
```

RESULT 14
ADE47675

ID   ADE47675 standard; DNA; 9698 BP.
XX
AC   ADE47675;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Human NOV14c gene SEQ ID NO.37.
XX
KW   ds; gene; human; cardiant; antiarteriosclerotic; hypotensive;
KW   immunosuppressive; dermatological; anorectic; cytostatic; antidiabetic;
KW   haemostatic; anti-HIV; antiasthmatic; antibacterial; virucide;
KW   neuroprotective; nootropic; antiparkinsonian; antilipaemic; gene therapy;
KW   vaccine.
XX
OS   Homo sapiens.
XX
PN   WO2003076642-A2.
XX
PD   18-SEP-2003.
XX
PF   02-AUG-2002; 2002WO-US024459.
XX
PR   02-AUG-2002; 2001US-0309501P.
PR   02-AUG-2001; 2001US-0309501P.
PR   03-AUG-2001; 2001US-0310291P.
PR   08-AUG-2001; 2001US-0311292P.
PR   09-AUG-2001; 2001US-0311951P.
PR   13-AUG-2001; 2001US-0311979P.
PR   14-AUG-2001; 2001US-0312203P.
PR   17-AUG-2001; 2001US-0313156P.
PR   17-AUG-2001; 2001US-0313201P.
PR   20-AUG-2001; 2001US-0313702P.
PR   21-AUG-2001; 2001US-0314031P.
PR   23-AUG-2001; 2001US-0314466P.
PR   28-AUG-2001; 2001US-0315403P.
PR   29-AUG-2001; 2001US-0315853P.
PR   31-AUG-2001; 2001US-0316508P.
PR   21-SEP-2001; 2001US-0323936P.
PR   03-DEC-2001; 2001US-0338078P.
PR   05-FEB-2002; 2002US-0354655P.
PR   05-MAR-2002; 2002US-0361764P.
PR   19-APR-2002; 2002US-0373825P.
PR   15-MAY-2002; 2002US-0380971P.
PR   15-MAY-2002; 2002US-0380980P.
PR   16-MAY-2002; 2002US-0381039P.
PR   28-MAY-2002; 2002US-0383761P.
PR   29-MAY-2002; 2002US-0383887P.
PR   01-AUG-2002; 2002US-00210130.
XX
PA   (CURA-) CURAGEN CORP.
XX
PI   Zerthusen BD, Patturajan M, Kekuda R, Miller CE, Rieger DK;
PI   Pena CEA, Shimkets RA, Li L, Berghs C, Zhong M, Casman SJ, Voss EZ;
PI   Boldog PL, Padigaru M, Anderson G, Shenoy SG, Ji W, Gorman L;
PI   Vernet CAM, Leite MW, Guo X, Anderson DW, Spytek KA, Gerlach VL;
PI   Burgess CE, Khramtsov NV, Ort T, Ellerman K, Rastelli L, Agee ML;
PI   Chaudhuri A, Chant JS, Dipippo VA, Edinger SR, Eisen A, Gangolli EA;
PI   Giot L, Ooi CE, Rothenberg ME, Spaderna SK, Hjalt T, Liu X;
PI   Taupier RJ, Catterton E;
XX
DR   WPI; 2003-779062/73.
DR   P-PSDB; ADE47676.
XX
PT   New NOVX polypeptides and nucleic acids, useful for preventing or
PT   treating NOVX-associated disorders, e.g. cancer, diabetes,
PT   atherosclerosis, asthma or AIDS, and in chromosome mapping, tissue typing
PT   or pharmacogenomics.
XX
PS   Claim 20; SEQ ID NO 37; 562pp; English.
XX
CC   The invention relates to a novel (NOVX) human polypeptide. A polypeptide
CC   of the invention has cardiant, antiarteriosclerotic, hypotensive,
CC   immunosuppressive, dermatological, anorectic, cytostatic, antidiabetic,
CC   haemostatic, anti-HIV, antiasthmatic, antibacterial, virucide,
CC   neuroprotective, nootropic, antiparkinsonian, and antilipaemic activity.
CC   A polynucleotide encoding a polypeptide of the invention may have a use
CC   in gene therapy, and as a vaccine. A polypeptide of the invention is
CC   useful in the manufacture of a medicament for treating a syndrome
CC   associated with a human disease, the disease selected from a pathology
CC   associated with the polypeptide. These may also be used in diagnosing,
CC   treating or preventing NOVX-associated disorders such as cardiomyopathy,
CC   atherosclerosis, hypertension, scleroderma, obesity, cancer, diabetes,
CC   haemophilia, graft-versus-host disease, AIDS, asthma, Crohn's disease,
CC   multiple sclerosis, infections, anorexia, cancer-associated cachexia,
CC   neurodegenerative disorders (e.g. Alzheimer's disease or Parkinson's
CC   disease), haematopoietic disorders, dyslipidaenias and other wasting
CC   disorders associated with chronic diseases. The nucleic acids are also
CC   used as hybridisation probes, in chromosome mapping, tissue typing,
CC   preventive medicine, and pharmacogenomics. The polypeptides are also
CC   useful as vaccines. The present sequence encodes a NOVX polypeptide of
CC   the invention.
XX
SQ   Sequence 9698 BP; 1693 A; 3352 C; 3163 G; 1490 T; 0 U; 0 Other;

```
Query Match             6.3%;  Score 327.6;  DB 9;  Length 9698;
Best Local Similarity  56.6%;
Matches  725;  Conservative    0;  Mismatches  519;  Indels   36;  Gaps    5;

Qy    256 CTCCCAGGGCCCCATCCATGCAGGTAACCATCGAGGATGTGCAGGACACAGACAGGCGGA 315
          |||||  ||| |||||   || || |||||  || ||||  |||||  ||| |  ||| ||||
Db   4324 CTGGCAGAGGCCCCTCGGTTTGAGTCATCATCGAGGACGTGGAGGTGGGGGCTGGGGAA 4383

Qy    316 ACGGGCCAATTCGAGGCTATCATTGAGGGCGACCCAGCCCTCGGTGACCTGGTACAAG 375
          ||   ||  || ||| || |   | || || || |||||| |||| ||| || ||||||
Db   4384 ACTGCTCGCTTTGCGGTGGTGGTCGAGGGAAAACCACTGCCCGGACATCATGTGGTACAAG 4443

Qy    376 GACAGCGTCCAGCTGGTGACACGACCCGGCTTAGCCAGCAGCAAGAAGGCACCACATAC 435
          |||   ||| || |||||| | | |||  |||   ||| ||||   ||| || ||   ||
Db   4444 GACGAGTGCTGCTGACCGAGCAGCAGCCATGTGAGCTTCGTGTACGAGGAGAATGAGTGC 4503

Qy    436 TCCCTGGTGTGTGAGGCATGTGCCTGAAGGATGCCGCGTTTACCTGGCGTTTACACCTGGCCCAA 495
          |||||||||||||      || | |||  |||| || |   ||| |  |||| ||||||  ||||
Db   4504 TCCCTGGTGTGTGCTCAGCACGCGGGCCCCAGGATGGAGGCGTCTACACCTGCACCGCCCAG 4563

Qy    496 AACACTGGTGGCCAGGTGCTCTGCAAGGCAGAGCTGCTGGTGC--------TT 540
          |||  ||  || || ||| | |  |||  |||| || || ||||       ||
Db   4564 AACCTGCGCGGTGAGGTCTTCCTGCAAAGCAGCAGTGGCTGTGTGCATTCAGCTCAGACAGCT 4623

Qy    541 GGGGGGACAATGAGCCGACTCAGAGAAGCAAAGCACCGGAGGAAGCTGCACTCCTTC 600
          |||||    ||||| ||  || | | ||||| |||| ||| || || | | || |||
Db   4624 ATGGAGGTCGAGGGGGTCGGGGAGGATGAGGACCCATCGAGGAAGGACCATCAGCGACTTT 4683

Qy    601 TATGAGGTCAAGGAGGAGATTGAAGGGGCGTGTGTTTGGCTTCGTAAAAGAGTGCAGCAC 660
          |||||  || || ||||| | ||   ||| ||| | ||||| |   | || || || |||
Db   4684 TATGACATCCACCAGGAGATCGGCCAGGGGGTGCTTCTCCTACTGCGCGCATAGTGGAG 4743

Qy    661 AAAGGAAAACAAGATCTTGTGCGCTGCCAAGTTCATCCCCCACGGAGCAGAACTCGGGCC 720
          ||  ||||  ||| |  | | |   ||||||||||||||| ||| | || | |   |||||
Db   4744 CGTAGCTCCCGGCGAGTTGCCCCAAGTTCATCCCCCACGGCCAGGCCAAGCCAAAGGCA 4803

Qy    721 CAGGCATACAGGAGGAGACAATCCTGGCCGCGCTGAGCCACCCGCTGGTCACGGGGCTG 780
          |||||    ||||| || ||| | |||| || || ||||| || |||| ||||  ||||
Db   4804 TCAGGCGGTCGGGGAGGCCCGGGCTGCTGCCAGCTCCAGCACGACGTGTTCTCTACTTC 4863

Qy    781 CTGGACCAGTTGAGACCCGCAGACCCTCATCCTCATCCTCGGGAGCTGTGCTCATCCGAG 840
          ||||| ||| | || | | |||  || |||||| |||| | ||  ||| || | ||||||
Db   4864 CATGAGGGCCTTCGAGGAGGCGCGGGGACTGGTCATTGTCACCGAGTCTGCACA--GAG 4920

Qy    841 GAGCTGCTGGACCCGCCTGTACAGGAAGGGCGTGTGACGGAGGCCGAGGTCAAGGTCTAC 900
          |||||||||| | |  || ||||||  | | | ||   |||| ||| ||| |||| ||||
Db   4921 GAGCTGCTGGAGCGAATCGCCAGGAAACCACCGTGTGTGATCTGTGAGATCGGGCCTAT 4980

Qy    901 ATCCAGCAGCTGGTGTGGAGGGGGGTGCACTAACCTGCACAGCCATGGGGTTCCCACCTGGAC 960
          ||  |||||||||| | | || || || |  ||  |||||| |||  |||||| |||||| ||
Db   4981 ATGGGGCAGGTGCTGAGGGAGGAATACCATACACCTGCACCCAGAGCAGCACGTGCTGCACCTCGAT 5040
```

PI Yan C, Gan W;
XX
DR WPI; 2003-722329/68.
DR P-PSDB; ADB79959.
XX
PT New peptides related to kinase protein subfamily useful for treating
PT disorders associated with abnormal expression of kinase protein in
PT testis, nervous tissue, fetal, lung, ovary tumor tissue.
XX
PS Claim 4; Fig 1A-C; 86pp; English.
XX
CC The present sequence encodes a human kinase protein (I), which is located
CC to chromosome 2. The present invention also describes an allelic variant
CC or orthologue of (I). (I) has cytostatic activity, and can be used in
CC gene therapy. (I) can be used in substantial and specific assays related
CC to functional information of the protein sequence, to raise antibodies or
CC to elicit immune responses, as reagents in assays to determine the levels
CC of protein in biological fluids. (I) can be used in drug screening assays
CC for identifying agents that are useful in treating disorders associated
CC with the absence of, inappropriate, or unwanted expression of kinase
CC protein in testis, nervous tissue, foetal, lung, brain anaplastic
CC oligodendroglioma, lung carcinoid tissue, soft tissue leiomyosarcoma,
CC ovary tumour tissue, or germ cell tumour tissue. The protein and nucleic
CC acid sequences of (I) are useful as models for the development of human
CC therapeutic targets, in the identification of therapeutic proteins and as
CC targets for the development of human therapeutic agents that modulate
CC protease activity in cells and tissues that express the kinase peptide.
XX
SQ Sequence 9807 BP; 1721 A; 3370 C; 3208 G; 1508 T; 0 U; 0 Other;

Query Match 6.3%; Score 327.6; DB 9; Length 9807;
Best Local Similarity 55.6%; Pred. No. 8.8e-50;
Matches 725; Conservative 0; Mismatches 519; Indels 36; Gaps 5;

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Qy    256 CTCCCAGGGCCCCATCCATGCAGGTAACCATCGAGGATGTGCAGGCACAGACAGGCGGA 315
          ||||||||  || |||| |||  ||| |||| | |||| || ||| | || |||||  |
Db   4441 CTGGCAGAGGCCCCTCGGTTTGAGTCATCATGGAGACGTGGAGGTGGGGGCTGGGGAA 4500

Qy    316 ACGGCCCAATTCGAGGCTATCATTGAGGGCGACCCACAGCCCTCGGTGACCTGGTACAAG 375
          ||| |||  || ||| || | |||||| | ||| ||||| |||||| || ||||||||||
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Qy    376 GACAGCGTCCAGCTGGTGGACAGCACCCGGCTTAGCGCAGCAGCAGCAAGGCAGCCACCATAC 435
          |||  || | ||| |||||||| | ||||| |||| || ||||| |||||| || ||| ||
Db   4561 GACAGGTGCTGCTGTGACCGAGCAGCCATGTGAGCTTCGTGTACGAGGAGAATGAGTGC 4620

Qy    436 TCCCTGGTGCTGAGGCATGGCATGTGGCTTCGAAGGATGCCCGGTTTACACCTGCTGGCCCAA 495
          || |||||| ||| |||||| || ||| ||||||| || ||||  || ||||| |||||||
Db   4621 TCCCTGGTGCTGTGCTCAGCACGGGGCCCCAGGATGATGGAGGCGGTCTCACACCTGCACCCGGCCCAG 4680

Qy    496 AACACTGGTGGCCAGGTGCTCTGCAAGCAGAGCCAGGAGAGCTGCTGGTGC----------TT 540
          |||||||||| ||||| || ||| |||||| ||||| || ||| |||| |         ||
Db   4681 AACCTGGCGGGTGAGGTCTCCTGCAAGCACAGTTGGCTGTGCATTCAGTCAGACAGCT 4740

Qy    541 GGGGGGACAATGAGCCGGACTCAGAGAAGCAAAGCCACCGGAGGAGCTGCACCTCCTTC 600
          |||  || |  ||| || ||| || || ||||| ||  || |||||| |||| ||||||
Db   4741 ATGGAGGTCGAGGGGTCGGGGGAGGGATGAGGACCATCGAGGAGGAAGGAGACTCAGCGACTTT 4800

Qy    601 TATGAGGTCAAGGAGGAGGATTGGAAGGGGCGTGTTGGCTTCGTAAAAAGAGTGCAGCAC 660
          || ||| || |||||| ||||| || ||| |   || || ||||| | || |||| ||
Db   4801 TATGACATCCACCAGGAGATCGGCAGGGTGCTTTCTCACTTGCGGCAGAACTCGGGCC 4860

Qy    661 AAAGGAAACAAGATCTTGTGCGCTGCCAAGTTCATCCCCTACAGGACGCAGAACTCGGGCC 720
          |||| ||||||| |  ||||| ||||| |||| ||| ||||||||| || || |||| |
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Qy    721 CAGGCATACAGGGAGCGAGACATCTCGGCCGCTGGTCACGGGGCTG 780
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Db   4921 TCAGCGCGTCGGGAGGCCCGGCTCGGCCAGGGCTCCAGCACGACTGTGTCCTCTACTTC 4980

Qy    781 CTGGACCAGTTGACACCCGCAAGACCCTCATCCTCCTGGAGCTGTGCTCATCCGAG 840
          |||  || | ||||||   |||| |||| |  ||| | || ||||||| ||||||
Db   4981 CATGAGGGCCTTCGAGAGGCGCCGGGGACCTGGGTCATTGTCACCGAGCTCTGCACA---GAG 5037
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RESULT 15
ADB79958
ID ADB79958 standard; cDNA; 9807 BP.
XX
AC ADB79958;
XX
DT 04-DEC-2003 (first entry)
XX
DE Human kinase protein encoding cDNA SEQ ID NO:1.
XX
KW human; kinase; enzyme; chromosome 2; cytostatic; gene therapy;
KW brain anaplastic oligodendroglioma; lung carcinoid;
KW soft tissue leiomyosarcoma; ovary tumour; germ cell tumour; gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..9807
FT /tag= a
FT /product= "kinase protein"
XX
PN WO2003076577-A2.
XX
PD 18-SEP-2003.
XX
PF 05-MAR-2003; 2003WO-US006666.
XX
PR 05-MAR-2002; 2002US-0361339P.
XX
PA (APPL-) APPLERA CORP.
XX

```
Qy    961 ATAAAGCCCTCTAACATCCTGATGGTGCATCCTGCCCGGGAAGACATTAAA------ATC 1014
          |||||  ||||  || ||| || || ||||| |||| ||| ||| |||  |       |||
Db   5041 GTCAAGCCTGAGAACCTGCTGGTGTGGGATGGTGCTGCGGCGAGCAGCAGGTGCGGATC 5100

Qy   1015 TGGGACTTGGCTTTGCCCAGAACATCACCCCAGCAGAGCTGCAGTTCAGCCAGTACGGC 1074
          ||| |||||| ||| || ||  |||| || | |||| ||| |||| |||||| || |||
Db   5101 TGTGACTTTGGGAATGCCCAGGAGCTGACTCCAGGAGAGCCCCAGTACTGCCAGTATGC 5160

Qy   1075 TCCCCTGAGTTCGTCTCCCCCGAGATCATCCAGCAGCAGAACCCTGTGAGCGAAGCCTCCGAC 1134
          ||||| ||||| ||| || ||| |||| ||||||| ||| ||||| || ||| ||||||||||
Db   5161 ACACCTGAGTTGTAGCACCCGGAGATTGTCAATCAGGAGCCCGTGTCTCGGAGTCACTGAC 5220

Qy   1135 ATTTGGGCCATGGGTGTCATCTCCTACCTCAGCCTGACCTTCATCCCCATTTGCCGGC 1194
          |||| || |||  |||| ||| ||| || |||| ||| || |||| ||| || ||||
Db   5221 ATCTGGCCTGTGGGTGTTGCCTTCCTCTCTGACAGGAATCTCCCCGTTTGTTGTGGG 5280

Qy   1195 GAGAGTGACCGGTGCCACCCTCCTGGAGGGCGCGGTCATGGAGCAGCCCC 1254
          ||||||||| |||||| |||| || |||  ||  | |||| || |||||||
Db   5281 GAAAATGATCACCGGACAACATTGATGAACATCCGAAACTACACAGTGGCCCTTCGAGGAGACC 5340

Qy   1255 ATGGCTGCCCACCTCAGCGAAGACGCCAAAGACTTCATCAAGGCTACGCGTCGCAGAGAGCC 1314
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Db   5341 ACATTCCTGAGCCTGAGCACGCAGGAGGCCCGGGCCTTCCTCATCAAAGTGTTGGTGCAGGAC 5400

Qy   1315 CCTCAGGCCCGGCCTAGTGCGGCCCAGTGCCTCTCCACCCTGGTTCCTGAAATCCATG 1374
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Db   5401 CGGGTG--AGACCTACCGCCAGAGAGACGACCCTAGAACATCCTTGGTT------CAAA 5448

Qy   1375 CCTGCGGAGGAGGGCCACTTCATCAACAACCAAGCAGCTCAAGTTCCTCCTGGCCGGAAGT 1434
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Db   5449 ACTCAGGCAAAGGGCGCAGAGGTGAGCAGGTGCACGGCCACAGCCTATTCCTTCCCCGGGCGG 5508

Qy   1435 CGTTGGCGAGCGTCCTGATGAGCTACAAGTCCATCCTGGTGATGCGCTCCATCCTGAG 1494
          ||||| || ||  | || ||  || || ||| || || || || |||| |  || |||||
Db   5509 AGGTGGCACGCGTCCCAGGATCAGCTACAAATGCCACCTGGTGCTGCGCGCCCCATCCCCAG 5568

Qy   1495 CTGCTGCGGGGCCACCCGA 1514
          ||||| |||||| ||||||
Db   5569 CTGCTGCGGGGCCCCCCCAGA 5588
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Qy   841  GAGCTGCTGGACCGCCTGTACAGGAAGGGCGTGGTGACGGAGGCCGAGGTCAAGGTCTAC   900
          ||||||||||| || ||  |||| | |  |  | ||  | ||| || || |||||| ||
Db  5038  GAGCTGCTGGGAGCGAATCGGCAGGAAACCACCGGTGTGTGAGTCTGAGATCCGGGGCTAT  5097

Qy   901  ATCCAGCAGCTGGTGGAGGGGCTGCACTACCTGCACAGCCATGGCGTTCTCCACCTGGAC   960
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Db  5098  ATGGCGCAGGTGCTAGAGGAGGGAATACACTACCTGCACCAGAGCCACGTGCTGCACCTCGAT  5157

Qy   961  ATAAAGCCCTCTAACATCCTGATGGTGCATCCTGCCCCGGAAGACATTAAA------ATC  1014
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Qy  1015  TGCGACTTTGGCTTTGCCCAGAACATCACCCCAGCAGAGCTGCCAGTTCAGCCAGTACGGC  1074
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Db  5218  TGTGACTTTGGGAATGCCCAGGAGCTGACTCCCAGGAGAGCCCCAGTACTGCCAGTATGGC  5277

Qy  1075  TCCCCTGAGTTCGTCTCCCCCGAGATCATCCAGCAGGACAACCCTGTGAGCGAAGCCTCCGAC  1134
          | |||||| || || | | | |||| || | ||| | || | || |   | | |||  ||||
Db  5278  ACACCTGAGTTTGTAGCACCGAGATTGTCAATCAGAGCCCCGTGTCTGGAGTCACTGAC  5337

Qy  1135  ATTTGGGCCATGGGTGTCATCTCCTACCTCAGCCTGACCTGCTCATCCCATTTGCCGGC  1194
          || ||| || || | || |  | ||| ||  | ||||  | ||  |  |||| |||||
Db  5338  ATCTGGCCTGTGGGGTGTGTTGTTGCCTTCCTTCCTGTCTGACAGGAATCTCCCGTTTGTTGGG  5397

Qy  1195  GAGAGTGACCGTGCCACCCTCCTGAACGTCCTGGAGGGGCGCGTGTCATGGAGCAGCCCC  1254
          || | ||| | | ||||| | | ||   |    || || |   |  ||| |||||| ||
Db  5398  GAAAATGACCGGACAACATTGATGAACATCCGAAACTACAACGTGGCCTTCGAGGAGACC  5457

Qy  1255  ATGGCTGCCCACCTCAGCGAAGACGCCAAAGACTTCATCAAGGCTACGCTGCAGAGAGCC  1314
          ||||| | |||  | ||| | | |||| ||| |||||||||| | || ||||| || ||
Db  5458  ACATTCCTGAGCCTGAGCAGGGAGCCCGGGGCTTCCTCATCAAAGTGTTGGTGCAGGAC  5517

Qy  1315  CCTCAGGCCCGGCCTAGTGCGGCCCAGTGCCTCTCCCACCCCTGGTTCCTGAAATCCATG  1374
          | | ||||| ||  | || | | ||  |  || |||| || |||||||     |  |
Db  5518  CGGCTG--AGACCTACCGCAGAAGAGACCCTAGAACATCCTTGGTT------CAAA  5565

Qy  1375  CCTGCCGGAGGAGGCCCACTTCATCAACAACAAGAGCTCAAGTTCCTCCTGGCCGAAGT  1434
          | | |  ||| |||| |||| ||| | || | ||||| | ||| |  |  || | |
Db  5566  ACTCAGCAAAGGGCGCAGAGGTGAGCACGGATCACCTGAAGCTATTCCTCTCCCGGCGG  5625

Qy  1435  CGCTTGCCAGCGTTCCCTGATGAGCTACAGTCATCCTGGTGATGCGGCTCATCCCTGAG  1494
          || | || |||  |  ||  || ||||| | | ||| |||||| ||||| |||||| ||
Db  5626  AGGTGGCAGCGCGCTCCCAGATCAGCTACAAAATGCCACCTGGTGCGCGCCCATCCCCGAG  5685

Qy  1495  CTGCTGCTGGGGGGCCCACCCGA  1514
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Db  5686  CTGCTGCGGCGGCCCCCCCAGA  5705
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Search completed: April 26, 2004, 09:08:04
Job time : 1258 secs

OM nucleic - nucleic search, using sw model

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

Run on: April 26, 2004, 08:13:13 ; Search time 8097 Seconds
(without alignments)
19203.702 Million cell updates/sec

Title: US-10-697-263-1
Perfect score: 5207
Sequence: 1 cagcacgaggaactccttct.........aaaaaaaaaaaaaaaaaaaaaa 5207

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27751289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estcov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
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21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | | Score | % Match | Query Length | DB | ID | Description |
|---|---|---|---|---|---|---|---|
| 1 | | 883.8 | 17.0 | 983 | 13 | BX460671 | BX460671 BX460671 |
| 2 | | 848.4 | 16.3 | 931 | 13 | BX409793 | BX409793 BX409793 |
| 3 | | 777.4 | 14.9 | 924 | 13 | BX409792 | BX409792 BX409792 |
| 4 | c | 713.4 | 13.7 | 715 | 12 | BM985339 | BM985339 UI-CF-EC1 |
| 5 | c | 666.8 | 12.8 | 731 | 12 | | BG818748 | BG818748 602779074 |
| 6 | c | 655.6 | 12.6 | 683 | 10 | | AW862431 | AW862431 RC0-CT038 |
| 7 | | 626.2 | 12.0 | 989 | 13 | | BX435097 | BX435097 BX435097 |
| 8 | | 541 | 10.4 | 622 | 12 | | BG999843 | BG999843 MR3-HN006 |
| 9 | | 478.4 | 9.2 | 480 | 13 | | BX280322 | BX280322 BX280322 |
| 10 | | 475 | 9.1 | 475 | 12 | | BI916955 | BI916955 603177768 |
| 11 | | 471 | 9.0 | 653 | 13 | | BY739930 | BY739930 BY739930 |
| 12 | | 463.2 | 8.9 | 768 | 10 | | BF134040 | BF134040 601777770 |
| 13 | | 453 | 8.7 | 477 | 12 | | BI916956 | BI916956 603177770 |
| 14 | c | 434 | 8.3 | 517 | 12 | | BG989614 | BG989614 MR2-HT116 |
| 15 | | 415.2 | 8.0 | 556 | 12 | | BI776197 | BI776197 468982 MA |
| 16 | c | 398.2 | 7.6 | 640 | 14 | | CD774776 | CD774776 UI-M-AQ0- |
| 17 | | 386.8 | 7.4 | 526 | 13 | | BQ554403 | BQ554403 H4027H08- |
| 18 | c | 377.4 | 7.2 | 622 | 14 | | CF176441 | CF176441 800530 MA |
| 19 | | 340.8 | 6.5 | 567 | 12 | | BI345924 | BI345924 374899 MA |
| 20 | | 331 | 6.4 | 479 | 10 | | BF651426 | BF651426 274209 MA |
| 21 | | 324.4 | 6.2 | 494 | 14 | | CF177813 | CF177813 806332 MA |
| 22 | c | 313.4 | 6.0 | 522 | 13 | | BQ554402 | BQ554402 H4027H08- |
| 23 | c | 311.4 | 6.0 | 493 | 10 | | BE110731 | BE110731 UI-R-BJ1- |
| 24 | | 307.8 | 5.9 | 447 | 10 | | BB848582 | BB848582 BB848582 |
| 25 | | 307 | 5.9 | 920 | 10 | | BF160452 | BF160452 60176924 |
| 26 | | 303.2 | 5.8 | 429 | 9 | | AI604658 | AI604658 vm45d02.y |
| 27 | | 296.6 | 5.7 | 494 | 14 | | CB713368 | CB713368 AMGNNUC:N |
| 28 | | 274.4 | 5.3 | 485 | 14 | | CB727068 | CB727068 AMGNNUC:N |
| 29 | | 274 | 5.3 | 397 | 10 | | AW479627 | AW479627 26563 MAR |
| 30 | | 274 | 5.3 | 427 | 9 | | AI006121 | AI006121 ua86g12.r |
| 31 | | 272.2 | 5.2 | 389 | 13 | | BY088395 | BY088395 BY088395 |
| 32 | | 267.2 | 5.1 | 311 | 10 | | BF855491 | BF855491 PM3-FN021 |
| 33 | | 257.4 | 4.9 | 570 | 12 | | BI345921 | BI345921 374896 MA |
| 34 | c | 255 | 4.9 | 328 | 10 | | AW482385 | AW482385 42756 MAR |
| 35 | | 246 | 4.7 | 279 | 10 | | BF762805 | BF762805 PM3-CS003 |
| 36 | | 246 | 4.7 | 397 | 12 | | BG986727 | BG986727 PM1-HT117 |
| 37 | c | 243.4 | 4.7 | 428 | 9 | | AI503993 | AI503993 vm45d02.x |
| 38 | c | 238.2 | 4.6 | 408 | 10 | | BF414891 | BF414891 UI-R-BJ2- |
| 39 | | 237 | 4.6 | 3241 | 11 | | AK035543 | AK035543 Mus muscu |
| 40 | c | 235.2 | 4.5 | 418 | 13 | | BX636992 | BX636992 BX636992 |
| 41 | | 231.6 | 4.4 | 445 | 13 | | BY588786 | BY588786 BY588786 |
| 42 | | 229.4 | 4.4 | 371 | 9 | | AJ573174 | AJ573174 AJ573174 |
| 43 | | 229.4 | 4.4 | 368 | 10 | | AW425352 | AW425352 57189 MAR |
| 44 | c | 229.2 | 4.4 | 411 | 12 | | BI186010 | BI186010 UNL-P-FN- |
| 45 | | 209.8 | 4.0 | 417 | 13 | | BY437537 | BY437537 BY437537 |

ALIGNMENTS

RESULT 1
BX460671
LOCUS       BX460671       983 bp    mRNA    linear    EST 22-MAY-2003
DEFINITION  BX460671 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
            CS0DF017YK06 5-PRIME, mRNA sequence.
ACCESSION   BX460671
VERSION     BX460671.1  GI:31023260
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 983)
AUTHORS     Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE       Full-length cDNA libraries and normalization
JOURNAL     Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 1025.r For
            more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CS0DF017BF03QPi&cluster=1025.r. Contact :
            Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InviTrogen Corporation 1600

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FEATURES    Location/Qualifiers
source      1..983
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="CS0DF017YK06"
            /tissue type="FETAL BRAIN"
            /dev_stage="fetal"
            /clone_lib="Homo sapiens FETAL BRAIN"
            /note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
            was primed with a NotI-oligo(dT) primer. Five prime end
            enriched, double-strand cDNA was digested with Not I and
            cloned into the Not I and EcoRV sites of the pCMVSPORT 6
            vector. Library was not normalized."

            Faraday Avenue Genoscope sequence ID : CS0DF017BF03QP1.

ORIGIN

Query Match    17.0%;  Score 883.8;  DB 13;  Length 983;
Best Local Similarity  99.0%;  Pred. No. 5.9e-114;
Matches 918;  Conservative 2;  Mismatches 4;  Indels 3;  Gaps 3;

Qy 2596 GTGGGCTCCTCCCAGGTGGCACAGAGCTGGCCCTCCCTGGATGCGAGGGCTGGACC 2655
        | ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   56 GGGATCTCCTCCCAGGTGGCACAGAGCTGGCCCTCCCTGGATGCGAGGGCTGGACC 115

Qy 2656 CAGGAGGCTGAGGATCTGTCCGACTCCACACCCACCTTGCAGCGGCCTCAGGAACAGGTG 2715
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  116 CAGGAGGCTGAGGATCTGTCCGACTCCACACCCACCTTGCAGCGGCCTCAGGAACAGGTG 175

Qy 2716 ACCATGCGCAAGTTCTCCCTGGGTGGTGCGCGGGGGCTACGCAGGCGGCTGGCTATGGC 2775
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  176 ACCATGCGCAAGTTCTCCCTGGGTGGTGCGCGGGGGCTACGCAGGCGGCTGGCTATGGC 235

Qy 2776 ACCTTGCCTTGGTGGAGATCCAGGGGGCATGCTGGGCAGGGGCCATGTGGGCCCAGG 2835
        |||||||||| ||||||||| ||||||||||||||||||||||||||||||||||||
Db  236 ACCTTGCCTTTGGTGGAGATGCAGGGGGCATGCTGGGCAGGGGCCATGTGGGCCAGG 295

Qy 2836 ATAGCCTGGGCTGTGTCCAGTCGGAGGAGGAGGAGGAGGAGGCTCAGGCTGAGTCC 2895
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Db  296 ATAGCCTGGGCTGTGTCCAGTCGGAGGAGGAGGAGGAGGAGGCCAGGGCTGAGTCC 355

Qy 2896 CAGTCGGAGGAGCAGCAGGAGGCCAGGGCTGAGAGCCCACTGCCCCAGGTCAGTGCAAGG 2955
        |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db  356 CAGTCGGAGGAGCAGCAGGAGGGCCAGGGCTGAGAGCCCACTGCCCCAGGTCAGTGCAAGG 415

Qy 2956 CCTGTGCCTGAGGTCGGCAGGGGCTCCCACCACAGGAGCTCTCCAGAGCCCATGGGAG 3015
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Db  416 CCTGTGCCTGAGGTCGGCAGGGGCTCCCACCACAGGAGCTCTCCAGAGCCCACCATGGGAG 475

Qy 3016 GACATCGGCAGGTCTCCCTGGTGCAGATCCGGGACCCGTCAGGTGATGCGGAGGGGGGC 3075
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Db  476 GACATCGGCAGGTCTCCCTGGTGCAGATCCGGGACCCGTCAGGTGATGCGGAGGGGGGC 535

Qy 3076 GACACAATATCCCTGGACATTCCGAGGTGGACCCCGCCTACCTCAACCTCTCAGACCTG 3135
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Db  536 GACACAATATCCCTGGACATTCCGAGGTGGACCCCGCCTACCTCAACCTCTCAGACCTG 595

Qy 3136 TACGATATCAAGTACCTCCCATTCGAGTTTATGATCTTCAGGAAAGTCCCCAAGTCCGCT 3195
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Db  596 TACGATATCAAGTACCTCCCATTCGAGTTTATGATCTTCAGGAAAGTCCCCAAGTCCGCT 655

Qy 3196 CAGCCAGAGCCGCCCTCCCCCATGGCTGAGGAGGAGCTGGCCGAGTTCCCGGAGCCCACG 3255
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Db  656 CAGCCAGAGCCGCCCTCCCCCATGGCTGAGGAGGAGCTGGCCGAGTTCCCGGAGCCCACG 715

Qy 3256 TGGGCCCTGGCAGGTGAACTGGGGCCCCCACGCAGGGCCT-GGAGATCACAGAGGAGTCAGA 3314
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Db  716 TGGGCCCTGGCAGGTGAACTGGGGCCCCCACGCAGGGCCTGGGAGATCACAGAGGAGTCAGA 775

Qy 3315 GGATCTGGACGCGCTGCTGCCAGAGGGCTGCCGTGGCAGAGGCTCCGTCTTCGCC 3374
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Db  776 GGATGTGGACGCGCTGCTGCCGGCAGAGGCTGCCGTGGCAGAGGCCAAGTGGTCTTCGCC 835
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Qy 3375 GTCACGCAGCGCCTCTTCCACTTCCC-TGGGAGGCACCTGCCGCTGCGATGAGCCTGCGAGC 3433
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Db  836 GTCACGCAGCGCCTCTTCCACTTCCCTTGGGAGGCACCTGCCGCTGCGATGAGCCTGCGAGC 895

Qy 3434 T-GGGGCTGCGGTGAGAGTGAAGGCCTCCGTGGGAGCACACTCCCGGATCCTGAAGGGC 3492
        | ||||||||||||||||||||||||||||||||||||||||:||:||||:|||||||||
Db  896 TGGGGGGCTGCGGTGAGAGTGAAGGCCTCCGTGGGAGCACATYTCCCGGAYTCCTGAAGGGC 955

Qy 3493 AGGCCGGAAGGTCTGGAGAAGGAGGGG 3519
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Db  956 AGGCCGGAAGGTCTGGAGAAGGAGGGG 982

RESULT 2
BX409793
LOCUS       BX409793                 931 bp    mRNA    linear    EST 13-MAY-2003
DEFINITION  BX409793 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
            CS0DF017YK06 5-PRIME, mRNA sequence.
ACCESSION   BX409793
VERSION     BX409793.1  GI:30640364
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 931)
AUTHORS     Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE       Full-length cDNA libraries and normalization
JOURNAL     Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 1025.r For
            more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CS0BAF014ZC08_AF01308_2&cluster=1025.r.
            Contact : Feng Liang Email : fliang@lifetech.com URL :
            http://fullength.invitrogen.com/ Invitrogen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0BAF014ZC08_AF01308_2.
FEATURES    Location/Qualifiers
source      1..931
            /organism="Homo sapiens"
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            /db_xref="taxon:9606"
            /clone="CS0DF017YK06"
            /tissue_type="FETAL BRAIN"
            /dev_stage="fetal"
            /clone_lib="Homo sapiens FETAL BRAIN"
            /note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
            was primed with a NotI-oligo(dT) primer. Five prime end
            enriched, double-strand cDNA was digested with Not I and
            cloned into the Not I and EcoRV sites of the pCMVSPORT 6
            vector. Library was not normalized."
ORIGIN

Query Match    16.3%;  Score 848.4;  DB 13;  Length 931;
Best Local Similarity  95.9%;  Pred. No. 5.3e-109;
Matches 896;  Conservative 0;  Mismatches 33;  Indels 5;  Gaps 3;

Qy 3410 TGCCGCTGCGATGAGCCTGCAGAGCTGCGGGGCTGCGTGAGAGCTGGAGGCCTCCGTGGAGC 3469
        ||||||||||  ||  |||||  |||| ||||||||||||  | | ||||   |||||||||||
Db    2 TGCCGCTGCGGAACCTGCANGACTGGGGCTGCGTGNGNGNGTGAAGCGCCTTCCGTGGAGC 61

Qy 3470 ACATCTCCCGGATCCTGAAGGGCCAGGGCGGAAGGTCTGGAGAAGGAGGGGGCCCCCAGGA 3529
        |||||||||||||||||||  |||| ||| ||||| ||||||||||||||||||||||||||
Db   62 ACATCTCCCGGATCCTGA--GGGCAGGCGCCGGAGGTCTGGAGAAGGAGGGGGCCCCCAGGA 119

Qy 3530 AGAAGCCAGGCCTTGCTTCCTTCCGGCTCTCAGGTCAGGTCGAAGAGTGTCTTCGCC 3589
        |||||||||||| ||||||||||||||||||||||||||||||||||||||  ||||
Db  120 AGAAGCCAGGCCCTTGCTTCCTTCCGGCTCTCAGGTCAGGTCGAAGAGTCTGGAGACCGCCGA 179
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Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 1025.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0BAF0142C08_AF01308_1&cluster=1025.r.
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0BAF0142C08_AF01308_1.

FEATURES             Location/Qualifiers
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                     /clone="CS0DF017YK06"
                     /tissue_type="FETAL BRAIN"
                     /dev_stage="fetal"
                     /clone_lib="Homo sapiens FETAL BRAIN"
                     /note="Organ: brain; Vector: pCMVSPORT_6; 1st strand cDNA
                     was primed with a NotI-oligo(dT) primer. Five prime end
                     enriched, double-strand cDNA was digested with Not I and
                     cloned into the Not I and EcoRV sites of the pCMVSPORT 6
                     vector. Library was not normalized."

ORIGIN

Query Match       14.9%;    Score 777.4;   DB 13;   Length 924;
Best Local Similarity   96.4%;    Pred. No. 4.6e-99;
Matches  848;   Conservative    0;   Mismatches   24;   Indels    8;   Gaps    5;
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Qy  3421 GAGCTGCGAGAGCTGGGGCTGCGTGAGGAGTGAAGGCCTCCGTGGAGCACATCTCCCGG 3480
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Db     1 GAGCTGCGAGAGCTGGGGCTGCGTGAGGAGTGAAGGCCTCCGTGGAGCACATCTCCCGG 60

Qy  3481 ATCCTGAAGGACCAGGCCCGGAAGTCTGGAGAAGAAGGAGGGGCCCCCAGGAGAAGGAGAAGGCCAGGC 3540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 ATCCTGAAGGACCAGGCCCGGAAGTCTGGAGAAGAAGGAGGGGCCCCCAGGAGAAGGAGAAGGC 120

Qy  3541 CTTGCTTCCTCCGGCTCTCAGTCTGAAGAGCTGGACGCCGGACCATCCTAAGG 3600
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 CTTGCTTCCTCCGGCTCTCAGTCTGAAGAGCTGGACGCCGGACATTCCTAAGG 180

Qy  3601 GAGCTCAGATGAGACTGTGTCCTCGGGCCCAGTCAGTGCTGCTGCCAGGTGTCA 3660
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Db   181 GAGCTCAGATGAGACTGTGTCCTCGGGCCCAGTCAGTGCTGCTGCCAGGTGTCA 240

Qy  3661 GCCCAGCCAGCTGCCCAGCCACCTGGAGCAAAGACCGGAGCCCCCAGGCAGCAGC 3720
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 GCCCAGCCAGCTGCCCAGCCACCTGGAGCAAGACGGAAGCAAGACGGCAGCAGC 300

Qy  3721 CGTGTCCCATCTCGCCACCCTCAAGAACTTCCAGCTTCGGTGGTGGTG 3780
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Db   301 CGTGTCCCATCTCGCCACCCTCAAGAACTTCCAGCTTCGGTGGTGGTG 360

Qy  3781 GCTGAGGACCTGGGTGTGTACACCTGAGCGTGAGCGAATGCGCTGGGAACAGTGACCACC 3840
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 GCTGAGGACCTGGGTGTGTACACCTGAGCGTGAGCGAATGCGCTGGGAACAGTGACCACC 420

Qy  3841 ACGGGCGTCCTCCGGAAGGCAGAGCGCCCCTCATCTTCGGCATGCCGGATATCGGGGAG 3900
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 ACGGGCGTCCTCCGGAAGGCAGAGCGCCCCTCATCTTCGGCATGCCGGATATCGGGGAG 480

Qy  3901 GTGTACGCGGGATGGGGTGCTGCTGGTCTGGAATCCTGGAAGCCCGTGGAATCCGTGACC 3960
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 GTGTACGCGGGATGGGGTGCTGCTGGTCTGGTCTGGAATCCTGGAAGCCCGTGGAATCCGTGACC 540

Qy  3961 TACATTGTGCAGTGCAGCCTAGAAGGCGGCAGCTGGACCACACTGGCCTTCGACATCTTT 4020
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 TACATTGTGCAGTGCAGCCTAGAAGGCGGCAGCTGGACCTGACCACCACTGGCCTNCGACATCTTT 600

Qy  4021 GACTGCTGCTACCTGACCAAGCACCTCCCGGGGTGGCACCTACCCTTCCGCACGGCA 4080
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Db   601 GACTGCTGCTACCTGACCAAGCACCTCCCGGGNGTGGCACCTACCCTTCCGCACGGCA 660

Qy  4081 TGTGTGCAGCAAGGCAGGAATGGGTCCCTACAGCAGCCCCCTACGGAGCAAGTCCTCCTGGGA 4140
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Qy  3590 CATTCCTAAGGAGGAGCTCTCAGATGAGACTGTGGTCCTCGGGCCAGTCAGTGACACTGGCCT 3649
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Db   180 CATTCCTAAGGGAGGAGCTCTCAGATGAGACTGTGGTCCTCGGGCCAGTCAGTGACACTGGCCT 239

Qy  3650 GCCAGGGTCAGCCCCAGCCAGCTGCCCAGGCCACCTGGAGCAAAGACGGAGCCCCCCTGG 3709
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Db   240 GCCAGGGTCAGCCCCAGCCAGCTGCCCAGGCCACCTGGAGCAAGAACGGAGCCCCCCTGG 299

Qy  3710 AGAGCAGCAGCCGTGTCCCATCTCTGCCACCCTCAAGAACTTCCAGCTTCGACCATCC 3769
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Qy  3770 TGGTGGTGGTGTGGCTGAGGACCTGGGTGTGTACACCTGAGCGGCAATGGCCTGGGGA 3829
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   360 TGGTGGTGGTGTGGCTGAGGACCTGGGTGTGTACACCTGAGCGGCAATGGCCTGGGGA 419

Qy  3830 CAGTGACCACCACGGGCGTCCTCCGGAAGGCAGAGCGCCCCTCATCTTCGGCATGCCCGG 3889
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Db   420 CAGTGACCACCACGGGCGTCCTCCGGAAGGCAGAGCGCCCCTCATCTTCGGCATGCCCGG 479

Qy  3890 ATATCGGGGAGGTGTACGCGGATGGGGTGCTGCTGGTCTGGTCTGGAAGCCCGTGGAATCCTACG 3949
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Db   480 ATATCGGGGAGGTGTACGCGGATGGGGTGCTGCTGGTCTGGTCTGGAAGCCCGTGGAATCCTACG 539

Qy  3950 GCCCTGACCACATTGTGCAGTGCAGCTGAAGAGGGCGCAGCTGGACCACACTGGCCT 4009
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Db   540 GCCCTGACCACATTGTGCAGTGCAGCTGCAGCTGAAGAGGCGCAGCTGGACCACACTGGCCT 599

Qy  4010 CCGACATCTTTGACTGCTGCTACCTGACCAAGCACGTCTCCCGGGGTGGCACCTACACCT 4069
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   600 CCGACATCTTTGACTGCTGCTACCTGACCAAGCACCTCTCCCGGNGTGGCACCTACACCT 659

Qy  4070 TCCGCACGGCACATGTGTCAGACAGGCAGGAATGGGTCCCTACAGCAGCCCCTCGGAGCAAG 4129
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Db   660 TCCGCACGGCACATGTGTCAGACAGGCAGGAATGGGTCCCTACAGCAGCCCCTCGGAGCAAG 719

Qy  4130 TCCTCCTGGGAGGGCCCAGCCACCTGGCTCTGGCTCCTGAGGAGAGAGCCAGGGCGGTCAGCCC 4189
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Db   720 TCCTCCTGGGAGGGCCCAGCCACCTGGCTCTGGCTCCTGAGGAGAGAGCCAGGGCCGGTCAGCCC 779

Qy  4190 AACCCCGCCAGCACAAAGACCTTCGCATTCGCAATTCCAGACACAGATCCAGAGGAGCCGCCTTCA 4249
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Db   780 AACCCCTGCCCAGCACCAAAGACCTTCGCATTCGCAATTCCAGACACCAGATCCAGAGGGCCGCCTTCA 839

Qy  4250 GCGTGTGCGCAATGCTGGGAGAAGGCAGCGGCGGGCGCGGGCGCGCCAAGATCATCC 4309
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Db   840 GCGTGGCGCGCAATGCTGGGAGAAGGCCANNCGGCGGGCGCCGGGCGCC -AGNACATCC 898

Qy  4310 CCTACCACCCCAAGGACAGACAAGCACAGCAGCAGTGCTGCG 4343
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Db   899 CCTACCACCCCA- -GGACAGNCAGCAGTGCTGCG 930
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RESULT 3
BX409792

LOCUS       BX409792          924 bp   mRNA    linear   EST 13-MAY-2003
DEFINITION  BX409792 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
            CS0DF017YK06 5-PRIME, mRNA sequence.
ACCESSION   BX409792
VERSION     BX409792.1   GI:30640362
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 924)
AUTHORS     Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE       Full-length cDNA libraries and normalization
JOURNAL     Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr; Web : www.genoscope.cns.fr
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RESULT 4

ORIGIN

Query Match     13.7%;    Score 713.4;  DB 12;  Length 715;
Best Local Similarity   99.9%;   Pred. No. 4.2e-90;
Matches 714;  Conservative   0;  Mismatches  1;  Indels  0;  Gaps   0;

RESULT 5

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Db    540 TTCGTGCGCAATCGCGAGAAGAGACGCGCGCGTCTGTCGTGACAAGAGGCACAACCTGGCCCAG 599
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   5098 GTGCGCTGAGGGTGCCCCGGCCACACCTGGCTCTCCCGCGTCCCGCGTCGGGGGTCGCGCAGACG 5157
          |||||| |||||| | |||||| ||||| || ||||| ||| ||||||||||||||||||||
Db    600 GTGCGCTGAGGGTCGCCCCGGCACACCCTTGTCTCCCCGCCTGGGGTTCGCTGCAGACG 659

Qy   5158 CGCCAATAAAAACGCACAGCCCGGGCGAGAAAAAAAAAAAAAAAAAAAAAA 5207
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Db    660 CGCCAATAAAAACGCACAGCCCGGGCCGAGAAAAAAAACAAAAAACAAAAA 709
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RESULT 6
AW862431
LOCUS       AW862431                683 bp    mRNA    linear   EST 19-MAY-2000
DEFINITION  RC0-CT0380-210300-035-a08 CT0380 Homo sapiens cDNA, mRNA sequence.
ACCESSION   AW862431
VERSION     AW862431.1  GI:7958129
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 683)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
            O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
   MEDLINE   20202663
   PUBMED    10737800
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=RC0-CT0380-210-
            300-035-a08&t3=2000-03-21&t4=1)
            Seq primer: puc 18 forward
            High quality sequence stop: 683.
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                     /db_xref="taxon:9606"
                     /dev_stage="Adult"
                     /clone_lib="CT0380"
                     /note="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2:
                     SmaI; A mini-library was made by cloning products derived
                     from ORESTES PCR (U.S. Letters Patent application NO.
                     196,716 - Ludwig Institute for Cancer Research) profiles
                     into the pUC 18 vector. Reverse transcription of tissue
                     mRNA and cDNA amplification were performed under low
                     stringency conditions."
ORIGIN

Query Match         12.6%;   Score 655.6;  DB 10;  Length 683;
Best Local Similarity   99.0%;   Pred. No. 5.1e-82;
Matches 669;  Conservative   0;  Mismatches   6;  Indels   1;  Gaps   1;

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Qy   3753 CCAGCTTCTGACCATCCTGGTGGTGGTGGTGACCTGGGTGTGGTGTACACCTGCAGCGT 3812
          |||||||||||||||||||||||||||||||||||  ||||||||||||||||||||||
Db      1 CCAGCTTCTGACCATCCTGGTGGTGGTGGTGGTGACCTGGGTGTGGTGTACACCTGCAGCGT 60
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REFERENCE   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            1  (bases 1 to 731)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: David N. Louis, M.D.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10821 row: d  column: 19
            High quality sequence stop: 693.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:4914402"
                     /tissue_type="anaplastic oligodendroglioma with 1p/19q
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                     /lab_host="DH10B (T1 phage-resistant)"
                     /clone_lib="NCI_CGAP_Brn67"
                     /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
                     Average insert size 2.3 kb. Constructed by Life
                     Technologies. Note: this is a NCI_CGAP Library."
ORIGIN

Query Match         12.8%;   Score 666.8;  DB 12;  Length 731;
Best Local Similarity   98.0%;   Pred. No. 1.4e-83;
Matches 696;  Conservative   0;  Mismatches  12;  Indels  12;  Gaps   2;

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Qy   4498 GAGGTGAAGGACTACCTGTGGCAGATGTTGAGTGCCACCCAGTACCTGACAACCAGCAC 4557
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Db      2 GAGGTGAAGGACTACCTGTGGCAGATGTTGAGTGCCACCCAGTACCTGCACAACCAGCAC 61

Qy   4558 ATCCTGACCTGGACCTGAGGTCCGAGAACATGATCATCACGAATACAACCTGCTCAAG 4617
          ||||||||||||||||||||||  ||||||||||||||||||||||||||||||||||
Db     62 ATCCTGACCTGGACCTGAGGTCCGAGAACATGATCATCACGAATACAACCTGCTCAAG 121

Qy   4618 GTCGTGGACCTGGCAATGCACAGAGCCTCAGCCAGGAGAAGGTGCTGCCCTCAGACAAG 4677
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    122 GTCGTGGACCTGGCAATGCACAGAGCCTCAGCCAGGAGAAGGTGCTGCCCTCAGACAAG 181

Qy   4678 TTCAAGGACTACCTAGAGACCATGGCTCCAGAGCTCCTGGAGGGGCCAGGGGGCTGTTCCA 4737
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Db    182 TTCAAGGACTACCTAGAGACCATGGCTCCAGAGCTCCTGGAGGGGCCA-GGGGCTGTTCCA 240

Qy   4738 CAGACAGACATCTGGGCCATCGGTCGTGTGACAGCCTTCATCATGCTGAGCGCGCCGAGTACCCG 4797
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Db    241 CAGACAGACATCTGGGCCATCGGTCGTGTGACAGCCTTCATCATGCTGAGCGCGCCGAGTACCCG 300

Qy   4798 GTGAGCAGCAGCGAGGGTGCACGCGACCTGCAGAGAGACTGCGCCAAGGGGCTGGTCCGGCTG 4857
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Db    301 GTGAGCAGCAGCGAGGGTGCACGCGACCTGCAGAGAGACTGCGCCAAGGGGCTGGTCCGGCTG 360

Qy   4858 AGCCGCTGCTACCGCGGGGCTGTTCCGGGGGCGCGTGGCCTTCCTGGCCAGCACTCGTGC 4917
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 AGCCGCTGCTACCGCGGGGCTGTTCCGGGGGCGCGTGGCCTTCCTGGCCAGCACTCGTGC 420

Qy   4918 GCCCAGCCCTGGGGCCGGCCCTGCGGTCCAGTGCCGTCCAGTGGCTAACAGAG 4977
          ||||| |||||||||||||||||||| |||||||||||||||||||||||||
Db    421 GCCCAGCCCTGGGGCCGGCCCTGCGGT-CAGCTGCCTGCCAGTGCCGTGGCTGGCTAACAGAG 479

Qy   4978 GAGGGCCCGGCCTGTTCGCGGGCCCCGGCGCCCGGACCTTCCCTACCGCGGCGCGGCGGTC 5037
          ||||| ||||||||||||||||||| ||||||||||||| |||||||||||||||||||||
Db    480 GAGGGCCCGGCCTGTTCGCGGGCCCCGGCGCCCGTTCCCTCACCGCGGCGGCGGTC 539

Qy   5038 TTCGTGCGCAATCGCGAGAAGAGACGCGCGCGTCTGTCGTGACAAGAGGCACAACCTGGCCCAG 5097
```

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Qy 3813 GAGCAATGCGGCTGGGACAGTGACCACCGGGCGGCGGTCCTCCGGAAGGCAGAGCCGCCCTC 3872
        |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db   61 GAGCAATGCGGCTGGGACAGTGACCACCGGGCGGCGGTCCTTCCCGGAAGGCAGAGCCGCCCTC 120

Qy 3873 ATCTTCGCCATGCCCGGATATCGGGAGGTGTACGGCGGATGGGTGTGCTGGTCTCGGAA 3932
        |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db  121 ATCTTCGCCATGCCCGGATATAGGGAGGTGTACGGCGGATGGGTGTGCTGGTCTCGGAA 180

Qy 3933 GCCCGTGGAATCCTACGGCCCTGACCTGACCATTGTGCAGTGCAGTCGAAGGCGGCAG 3992
        |||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Db  181 GCCCGTGGAATCCTACGGCCCTGACCTGACCATTGTGCAGTGCAGCCTAGAAGGCGGCAG 240

Qy 3993 CTGGACCACCACTGGCCTCCGACAATCTTTGACTGCTGCTGTACCTGACCAGCAAGCTCTCCCG 4052
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 CTGGACCACCACTGGCCTCCGACAATCTTTGACTGCTGCTGTACCTGACCAGCAAGCTCTCCCG 300

Qy 4053 GGGTGGCACCTACACCTTCCGCACGGCATGTGTCAGCAAGGCAGGAATGGGTGTCCCTACAG 4112
        ||||||||||||||||||||||||||||||||||| |||||||||||||||||||| ||||||
Db  301 GGGTGGCACCTACACCTTCCGCACGGCATGTGTCAGGAGGAAGGCAGGAATGGGTGTCCCCACAG 360

Qy 4113 CAGCCCCTCGGAGCAAGTCCTCCTGGGAGGGGCCCAGCCACCTGGCCTTCTGAGGAGGAGAG 4172
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 CAGCCCCTCGGAGCAAGTCCTCCTGGGAGGGGCCCAGCCACCTGGCCTTCTGAGGAGGAGAG 420

Qy 4173 CCAGGGCGGCGTCAGCCAACCCCTGCCCCAGCACAAAGACCTTCGCATTCCAGACACAGAT 4232
        |||||| ||||||||||| |||||||||||||||||| ||||||||||||||||||||||||
Db  421 CCAGGGGCGGCGTCAGCCCCAACCCCTGCCCCAGCACAATCCTTCGCATTCCAGACACAGAT 480

Qy 4233 CCAGAGGGGCCGCTTCAGCGTGGTGCGGCCAATGCTGGGAGAAGGCCAGCGGCGGGCGGCT 4292
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  481 CCAGAGGGGCCGCTTCAGCGTGGTGCGGCCAATGCTGGGAGAAGGCCAGCGGCGGGCGGCT 540

Qy 4293 GGCCGCCAAGATCATCCCCTACACCCCCAAGGACAACAGCAGCAGTGCTGCGGCGAATACGA 4352
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  541 GGCCGCCAAGATCATCCCCTACACCCCCAAGGACAACAGCAGCAGTGCTGCGGCGAATACGA 600

Qy 4353 GGCCCTCAAGGGGCTGCGCCACCCGCACCTGCCCAGCTGCACGAGCAGCCTCACCTCAGCCC 4412
        ||||||||| |||| |||||||||||||||| ||||||||||||||||||||||||||| |||
Db  601 GGCCCTCAGAGGGCCTGCGGCGCCACCCGCACCTGGNCCAGCTGCACGAGCAGCCTCACCTCAGNCC 660

Qy 4413 CCGGCACCTGGTGTC 4428
        || |||||||||||||
Db  661 CC-GCACCTGGTGTC 675
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RESULT 7
BX435097/c
LOCUS       BX435097                989 bp    mRNA    linear   EST 15-MAY-2003
DEFINITION  BX435097 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
            CS0DF017YK06 3-PRIME, mRNA sequence.
ACCESSION   BX435097
VERSION     BX435097.1  GI:30783342
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 989)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web.: www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 1025.r For
            more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CS0BAK036AC04NM1&cluster=1025.r. Contact :
            Feng Liang Email : fliang@lifetech.com URL :
            http://fullength.invitrogen.com/ Invitrogen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0BAK036AC04NM1.

FEATURES             Location/Qualifiers
     source          1..989
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DF017YK06"
                     /tissue_type="FETAL BRAIN"
                     /dev_stage="fetal"
                     /clone_lib="Homo sapiens FETAL BRAIN"
                     /note="Organ: brain; Vector: pCMVSPORT 6, 1st strand cDNA
                     was primed with a NotI-oligo(dT) primeI. Five prime end
                     enriched, double-strand cDNA was digested with Not I and
                     cloned into the Not I and EcoRV sites of the pCMVSPORT 6
                     vector. Library was not normalized."

ORIGIN

```
Query Match           12.0%;  Score 626.2;  DB 13;  Length 989;
Best Local Similarity 96.7%;  Pred. No. 6.4e-78;
Matches  672;  Conservative   0;  Mismatches  18;  Indels   5;  Gaps   3;

Qy 4477 AGGGCCTCCTACTCAGAA--TCTGAGGTGAGGACTACCTGTGGCAGATGTTGAGTGCCA 4534
        ||||||||| ||||||||  |  ||||||||| |||||||||||||||||||||||||||
Db  755 AGGGCCTCCAGCTCAGAAACTCGAGGTGAAGGGGTCACCTGTGGCAGATGTTGAGTGCCA 696

Qy 4535 CCCAGTACCTGCACAACCTGCAC-ATCCTGACACCTGACCTGAGGTCCGAGAACATGATC 4593
        |||||||||||||||||| ||||| ||||||||  |||||||||||||||||||||||||
Db  695 CCCAGTACCTGCACAACCAGCACAATCCTGACCTGACCTGAGGTCCGAGAACATGATC 636

Qy 4594 ATCACCGAATACAACCTGCTCAAGGTCGTGACCTGGGCAATGCACAGAGCCTCAGCCAG 4653
        |||||||||| |||||||||||||||||||||||||||||||||||||||||||  ||||
Db  635 ATCACCGAATTCAACCTGCTCAAGGTCGTGACCTGGGCAATGCACAGAGCCTCACCCAG 576

Qy 4654 GAGAAGGTGCTGCCCTCAGACAGTTCAAGGACTACCTAGAGACCATGGCTCCCAGAGCTC 4713
        ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db  575 GAGAAGGTGCTGCCCTCAGACAAGTTCAAGGACTACCTAGAGACCATGGCTCCCAGAGCTC 516

Qy 4714 CTGGAGGGCCAAGGGGCTGTTCCACAGACAGCAATCTGGGCCTCGGTGTGACAGCCTTC 4773
        ||||||||||| ||||| ||||||||||||||||  |||||| ||||||||||||||| |
Db  515 CTGGAGGGCCAGGGGGTGTTCCACAGACAGCACAGACAGCATCGGGCATCGGTGTGACAGCCTC 456

Qy 4774 ATCATGTGAGCGCGAGTACCCGGTGAGCCGCTGCACCGGGGCTGTCCGGGGGGCCCGTG 4833
        ||||||||||||| ||||||||||||||| ||||||||||||||||||||||||||||||
Db  455 ATCATGTGAGCGCCAGTACCCGGTGAGCAGGTGCACCGGGGCTGTCCGGGGGGCCCGTG 396

Qy 4834 CTGCGCAAGGGGCTGGTCCGGCTGAGCCGCTGCACCGGGGCTGTCCGGGGGCCCGTG 4893
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  395 CTGCGCAAGGGGCTGGTCCGGCTGAGCCGCTGCACCGGGGCTGTCCGGGGGCCCGTG 336

Qy 4894 GCCTTCCTGCGCAGCACTCGTGCGCCCCAGCCCTGCGGCCCGTCGCGTCCAGCTGC 4953
        ||||||||||||||||||||||||||| |||||||| ||||| |||||||||||||
Db  335 GCCTTCCTGCGCAGCACTCGTGCGCCCAGCCCTGGGCCCGGTCGCGTCCAGCTGC 276

Qy 4954 CTGCAGTGCCCGTGGCTAACAGAGGAGGGCCCGGCCCGTGTTCGCGGCCCCGTGACC 5013
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  275 CTGCAGTGCCCGTGGCTAACAGAGGAGGGCCCGGCCCGTGTTCGCGGCCCCGTGACC 216

Qy 5014 TTCCCTACCGCGGCTGCGGCGTCTTCGTCGCGCAATCGGCGAGAAGAGGACGCGCCGCTGCTG 5073
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  215 TTCCCTACCGCGGCTGCGGCGTCTTCGTCGCGCAATCGGCGAGAAGAGGACGCGCCGCTGCTG 156

Qy 5074 TACAAGAGGCACAACCTGCGCCCAGGTGCGGTGAGGGTCGGCCCCGGTCGCACACCCTTGGTCT 5133
        |||||||||||||||||| |||||| |||||||||||||||||||||||||||      |||| 
Db  155 TACAAGAGGCACAACCTGGCCGGTGCGGTGAGGGTCGGCCCCGGTCGCCCCGGCCACACCCTT--GGTC 98

Qy 5134 CCCGCGTGGGGGTTCGTCGACAGCGGCGGCAATAAAA 5168
        ||||| ||||||| |||| |  |||| ||| ||||||
Db   97 TCCCCGTGGGGGTCGGTCGGTCAGACGCGCCCAAAAAA 63
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RESULT 8
BG999843/c
LOCUS       BG999843                622 bp    mRNA    linear   EST 13-JUN-2001
DEFINITION  MR3-HN0063-030101-001-h03 HN0063 Homo sapiens cDNA, mRNA sequence.

ACCESSION   BG999843
VERSION     BG999843.1  GI:14403915
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 622)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
            O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
  MEDLINE   20202663
   PUBMED   10737800
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research.
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?ti=MR3&t2=MR3-HN0063-
            030101-001-h03&t3=2001-01-03&t4=1)
            Seq primer: puc 18 forward
            High quality sequence stop: 621.
FEATURES            Location/Qualifiers
     source          1..622
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /dev_stage="Adult"
                     /clone_lib="HN0063"
                     /note="Organ: head normal; Vector: puc18; Site_1: SmaI;
                     Site_2: SmaI; A mini-library was made by cloning products
                     derived from ORESTES PCR (U.S. Letters Patent application
                     No.196,716 - Ludwig Institute for Cancer Research)
                     profiles into the pUC 18 vector. Reverse transcription of
                     tissue mRNA and cDNA amplification were performed under
                     low stringency conditions."
ORIGIN

Query Match          10.4%;  Score 541;  DB 12;  Length 622;
Best Local Similarity 98.8%;  Pred. No. 5.6e-66;
Matches  566;  Conservative    0;  Mismatches    5;  Indels    2;  Gaps    2;

Qy   2933 CACTGCCCCAGGTCAGTGCAAGGCCTGCAAGGCCTGAGGTCGGCAGGGCTCCACCA-GGAGC 2991
          ||||||||||| ||| | |||||||||| |||||||||||||||||||||| |||| ||||
Db    622 CACTGCCCCAGTTCA-TCCAAGGCCTGTTCCTGAGGTCGGCAGGGCTCCCACCAGGGGAGC 564

Qy   2992 TCTCCAGAGCCACCCACCCCATGGGAGGACATCGGGCAGGTCTCCCTGGTGCAGATCCGGAC 3051
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    563 TCTCCAGAGCCACCCACCCCATGGGAGGACATCGGGCAGGTCTCCCTGGTGCAGATCCGGAC 504

Qy   3052 CTGTCAGGTGATGGGAGGCGGCCGCCGACACAATATCCCTGGACATTCCGAGGTGGACCCC 3111
          ||||||||||||||||||||||| |||||||||||||| ||| |||||||||||| |||||
Db    503 CTGTCAGGTGATGGGAGGCGGCGGCCGCCGACACAATATGCCGGACATTTCCGAGGTGGGACCCCC 444

Qy   3112 GCCTACCTCAACCTTCTCAGACCTTGTACGATATCAAGTACCTCCCATTCGAGTTTATGATC 3171
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    443 GCCTACCTCAACCTTCTCAGACCTTGTACGATATCAAGTACCTCCCATTCGAGTTTATGATC 384

Qy   3172 TTCAGGAAAGTCCCCAAGTCCGCTCAGCCAGACGCCGCCTCCCCCATGGCTGAGGAGGAG 3231
          ||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db    383 TTCAGGAAAGTCCCCAAGTCCCGCTCAGCCAGAGCCGCCTCCCCCATGGCTGAGGAGGAGGAG 324

Qy   3232 CTGGCGAGTTCCCGGAGCCCACGTGGCCCTGGCCAGGTGAACTGGCCCCACGCAGGC 3291
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    323 CTGGCGAGTTCCCGGAGCCCACGTGGCCCTGGCCAGGTGAACTGGCCCCACGCAGGC 264

Qy   3292 CTGGAGATCACAGAGGAGTCAGAGGATGGGACGCGCGTGCTGGCAGAGGCTGCCGTGGGC 3351
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    263 CTGGAGATCACAGAGGAGTCAGAGGATGGGACGCGCGTGCTGGCAGAGGCTGCCGTGGGC 204

Qy   3352 AGGAAGGCGAAGTGGTCCTCCGGGTCACGCAGCCTCTTCCACTTCCCTGGGAGGCCACCTG 3411
          ||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    203 AGGAAGGCCAAGTGGTCCTCCGGGTCACGCAGCCTCTTCCACTTCCCTGGGAGGCCACCTG 144

Qy   3412 CCGCTGGATGAGCCTGCAGAGCTGGGCGTCCGTGAGGAGAGTGAAGGCCTCCGTGGAGCAC 3471
          |||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Db    143 CCGCTGGATGAGCCTGCGAGAGCTGGGCGTCCGTGAGGAGAGTGAAGGCCTCCGTGGAGCAC 84

Qy   3472 ATCTCCCGATCCTGAAGGGCAGGCCGGAAGT 3504
          |||||||||||||||||||||||||||||||
Db     83 ATCTCCCGATCCTGAAGGGCAGGCCGGAAGT 51


RESULT 9
BX280322
LOCUS       BX280322      480 bp    mRNA    linear   EST 04-MAR-2003
DEFINITION  BX280322 NCI_CGAP Brn67 Homo sapiens cDNA clone IMAGp998D1910821 ;
            IMAGE:4914402, mRNA sequence.
ACCESSION   BX280322
VERSION     BX280322.1  GI:28612364
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 480)
  AUTHORS   Ebert,L., Heil,O., Hennig,S., Neubert,P., Partsch,E., Peters,M.,
            Radelof,U., Schneider,D. and Korn,B.
  TITLE     Human UnigeneSet - RZPD3
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Ina Rolfs
            RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
            Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
            RZPD; IMAGp998D1910821.
            RZPDLIB; I.M.A.G.E. cDNA Clone Collection;
            Human UnigeneSet - RZPD3 (RZPDLIB No.972)
            http://www.rzpd.de/CloneCards/cgi-
            bin/showLib.pl.cgi/response?ibNo=972 Contact: Ina Rolfs
            RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
            Heubnerweg 6, D-14059 Berlin, Germany
            Tel: +49 30 32639 101
            Fax: +49 30 32639 111
            www.rzpd.de
            This clone is available royalty-free from RZPD;
            contact RZPD (clone@rzpd.de) for further information. Seq primer:
            M13u, Primer sequence: CGTTGTAAAACGACGGCCAGT.
FEATURES            Location/Qualifiers
     source          1..480
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGp998D1910821 ; IMAGE:4914402"
                     /tissue_type="anaplastic oligodendroglioma with 1p/19q
                     loss"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /clone_lib="NCI_CGAP_Brn67"
                     /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
                     Average insert size 2.3 kb. Constructed by Life
                     Technologies. Note: this is a NCI_CGAP Library."
ORIGIN

Query Match           9.2%;  Score 478.4;  DB 13;  Length 480;
Best Local Similarity 99.8%;  Pred. No. 3.3e-57;
Matches  479;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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                   directionally cloned (EcoRV site is destroyed upon
                   cloning).  Average insert size 1.7 kb, insert size range
                   0.7-3.5 kb.  Library is normalized and enriched for
                   full-length clones and  was constructed by C. Gruber
                   (Invitrogen).  Research Genetics  tracking code 017: Note:
                   this is a NIH_MGC Library."

ORIGIN

     Query Match          9.1%;  Score 475;  DB 12;  Length 475;
     Best Local Similarity  100.0%; Pred. No. 9.8e-57;
     Matches 475;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy   3637 GTGACACTGGCCTGCCAGTGTGCCAGCTGCCAGCTGCCCAGGCCACCTGGAGCAAAGAC 3696
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 GTGACACTGGCCTGCCAGTGTGCCAGCTGCCAGCTGCCCAGGCCACCTGGAGCAAAGAC   60

Qy   3697 GGAGCCCCCTGGAGAGCAGCAGCCGTGTCCTCATCTCTGCCACCTCAAGAACTTCCAG 3756
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GGAGCCCCCTGGAGAGCAGCAGCCGTGTCCTCATCTCTGCCACCTCAAGAACTTCCAG  120

Qy   3757 CTTCTGACCATCCTGGTGGTGGCTGAGGACCTGGGTGTGTACACCTGCAGCGTGAGC 3816
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 CTTCTGACCATCCTGGTGGTGGCTGAGGACCTGGGTGTGTACACCTGCAGCGTGAGC  180

Qy   3817 AATGCGTTGGGACAGTGACCACCAGGGCGTCCTCCGGAAGGCAGAGCGCCCCTCATCT 3876
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 AATGCGTTGGGACAGTGACCACCAGGGCGTCCTCCGGAAGGCAGAGCGCCCCTCATCT  240

Qy   3877 TCGCCATGCCCGGATATCGGGAGGGTGTACCGCGGATGGGGTGCTGGTCTGGAAGCCC 3936
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 TCGCCATGCCCGGATATCGGGAGGGTGTACCGCGGATGGGGTGCTGGTCTGGAAGCCC  300

Qy   3937 GTGGAATCCTACGGCCCTGACCTACATTGTGCAGTGTGCAGTGCAGCGCAGCTGG 3996
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 GTGGAATCCTACGGCCCTGACCTACATTGTGCAGTGTGCAGTGCAGCGCAGCTGG  360

Qy   3997 ACCACACTGGCCTCCGACATCTTGACTGCTGCTACCTGACCAAGCTCTCCCGGGGT 4056
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 ACCACACTGGCCTCCGACATCTTTGACTGCTGCTACCTGACCAAGCTCTCCCGGGGT  420

Qy   4057 GGCACCTACACCTTCCGCACGGCATGTGTCAGCAAGGCAGGAATGGGTCCCTACA 4111
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 GGCACCTACACCTTCCGCACGGCATGTGTCAGCAAGGCAGGAATGGGTCCCTACA  475
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RESULT 11

BY739930

LOCUS       BY739930               653 bp    mRNA    linear   EST 17-DEC-2002
DEFINITION  BY739930 RIKEN full-length enriched, pooled tissues, 16 days
            embryo, etc. Mus musculus cDNA clone I920063N21 5', mRNA sequence.
ACCESSION   BY739930
VERSION     BY739930.1  GI:27163955
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 653)
  AUTHORS   Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
            Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I.,
            Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,
            Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C.,
            Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H.,
            Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V.,
            Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A.,
            Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T.,
            Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S.,
            Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A.,
            Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A.,
            Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R.,
            Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T.,
            Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G.,
            Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S.,
```
                   CTGAGGTGAAGGACTACCTGTGGCAGATGTTGAGTGCCACCCAGTACCTGCACAACCAGC 4555
                   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
                 1 CCGAGGTGAAGGACTACCTGTGGCAGATGTTGAGTGCCACCCAGTACCTGCACAACCAGC   60

Qy   4556 ACATCCTGCACCTGACCTGAGCTCCGAGAACATGATCATCACCGAATACAACCTGCTCA 4615
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 ACATCCTGCACCTGACCTGAGCTCCGAGAACATGATCATCACCGAATACAACCTGCTCA  120

Qy   4616 AGGTGTGGACCTGGCAATGCACAGAGGTCAGCCAGGAGAAGGTGCTGCCCTCAGACA 4675
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 AGGTGTGGACCTGGCAATGCACAGAGGTCAGCCAGGAGAAGGTGCTGCCCTCAGACA  180

Qy   4676 AGTTCAAGGACTACCTAGAGACCATGGCTCCAGAGCTCCTGGAGGGCCAGGGGCTGTTC 4735
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 AGTTCAAGGACTACCTAGAGACCATGGCTCCAGAGCTCCTGGAGGGCCAGGGGCTGTTC  240

Qy   4736 CACAGACAGACATCTGGGCCATCGGTGTGACAGCCTTCATCATGTGCTGAGCGGCGAGTACC 4795
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 CACAGACAGACATCTGGGCCATCGGTGTGACAGCCTTCATCATGTGCTGAGCGGCGAGTACC  300

Qy   4796 CGGTGAGCGAGGGTGCACGGGACCTGCAGAGAGACTGCGCAAGGGGCTGGTCCGGC 4855
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CGGTGAGCGAGGGTGCACGGGACCTGCAGAGAGACTGCGCAAGGGGCTGGTCCGGC  360

Qy   4856 TGAGGCCGCTGCTACGGCGGGGCTGTCCGGGGGCCGTGCCTTCCTGCGCAGCACTCTGT 4915
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 TGAGGCCGCTGCTACGGCGGGGCTGTCCGGGGGCCGTGCCTTCCTGCGCAGCACTCTGT  420

Qy   4916 GCGCCCAGCCCTGGGGCCGGCCGCCGGGCCCTGGCCTTCGCAGTGCCCGTGGCTCAACAG 4975
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Db    421 GCGCCCAGCCCTGGGGCCGGCCGCCGGGCCCTGGCCTTCGCAGTGCCCGTGGCTCAACAG  480
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RESULT 10

BI916955

LOCUS       BI916955               475 bp    mRNA    linear   EST 16-OCT-2001
DEFINITION  601777768F1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5242025 5',
            mRNA sequence.
ACCESSION   BI916955
VERSION     BI916955.1  GI:16180909
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 475)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM1610 row: g  column: 18
            High quality sequence stop: 475.
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                     /mol_type="mRNA"
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                     /clone="IMAGE:5242025"
                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_121"
                     /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: EcoRV (destroyed); RNA source anonymous pool of 3
                     fetal brains, female age 20 weeks, female age 24 weeks,
                     and male age 26 weeks. Library is oligo-dT primed and

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Qy   3430  GAGTGGGGCTGCGTGGTGAGAGAGTGAAGGCCTCCGTGGATCGACAATCTCCCGGATCCTGAAG  3489
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5  GAGCTTGGGCTGCGCGCCAGGGGTGAAGGCTTCCATGGCTCACATCTCCAGGATCCTCAAG    64

Qy   3490  GGCAGGCCGAAGGTCTGAGAGGAGAGGGCGCCCCCAGGAGAGAAGCCAGGGCCTTGCTTCC  3549
                 ||||||||||||||||||||||||||||||||||||||||
Db     65  GGCAGGCCGAAGGTCCTGAGGGGAAGGGCCTCCCAGAAAGAAGGCAGGGCCTAGCTTCT   124

Qy   3550  TTCCGGCTCTCAGGTCTGAAGAGCTGGGACCCGAGGCCGACATTCCTTAAGGGAGTCTCA  3609
                 |||||||||||||||||||||||||||||||||||||
Db    125  TTCCGGCTCTCAGGCCTGAAGGGCAGGGACCAAGCACCAATCCTTCCTTAAGAGAACTCTCA   184

Qy   3610  GATGAGACTGTGGTCCTGGGCCAGTCAGTGACACTGGCCTGCCAGGTGTCAGCCCAGCCA  3669
                 ||||||||||||||||||
Db    185  GACGAGGCTGTGTGGTCCTGGGCCAATCAGTGACACTGGCCTGCCAGTGTTGCCCAGCCA   244

Qy   3670  GCTGCCCAGGCCACCTGAGCAAAGACGGAGCCCCCTGGAGAGCACCGTGTCCTC  3729
                 ||||||||||||||||||
Db    245  ACTGCCCCAGGCTACCTGGAGCAAAGATGGGGTCCTCCTGGAGCAGCAGCGGCCGCACCTCCTC   304

Qy   3730  ATCTCTCCACCCTCAAGAACTTCCAGCTTCGACCATCCTCGGTGGTGGGGCTGAGGAC  3789
                 |||||||||||||||||
Db    305  ATCTCCTCCACCCTGAAGAACTTCCAGCTGCTTGACCATCCTGGTGGTGGGTGAAAGAGGAGGAT   364

Qy   3790  CTGGGTGTACACCTGCAGCGTGAGCAATGCGCTGGGGACCAGTGACCACCACGGGCGTC  3849
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Db    365  CTGGGCACATATACCTGCTGTGGTGAGCAACCCGCTGGGGACAGCAGTCACCACAGTGTC   424

Qy   3850  CTCCGGAAGGCAGAGCGCCCCCATCTTCGCCATGCCGCGGATATCGGGAGGGTGTACGGG  3909
                 |||||||||||||||||||
Db    425  CTCCGGAAAGCAGAGCGGCCCTTCATCTTCTCCACGGCCTCAGGGTGGGGGAACTATACAAG   484

Qy   3910  GATGGGTTGCTGCGTGGTCTGGAAGCCCGTGGAATCCTGAATCCTGTGACCTACCACATTGTG  3969
                 ||||||||||||||||||||||||||||||||||
Db    485  GATGCGGGTTGCTGCTGGTCTGGTCTGGAAGCCGTGTGGCCCGGTGACCTACATTGTG   544

Qy   3970  CAGTGCAGCCAGCTAGGAAGGGGCAGCTGGACGCCACCTGGCCTCCGACATCTTTGACTGCTGC  4029
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Db    545  CAGTGCTGTATAGAGAGGAGGGCAGCTGGACAACCCCTGGCTTCAGACATCTCTGACTGCTGC   604

Qy   4030  TACCTGACCAGCAAGCTCTCCCGGGGTGGGCACCACCTTCCGCACGG  4078
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Db    605  TACCTCACTGGNCAGCTATCGAGGGGTGCATGTATATCTTNCGGACAG   653
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RESULT 12
BF134040
LOCUS       BF134040          768 bp      mRNA      linear     EST 24-OCT-2000
DEFINITION  601778492F1 NCI_CGAP_Lu10 Mus musculus cDNA clone IMAGE:4006702 5',
            mRNA sequence.
ACCESSION   BF134040
VERSION     BF134040.1    GI:10973080
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 768)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Gilbert Smith, Ph.D.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM9238 row: g  column: 23
            High quality sequence stop: 736.

            Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M.,
            Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K.,
            Sulkana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M.,
            Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y.,
            Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I.,
            Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P.,
            Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M.,
            Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K.,
            Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y.,
            Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K.,
            Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S.,
            Rogers,J., Birney,E. and Hayashizaki,Y.
TITLE       Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
JOURNAL     Nature 420, 563-573 (2002)
MEDLINE     22354683
PUBMED      12466851
COMMENT     Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.go.jp,
            URL:http://genome.gsc.riken.go.jp/
            Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P.,
            Fukuda,S., Hashizume,W., Hayashida,K., Hirozane,T., Hori,F.,
            Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kawai,J., Kojima,Y.,
            Kondo,S., Konno,M., Koya,S., Miyazaki,A., Murata,M., Nakamura,N.,
            Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Saito,R., Sakazume,N.,
            Sano,H., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M.,
            Takeda,Y., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y.
            Direct Submission
            Computational Analysis of Full-Length Mouse cDNAs Compared with
            Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
            Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new
            Genes. Genome Res. 10 (10), 1617-1630 (2000)
            RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer. Genome Res.
            10 (11), 1757-1771 (2000)
            Computer-based methods for the mouse full-length cDNA
            encyclopedia: real-time sequence clustering for construction of a
            nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
            cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in.RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
            Please visit our web site (http://genome.gsc.riken.go.jp) for
            further details.
FEATURES             Location/Qualifiers
     source          1..653
                     /organism="Mus musculus"
                     /mol_type="mRNA"
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                     /clone="r920063N21"
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                     days embryo, etc."
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                     embryo,tissue_type=kidney,sex=mix),(dev_stage=17 days
                     embryo,tissue_type=heart,sex=mix),(dev_stage=17 days
                     embryo,tissue_type=stomach,sex=mix),(dev_stage=17 days
                     embryo,tissue_type=kidney,sex=mix),(dev_stage=17 days
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                     (dev_stage=13 days embryo,tissue_type=liver,sex=mix)"
ORIGIN
Query Match    9.0%;    Score 471;    DB 13;    Length 653;
Best Local Similarity  82.7%;    Pred. No. 3.4e-56;
Matches 537;    Conservative  0;    Mismatches 112;    Indels  0;    Gaps    0;

RESULT 13

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LOCUS       BI916956
DEFINITION  BI916956
            603177770F1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5242121 5',
            mRNA sequence.
            601777770F1 NIH_MGC_121 Homo sapiens    477 bp    mRNA    linear    EST 16-OCT-2001
ACCESSION   BI916956
VERSION     BI916956.1  GI:16180910
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 477)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM1610 row: k column: 18
            High quality sequence stop: 477.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:5242121"
                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_121"
                     /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: EcoRV (destroyed); RNA source anonymous pool of 3
                     fetal brains, female age 20 weeks, female age 24 weeks,
                     and male age 26 weeks. Library is oligo-dT primed and
                     directionally cloned (EcoRV site is destroyed upon
                     cloning). Average insert size 1.7 kb, insert size range
                     0.7-3.5 kb. Library is normalized and enriched for
                     full-length clones and was constructed by C. Gruber
                     (Invitrogen). Research Genetics tracking code 017. Note:
                     this is a NIH_MGC Library."
ORIGIN
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Query Match    8.7%;  Score 453;  DB 12;  Length 477;
Best Local Similarity   99.6%;  Pred. No. 1.2e-53;
Matches  475;  Conservative   0;  Mismatches   0;  Indels   2;  Gaps   2;

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Qy   3637 GTGACACTGGCCTGCCCAGTGTCAGCCCA-GCAGCTGCCCAGGCCACCTGGAGCAA-AG 3694
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Db      1 GTGACACTGGCCTGCCCAGTGTCAGCCCATGCAGCCCATGCCCAGGCCACCTGGAGCAAGAG 60

Qy   3695 ACGGAGCCCCCTGGAGAGCAGCAGCCGCGTGTCCTCATCTGTGCCACCCTCAAGAACTTCC 3754
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 ACGGAGCCCCCTGGAGAGCAGCAGCCGCGTGTCCTCATCTGTGCCACCCTCAAGAACTTCC 120

Qy   3755 AGCTTCTGACCATCCTGGTGGTGGTGCTGAGGACCTGGGTGTGTACACCTGCAGCGTGA 3814
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 AGCTTCTGACCATCCTGGTGGTGGTGCTGAGGACCTGGGTGTGTACACCTGCAGCGTGA 180

Qy   3815 GCAATGGCTGGGACAGTGACCACCACGGGCGTCCTCCGGAAGGCAGCGAGCGCCCCTCAT 3874
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GCAATGGCTGGGACAGTGACCACCACGGGCGTCCTCCGGAAGGCAGCGAGCGCCCCTCAT 240

Qy   3875 CTTCGCCATGCCCGGATATCGGGGAGTGTACGCGGATGGGGTGCTCGTGTCTGGAAGC 3934
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Db    241 CTTCGCCATGCCCGGATATCGGGGAGTGTACGCGGATGGGGTGCTCGTGTCTGGAAGC 300

Qy   3935 CCGTGGAATCCTACGGCCCTGTGACCTACATTGTGCAGTGCGGCAGCTAGAAGGCGCAGCT 3994
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                     /clone="IMAGE:4006702"
                     /tissue_type="tumor, metastatic to mammary"
                     /lab_host="DH10B"
                     /clone_lib="NCI_CGAP_Lu30"
                     /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; transgenic model WNT-1, expression driven by
                     MMTV-LTR enhancer; Cloned unidirectionally. Primer: Oligo
                     dT. Library constructed by Life Technologies.
                     Investigator providing samples: Gilbert Smith, NIH"
ORIGIN

Query Match    8.9%;  Score 463.2;  DB 10;  Length 768;
Best Local Similarity   81.0%;  Pred. No. 4.2e-55;
Matches  601;  Conservative   0;  Mismatches  133;  Indels   8;  Gaps   5;

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Db      2 CCTTCAGCAGCCCCTCAGAACAGTGTCCTCCTCGGAGGAGCCAACCACCTGGCCTCTGAG 61

Qy   4165 GAGGA---GAGCCAGGGGCGGTCAGCCAACCCCTGCCCAGCACAAAGAGCTTCGCATTC 4221
          |||||   |||||||||| ||| |||||||| ||||| |||||||||||  |||||| |
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Db    122 CAGATGCAGATCCGGGAGGGCCGCTTCAGTGTGCGGCGGCAGTGGGAGGAGAAGGCAAGT 181

Qy   4282 GGGCGGGCGGCTGGCCGCCAAGATCATCCCTACCACCCCAAGGACAAGACAGCAGTGCTG 4341
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Db    182 GGGCGGGCCCTAGCTGCTAAGATCGTTCCTACCACCACCAACTGAGACAAGACAGCGTGCTG 241

Qy   4342 CGCGAATACGAGAGGCCCTCAAGGGCTGGCCACCCGCCAGCTGCACGCAGCC 4401
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Db    242 AGAGAATACGAGGCACTTAAGAGACTGACCACCTCGGCCACCATCCATGCCGCC 301

Qy   4402 TACTTCAGCCCCCGGCACCTGGTGCTCATCTTGGAGCTGTGCTCTGGGCCCGAGCTGCTC 4461
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Db    302 TACTTCAGTCCCCGGCACCTGGTGCTCATCCTGGAGCTGTGCTCTGCCCCTGAGCTGCTA 361

Qy   4462 CCCTGCCTGGCCGAGAGGGCCTCCTACTCAGAATCTGAGGTGAAAGGACTACCTGTGGCAG 4521
          |||  || |||||||| |||| |||||||||| |||||| ||||||| ||||||||||||
Db    362 CCCTCTTTGGCGGAGAGGAATCCTACTCAGAGTCTGATGTGAAAGAGACTACCTGTGGCAG 421

Qy   4522 ATGTTGAGTGCCACCAGTACCTGCACAAACCAGCACATCCTGCACCTGGACCTGAGGTCC 4581
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Db    422 ATGCTGAGTGCCACCAGTACTTGCATGCCAACACATCCTGCACCTGGACCTGAGGTCC 481

Qy   4582 GAGAACATGATCATCACCGAATACAACCTGCTCAAGGTCGTGGACCTGGGCAATGCACAG 4641
          ||||||||||||| | |||| ||||||||| | |||| |||| |||||||||||||||
Db    482 GAGAACATGATGGTCACTGAGTACAACTGCTTAAGGTTATAGACCTGGGAAAATGCCCAG 541

Qy   4642 AGCTTCAGCCAGGAGAAGGTGCTGCCCAGACAAGTTCAAGGACTACCTAGAGACCATG 4701
          || ||| || ||||| ||||||||||||| ||| || |||||| ||||  |||||||
Db    542 AGTCTGACCAAGAGAAGAAGGTCCCAGCCCCTGTGAACTTCAAAGACTACCTGGAGACCATG 601

Qy   4702 GCTCCAGAGCTCCTGGGAGGGGCCAGGGGGCTGTTCCACAGACAGAATCTGGGCCATCGGT 4761
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Db    602 GCTCCAGAACTCCTGGAGGTCAC GGGGGCTGTTCCACAGACA--TTGGGCTATGGT 659

Qy   4762 GTGACAGCCTTCATCATGCTGAGCGCCGAGTACCCGGTGAGCGAGGGTGCACGCGAC 4821
          ||||| | || |||| ||||||||| |||| ||||| | | ||||| | |||||||
Db    660 GTAACAG-CTTCATTATCTGCGTGGGGGAGTA-CCAGAGCAGCAGGAGGGGGGGACTCGTGA- 716

Qy   4822 CTGCAGAGGAGGACTGCGCAAGG 4843
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Db    717 CTTGGAGAAAGGCTTCGCGCAGGGG 738
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RESULT 14

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Db    301 CCGTGGAATCCTACGGCCCTGTGACCTACATTGTGCAGTGCAGCCTAGCAAGGCGGCAGCT 360
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Qy   3995 GGACCACACTGGCCTCCGACATCTTGACTGCTGCTACCTGACCAGCAAGTCTCCCGGG 4054
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Db    361 GGACCACACTGGCCTCCGACATCTTTGACTGCTGCTACCTGACCAGCAAGCTCTCCCGGG 420
Qy   4055 GTGGCACCTACACCTTCCGCACGGCGATGTGTCAGCAAGGCAGGAATGGGTCCTACA 4111
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Db    421 GTGGCACCTACACCTTCCGCACGGCGATGTGTCAGCAAGGCAGGAATGGGTCCTACA 477
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RESULT 14
BG989614/c

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LOCUS       BG989614               517 bp    mRNA    linear   EST 13-JUN-2001
DEFINITION  MR2-HT1160-190101-013-e11 HT1160 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BG989614
VERSION     BG989614.1  GI:14393684
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 517)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W.Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
            O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
  MEDLINE   20202663
   PUBMED   10737800
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPSP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?ti=MR2&t2=HT1160-
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                     /note="Organ: head neck; Vector: puc18; Site 1: SmaI;
                     Site_2: SmaI; A mini-library was made by cloning products
                     derived from ORESTES PCR (U.S. Letters Patent application
                     No. 196,716 - Ludwig Institute for Cancer Research)
                     profiles into the pUC 18 vector. Reverse transcription of
                     tissue mRNA and cDNA amplification were performed under
                     low stringency conditions."
ORIGIN
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Query Match         8.3%; Score 434; DB 12; Length 517;
Best Local Similarity 94.5%; Pred. No. 5.3e-51;
Matches 482; Conservative 0; Mismatches 25; Indels 3; Gaps 3;

Qy    964 AAGCCCTCAACATCCTGATGGTGCATCCTGCCCGGGAAGACATTAAAATCTGCGACTTT 1023
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Db    508 AAGCCCTCACCATCCTGATGGT-CATCCTGCCCGGCAGACATTAAAATCTGCGACTTT 450
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RESULT 15

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Qy   1024 GGCTTTGCCCAGAACATCACCCCAGCAGAGCTGCAGTTCAGCCAGTACGGCTCCCCTGAG 1083
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Qy   1084 TTCGTCT-CCCCCAGATCATCCAGCAGCAGAACCCTGTGAGCGAAGCCTTCGGC 1142
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Qy   1143 CATGGGTGTCATCTCCTACCTCAGCCTGACCTGCTCATCCCCATTTGCCGGGCGAGAGTGA 1202
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RESULT 15
BI776197

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DEFINITION  468982 MARC 2BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION   BI776197
VERSION     BI776197.1  GI:15777174
KEYWORDS    EST.
SOURCE      Bos taurus (cow)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
            Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 556)
  AUTHORS   Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
            Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C.,
            Bennett,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A.,
            Chitko-McKown,C.G., Pertea,G., Holt,I., Karamycheva,S., Liang,F.,
            Quackenbush,J. and Keele,J.W.
  TITLE     Sequence evaluation of four pooled-tissue normalized bovine cDNA
            libraries and construction of a gene index for cattle
  JOURNAL   Genome Res. 11 (4), 626-630 (2001)
  MEDLINE   21180013
   PUBMED   11282978
COMMENT     Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called and alt trimmed with phred
            v0.980904.e. Vector identified by cross_match with the -minscore 18
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            PCR Primers
            FORWARD: AGGAAACAGCTATGACCAT
            BACKWARD: GTTTTCCCAGTCACGACG
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FEATURES             Location/Qualifiers
     source          1..556
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ORIGIN

Query Match          8.0%;   Score 415.2; DB 12; Length 556;
Best Local Similarity 85.4%;  Pred. No. 2.2e-48;
Matches 475; Conservative 0; Mismatches 78; Indels 3; Gaps 1;

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Qy  3745 AAGAACTTCCAGCTTCTGACCATCCTGGTGGTGGCTGAGGACCTGGGTGTGTACACC 3804
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Qy  3805 TGCAGCGTGAGCAATGGCTGGGGACAGTGACCACCACGGGCGTCCTCCGGAAGGCAGAG 3864
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Qy  3865 CGCCCCTCATCTTCGCCATGCCCGGATATCGGGGAGGTGTACGCGGATGGGTGCTGCTG 3924
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Search completed: April 26, 2004, 15:00:43
Job time : 8103 secs

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          Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:    April 26, 2004, 08:18:58 ; Search time 242 Seconds
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Title:          US-10-697-263-1
Perfect score:  5207
Sequence:       1 cagcacgaggaactcctct.........aaaaaaaaaaaaaaaaaaaa 5207

Scoring table:  IDENTITY_NUC
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Searched:       682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters:     1365418

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

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| 2 | 5207 | 100.0 | 5207 | 4 | US-10-274-978-1 | Sequence 26, Appli |
| 3 | 5207 | 100.0 | 5207 | 4 | US-10-274-978-3 | Sequence 3, Appli |
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ALIGNMENTS

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; Sequence 1, Application US/09858664A
; Patent No. 6482624
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui, et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL000927-CIP
; CURRENT APPLICATION NUMBER: US/09/858,664A
; CURRENT FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: 09/711,134
; PRIOR FILING DATE: 2000-11-11
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 5207
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-858-664A-1

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Best Local Similarity   100.0%;  Pred. No. 0;
Matches 5207;   Conservative 0;  Mismatches 0;  Indels 0;   Gaps 0;

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Qy    901  ATCCAGCAGCTGGTGGAGGGGCTGCACTACCTGCACACAGCCATGGCGTTCTCCACCTGGAC  960
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Qy   1141  GCCATGGGTGTCATCTCCTACCTCAGCCTGACCTGCTCATCCCATTGCCGGCGAGAGT  1200
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Qy   1261  GCCACCTCAGCGAAGAGCCAAAGACTTCATCAAGGCTACGCTGCAGAGAGCCCCTCAG  1320
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Qy   1321  GCCCGGCTAGTCGGGCCCAGTGCCTCTCCCACCCGGTTCCTGAAATCCATGCCTGCG  1380
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Qy   1381  GAGGAGGCCCACTCATCAACACCAAGCAGCTCAAGTTCCTCCTGCGCCCGAAGTCGCTG  1440
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Qy   1441  CAGCGGTTCCCTGATGAGTCACAAGTCCATCCTGGTGATGCGTCCATCCTCCTGAGCTGCTG  1500
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Db   1621  TCACTGCCACCCTCCCCCGGTGACACTCACCACTGCTGACCCCCGGGGGCTTCCTGCGG  1680

Qy   1681  CCCTCGGCCAGCAGCTGCTGAGGAAGCCAGGGCAGTGAGTGAGCGCCCCAGCT  1740
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681  CCCTCGGCCAGCAGCTGCTGAGGAAGCCAGGGCAGTGAGTGAGCGCCCCAGCT  1740

Qy   1741  CGGCCTGCATCTCCGAGCCTGTTCTACCACAGGGCCCGGCTCGTGCCCCGGCCAC  1800
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741  CGGCCTGCATCTCCGAGCCTGTTCTACCACAGGGCCCGGCTCGTGCCCCGGCCAC  1800

Qy   1801  AGGGTCATCCGACAGCCGTGTTCTACCACCAGGGGTGAGAGCCCTGAGCACGGGCCCTG  1860
           ||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db   1801  AGGGTCATCCGACAGCCGTGTTCTACCACCAGGGGTGAGAGCCCTGAGCACGGGGCCCTG  1860

Qy   1861  GCCCGGGGACAGCGGCGCACCCGGCCCGGCGGCCGCTGCTGAAGGGCCGCTACATT  1920
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861  GCCCGGGGACAGCGGCGCACCCGGCCCGGCGGCCGCTGCTGAAGGGCCGCTACATT  1920

Qy   1921  GCGGGGGCGCTGCCAGGCCACTGATGAGCACCGGCGTGCTGGAG  GGAG  1980
           ||||||||||||||||||||||||||||||||||||||||||||  ||||
Db   1921  GCGGGGGCGCTGCCAGGCCACTGATGAGCACCGGCGTGCTGGAG  GGAG  1980

Qy   1981  GCCGCCAGGGAGGAGCAGGCCACCCTCCTGGCCAAAGCCCCCTCATTGCGACTGCCCTC  2040
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981  GCCGCCAGGGAGGAGCAGGCCACCCTCCTGGCCAAAGCCCCCTCATTGCGACTGCCCTC  2040

Qy   2041  CGGCTGCCTGCCTCTGGCCACCCACTTGGCCCCTGGAGGCTGCGGTGGAGGCGCAGCAGCTGGAACATGAC  2100
           |||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db   2041  CGGCTGCCTGCCTCTGGCCACCCACTTGGCCCCTGGAGGCTGCGGTGGAGGCGCAGCACAGCTGGAACATGAC  2100

Qy   2101  TCTTCCGAGCACCCCCGCCCCCCGGGGGGCCCCTATCAGGAGCTCAGGGCTCCAAGCAGCTT  2160
           ||||||||||||||||| ||||||||||||||||||||||||||||||||||||||| |||
Db   2101  TCTTCCGAGCACCCCCGCCCCCCTGGGGGGCCCCTATCAGGAGCACCCTGAGGCTCAGGGCTCCAAGCAGCTT  2160

Qy   2161  GCCCCCTCCGGGGGGCCCCTATCAGGAGCACTGCTCAGCGAGAGGCATCCCCGGACAGCCCT  2220
           ||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db   2161  GCCCCTCCGGGGGGCCCCTATCAGGAGCACTGCTCAGCGAGAGGCATCCCCGGACAGCCCT  2220

Qy   2221  CCATCCACTGGTGGCCACCCAGCCCACTGCTCAGCGAGAGGCATCCCCCGGACAGCCCT  2280
           || ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db   2221  CCATCCACTGGTGGCCACCCAGCCCACTGCTCAGCGAGAGGCATCCCCCGGACAGCCCT  2280

Qy   2281  TGGGGGCAGCCAGCCCCCTTTCTGCCACCCCCAGGAGGCTGTTCGCCCCAGGGAGGCTGCTGCAAA  2340
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281  TGGGGGCAGCCAGCCCCCTTTCTGCCACCCCCAGGAGGCTGTTCGCCCCAGGGAGGCTGCTGCAAA  2340

Qy   2341  AGCCCCACCCCAGTTGCCCATGCCCTGCTGGGCTCCTCCTCCTCCAGGATCTTGCAAA  2400
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341  AGCCCCACCCCAGTTGCCCATGCCCTGCTGGGCTCCTCCTCCTCCAGGATCTTGCAAA  2400

Qy   2401  GAGGCCCCTTAGTACCCTCAAGCCCCTTCTTGGGACAGCCCCAGCACCCCCTGCCCCT  2460
           |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db   2401  GAGGCCCCTTAGTACCCTCAAGCCCCTTCTTGGGACACAGCCCCAGCACCCCCTGCCCCT  2460

Qy   2461  GCCAAAGCAAGCCCCCCATTTGACTCTTAAGATGGGCCTGAGACTCTTGGG  2520
           |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2461  GCCAAAGCAAGCCCCCCATTTGACTCTTAAGATGGGCCTGAGACTCTTGGG  2520

Qy   2521  AGGCCAAAACCCGGCCCCCTCCCGCAGTTCCCAGGTCAGCTGAGCGCTCTTCCCCAA  2580
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Left column:

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Db   2521 AGGCCAAAACCGGCGCCCCTGCAGTTCCCAGGGTCAGCCTCCCAGGCGAGCTCTTCCCAA 2580
Qy   2581 GTGAGCCCCTCAGGGTGGGCTCCTCCCAGTGGGCACAGAGCCTGGCCCTTCCCCCCTGAT 2640
          |||||||  ||||||||||||||||||||||||||||||||  ||||||||  ||||||||
Db   2581 GTGAGC--CTCCTTCCCTCAGGGTGGGCTGGGCCCTTCCCCAGTGGGCACAGAGCCCCTGGCCCTTCCCCCCTGAT 2640
Qy   2641 GCGGAGGGCTGACCCAGGAGGCTGAGGATCGTCCGACTCCACACCCACCTTGCAGCGG 2700
          ||||||||||||||||||||||||||||||||  ||||||||||||||||||||||||
Db   2641 GCGGAGGGCTGACCCAGGAGGCTGAGGATCTGTCCGACTCCACACCCACCTTGCAGCGG 2700
Qy   2701 CCTCAGGAAACAGGTGACCATGCCACATGCGCCAAGTTCTCCCGGGTGGTCGCGGGGGCTACGCAGGC 2760
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2701 CCTCAGGAAACAGGTGACCATGCCACATGCGCCAAGTTCTCCCGGGTGGTCGCGGGGGCTACGCAGGC 2760
Qy   2761 GTGGCTGGCTATGGCACCTTTGCCTTTGGTGGAGATGCAGGGGGCATGTCGGGGCAGGGG 2820
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2761 GTGGCTGGCTATGGCACCTTTGCCTTTGGTGGAGATGCAGGGGGCATGTCGGGGCAGGGG 2820
Qy   2821 CCCATGTGGGCCAGGATAGCCTGGGCTGTGTCCCAGTCGGACAGCAGGAGGAGCCCCACTGCCC 2880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2821 CCCATGTGGGCCAGGATAGCCTGGGCTGTGTCCCAGTCGGACAGCAGGAGGAGCCCCACTGCCC 2880
Qy   2881 GCCAGGGCTGAGTCCCAGTCGGAGGACAGCAGGAGGCCAGGGCTGAGGCCCCACTGCCC 2940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2881 GCCAGGGCTGAGTCCCAGTCGGAGGACAGCAGGAGGCCAGGGCTGAGGCCCCACTGCCC 2940
Qy   2941 CAGGTCAGTGCAAGGCCTGTCGGTCGGCAGGGCTCCCACCAGGAGCTCTCAGAGCTCTCCAGAG 3000
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2941 CAGGTCAGTGCAAGGCCTGTCGGTCGGCAGGGCTCCCACCAGGAGCTCTCAGAGCTCTCCAGAG 3000
Qy   3001 CCCACCCCATGGGAGGACAATCGGGCAGGTCTCCCTGGTGCAGATTCCCGGGACCTGTCAGGT 3060
          ||||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||
Db   3001 CCCACCCCATGGGAGGACACATCGGGCAGGTCTCCCTGGTGCAGATTCCGGGACCTGTCAGGT 3060
Qy   3061 GATGGCGGAGGCGGCCGACACCAATATCCCTGGACATTCCCATTCGAGGTGGTTATGATCTTCAGATC 3120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3061 GATGGCGGAGGCGGCCGACACCAATATCCCTGGACATTCCCATTCGAGGTGGTTATGATCTTCAGATC 3120
Qy   3121 AACCTCTCAGACCTGTACGATATCAAGTACCTCCCATTCGAGTTTATGATCTTCAGAAA 3180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3121 AACCTCTCAGACCTGTACGATATCAAGTACCTCCCATTCGAGTTTATGATCTTCAGAAA 3180
Qy   3181 GTCCCCAAGTCCGCTCAGCCAGAGCGCGCCCTCCCCCATGGCGTGAGGAGGAGCCTGGCCGAG 3240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3181 GTCCCCAAGTCCGCTCAGCCAGAGCGCGCCCTCCCCCATGGCGTGAGGAGGAGCCTGGCCGAG 3240
Qy   3241 TTCCCGGAGCCCACGTGGCCCTGGCCAGTGAACTGGGCCCCACGCAGCAGGCCTGGGAGATC 3300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3241 TTCCCGGAGCCCACGTGGCCCTGGCCAGTGAACTGGGCCCCACGCAGCAGGCCTGGGAGATC 3300
Qy   3301 ACAGAGGAGTCAGAGGATGTGAGCGGCTGCTGCCGTGGCCGTCGCGTGGGCAGGAGGCGC 3360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3301 ACAGAGGAGTCAGAGGATGTGAGCGGCTGCTGCCGTGGCCGTCGCGTGGGCAGGAGGCGC 3360
Qy   3361 AAGTGGTCCTCGGCCGTCACGCAGCCTCTTCCACTTCCCTGGAGGCACCTGCCGCGTTGGAT 3420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3361 AAGTGGTCCTCGGCCGTCACGCAGCCTCTTCCACTTCCCTGGAGGCACCTGCCGCGTTGGAT 3420
Qy   3421 GAGCCTGCAGAGCTGGGGCTGGGGGTGGGGCGTGGGCGTGAAGGCCTCCTGGAGCACATCTCCCGG 3480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3421 GAGCCTGCAGAGCTGGGGCTGGGGGTGGGGCGTGGGCGTGAAGGCCTCCTGGAGCACATCTCCCGG 3480
Qy   3481 ATCCTGAAGGGCAGGCCGGAAGGTCTGGAAGAGGTCTGAAGAGGCCTCCGGACATTCCTTAAGG 3540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3481 ATCCTGAAGGGCAGGCCGGAAGGTCTGGAAGAGGTCTGAAGAGGCCTCCGGACATTCCTTAAGG 3540
Qy   3541 CTTGCTTCCTTCCCGGCTTCCCAGGTCTGAGAAGTCTCAGTGACACTGGCCTGCCAGGTGTCA 3600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3541 CTTGCTTCCTTCCCGGCTTCCCAGGTCTGAGAAGTCTCAGTGACACTGGCCTGCCAGGTGTCA 3600
Qy   3601 GAGCTCTCAGATGAGACTGTGGTCCTCGGGACCAGTCAGTCAGTGACACTGGCCTGCCAGGTGTCA 3660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3601 GAGCTCTCAGATGAGACTGTGGTCCTCGGGACCAGTCAGTCAGTGACACTGGCCTGCCAGGTGTCA 3660
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Right column:

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Qy   3661 GCCCAGCCAGCTGCCCAGCCGACCACCTGGAGCAAAGACGGAGCCCCCTGAGAGCAGCAGC 3720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3661 GCCCAGCCAGCTGCCCAGCCGACCACCTGGAGCAAAGACGGAGCCCCCTGAGAGCAGCAGC 3720
Qy   3721 CGTGTGTCCTCATCTCTGCCACCCTCAAGAGACTTCAGCTTCTGACCATCCTGGTGTGGTGTG 3780
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3721 CGTGTGTCCTCATCTCTGCCACCCTCAAGAGACTTCAGCTTCTGACCATCCTGGTGTGGTGTG 3780
Qy   3781 GCTGAGGACCTGGGTGTGTACACCTGCAGCGTCAGCGTGAGCAATGGCTGGGACAGTGACCACC 3840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3781 GCTGAGGACCTGGGTGTGTACACCTGCAGCGTCAGCGTGAGCAATGGCTGGGACAGTGACCACC 3840
Qy   3841 ACGGGCGTCCTCCGGAAGGCAGAGCGCCCCCTCATCTTCGCCATGCCCATGCCCGGATATCGGGGAG 3900
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3841 ACGGGCGTCCTCCGGAAGGCAGAGCGCCCCCTCATCTTCGCCATGCCCATGCCCGGATATCGGGGAG 3900
Qy   3901 GTGTACGCGGATGGGGTGCTGTCGTGGTCGGGAATCCTGGAAGCCGTTGGAATCCTACGGCCCTGTGACC 3960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3901 GTGTACGCGGATGGGGTGCTGTCGTGGTCGGGAATCCTGGAAGCCGTTGGAATCCTACGGCCCTGTGACC 3960
Qy   3961 TACATTGTGCAGTGCAGCTAGAAGGCGGCAGCTGGACCACACTGGCCTTCCGACATCTTT 4020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3961 TACATTGTGCAGTGCAGCTAGAGAGGCGGCAGCTGGACCACACTGGCCTTCCGACATCTTT 4020
Qy   4021 GACTGCTGCTACCTGACCAGCAAGCTCTCCCGGGTGGCACCTACACCTTCCGCACGGCA 4080
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4021 GACTGCTGCTACCTGACCAGCAAGCTCTCCCGGGTGGCACCTACACCTTCCGCACGGCA 4080
Qy   4081 TGTGTCAGCAAGGCAGGAATGGGTTCCCTGAGGAGGAGAGCCCCCTGTCAGCGAAGTCTCTCCTGGA 4140
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4081 TGTGTCAGCAAGGCAGGAATGGGTTCCCTGACGAGGAGAGCCCCCTGTCAGCGAAGTCCTCCTGGA 4140
Qy   4141 GGGCCCAGCCACCTGGCTCCCTGGCCTCCCGGAGCCCCTGCCCAGTGCCCAACCCCTGCCC 4200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4141 GGGCCCAGCCACCTGGCTCCCTGGCCTCCCGGAGCCCCTGCCCAGTGCCCAACCCCTGCCC 4200
Qy   4201 AGCACAAAGACCTTCGCATTCGCACATTCGAGACACAGATCCAGAGACACCAGATCCAGAAA 4260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4201 AGCACAAAGACCTTCGCATTCGCACATTCGAGACACAGATCCAGAGACACCAGATCCAGAAA 4260
Qy   4261 CAATGCTGGGAGGAGGCCAGCGGCGGGGCGGCCTGCGGAATCATCCCTACCACCCCC 4320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4261 CAATGCTGGGAGGAGGCCAGCGGCGGGGCGGCCTGCGGAATCATCCCTACCACCCCC 4320
Qy   4321 AAGGACAAGACAGCAGTGCTGCGGCAGCCTCACCTGCAGCCCCGGACCCGCCACCCCCAC 4380
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4321 AAGGACAAGACAGCAGTGCTGCGGCAGCCTCACCTGCAGCCCCGGACCCGCCACCCCCAC 4380
Qy   4381 CTGGCCCAGCTGCACGCAGCCTACCTGGCACCTGTGCTGCTCATCTTGGAGCTG 4440
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4381 CTGGCCCAGCTGCACGCAGCCTACCTGGCACCTGTGCTGCTCATCTTGGAGCTG 4440
Qy   4441 TGCTCTGGGGCCCAGAGCTCTCCCGGAGGCACCTGCCGCGCTTCCTACTCAGAATCTGAG 4500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4441 TGCTCTGGGGCCCAGAGCTCTCCCGGAGGCACCTGCCGCGCTTCCTACTCAGAATCTGAG 4500
Qy   4501 GTGAAGGACTACCTGTGCAGATGTTGAGTGCCACCCAGTAGTGCACAACCAGCACATC 4560
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4501 GTGAAGGACTACCTGTGCAGATGTTGAGTGCCACCCAGTAGTGCACAACCAGCACATC 4560
Qy   4561 CTGCACCTGACCTGGGCAATGCACAGCCTGAGGTCCGAGAACATGATCATCACCGGCAAGGTC 4620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4561 CTGCACCTGACCTGGGCAATGCACAGCCTGAGGTCCGAGAACATGATCATCACCGGCAAGGTC 4620
Qy   4621 GTGGACCTGGGCAATGCACAGAGAGGTGCTGCCCTAGAAGGGCGCGGTGTTCCTTAAGG 4680
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4621 GTGGACCTGGGCAATGCACAGAGAGGTGCTGCCCTAGAAGGGCGCGGTGTTCCTTAAGG 4680
Qy   4681 AAGGACTACCTAGAGACCATGGCTCCAGAGCTCCTGGAGGGGCGTGTTCCACAG 4740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4681 AAGGACTACCTAGAGACCATGGCTCCAGAGCTCCTGGAGGGGCGTGTTCCACAG 4740
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Qy  181  CCAAGCATGGTAGGCTGTGGCTGGCACCCAGGGTTGTGTGGCTGGGAGGTGGTCTCCAC  240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181  CCAAGCATGGTAGGCTGTGGCTGGCACCCAGGGTTGTGTGGCTGGGAGGTGGTCTCCAC  240

Qy  241  AGTTCCTCCCTGCCTCCCAGGGCCCCATCCATGCAAGGACTGCGCAAGGAGGATGTGCAG  300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241  AGTTCCTCCCTGCCTCCCAGGGCCCCATCCATGCAAGGACTGCGCAAGGAGGATGTGCAG  300

Qy  301  GCACAGCAGGCGGAACGGCCCAATTCGAGGCTATCATTGAGGGCGACCACAGCCCTCG  360
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301  GCACAGCAGGCGGAACGGCCCAATTCGAGGCTATCATTGAGGGCGACCCCAGCCCTCG  360

Qy  361  GTGACCTGGTACAAGGACAGCGTCCAGCTGGTGCAGCACCCGGCTTAGCCAGCAGCAA  420
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361  GTGACCTGGTACAAGGACAGCGTCCAGCTGGTGCAGCACCCGGCTTAGCCAGCAGCAA  420

Qy  421  GAAGGCACCACATACTCCCTGGTGCTGAGGCATGTGGCCTCGAAGGATGCCGGCGTTTAC  480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421  GAAGGCACCACATACTCCCTGGTGCTGAGGCATGTGGCCTCGAAGGATGCCGGCGTTTAC  480

Qy  481  ACCTGCTGCCCAAAACTGGTGGCCAAGGTGCTCTGCAAGAGGCACAACCTGGCCCAGGTG  540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  481  ACCTGCTGCCCAAAACTGGTGGCCAAGGTGCTCTGCAAGAGGCACAACCTGGCCCAGGTG  540

Qy  541  GGGGGGACAATGAGCCGACTCAGAGAAGCAAAGCCACCGGAGGAGCTGCACTCCTTC  600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  541  GGGGGGACAATGAGCCGACTCAGAGAAGCAAAGCCACCGGAGGAGCTGCACTCCTTC  600

Qy  601  TATGAGGTCAAGGAGGATTGGAAGGGGCGTGTTTGGCTTCGTAAAAAGAGTGCAGCAC  660
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  601  TATGAGGTCAAGGAGGATTGGAAGGGGCGTGTTTGGCTTCGTAAAAAGAGTGCAGCAC  660

Qy  661  AAAGGAAACAAGATCTTGTGCGCTGCCAAGTTCATCCCCTACGGAGCAGAACTCGGGCC  720
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  661  AAAGGAAACAAGATCTTGTGCGCTGCCAAGTTCATCCCCTACGGAGCAGAACTCGGGCG  720

Qy  721  CAGGCATACAGGGAGGGAGCACATCCTGCCGCGCTGGAGCTGTCACGGGGCTG  780
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  721  CAGGCATACAGGGAGGGAGCACATCCTGCCGCGCTGGAGCTGTCACGGGGCTG  780

Qy  781  CTGACCAGTTTGAGACCCGCAAGACCCTCATCCTGGAGCTGTGCTCATCCGAG  840
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  781  CTGACCAGTTTGAGACCCGCAAGACCCTCATCCTGGAGCTGTGCTCATCCGAG  840

Qy  841  GAGCTGCTGACGCCTCGTACAGGAAGGCGGTGGTGACGAGGCCGAGGTCAAGGGTCTAC  900
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  841  GAGCTGCTGACGCCTCGTACAGGAAGGCGGTGGTGACGAGGCCGAGGTCAAGGGTCTAC  900

Qy  901  ATCCAGCAGCTGGTGGAGGGGCTGCACTACCTGCACAGCCAATGGCGGTTCTTCCACCTGGAC  960
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  901  ATCCAGCAGCTGGTGGAGGGGCTGCACTACCTGCACAGCCAATGGCGGTTCTTCCACCTGGAC  960

Qy  961  ATAAAGCCCTCTAACATCCTGATGGTGCATCCTGAGGTGCATCCTGCGCGAC  1020
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  961  ATAAAGCCCTCTAACATCCTGATGGTGCATCCTGAGGTGCATCCTGCGCGAC  1020

Qy 1021  TTTGGCTTTGCCCAGGCTGCAGTTCAGTCAGTAGCGGCTCCCCT  1080
         ||||||||||||||||||||||||||||||||||||||||||||
Db 1021  TTTGGCTTTGCCCAGGCTGCAGTTCAGTCAGTAGCGGCTCCCCT  1080

Qy 1081  GAGTTCGTCTCCCCGAGATCATCCAGCAGAACCCTGTGAGCGGAGGCCTCCGACATTTGG  1140
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1081  GAGTTCGTCTCCCCGAGATCATCCAGCAGAACCCTGTGAGCGGAGGCCTCCGACATTTGG  1140

Qy 1141  GCCATGGGTGTCATCTCCTACCTCAGCGTCCCATTTGCCGGCGGAGAGT  1200
         |||||||||||||||||||||||||||||||||||||||||||||||||
Db 1141  GCCATGGGTGTCATCTCCTACCTCAGCGTCCCATTTGCCGGCGGAGAGT  1200

Qy 1201  GACCTGCCACCCTCGTGAACGTCCTGGAGGGGCGGGTGTCATGAGCGCCCATGGCT  1260
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1201  GACCTGCCACCCTCGTGAACGTCCTGGAGGGGCGGGTGTCATGAGCGCCCATGGCT  1260

Qy 1261  GCCCACCTGCGGAAGACGCCAAAGACTTCATCAAGGCTACGCTGCAGAGAGCCCCTCAG  1320
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Qy 4741  ACAGACATCTGGGCCATCGGTGTGACAAGCCTCATCATGCTGAGCGCCGAGTACCGGTG  4800
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4741  ACAGACATCTGGGCCATCGGTGTGACAAGCCTCATCATGCTGAGCGCCGAGTACCGGTG  4800

Qy 4801  AGCAGCGAGGGTGCACGCGACTGCAGAGAGACTGCGCAAGGGGCTGGTCCGGCTGAGC  4860
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4801  AGCAGCGAGGGTGCACGCGACTGCAGAGAGACTGCGCAAGGGGCTGGTCCGGCTGAGC  4860

Qy 4861  CGCTGCTACGCGGGGGTGTCCGGGGGCCGTGGCCTTCCTGCGCAGCACTCTGTGCGCC  4920
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4861  CGCTGCTACGCGGGGGTGTCCGGGGGCCGTGGCCTTCCTGCGCAGCACTCTGTGCGCC  4920

Qy 4921  CAGCCCTGGGGCCGGCCGCCCTGCGCGGTCCAGCTGCCTGCAGCTGCCGTCCCTGGCTAACAGAGGAG  4980
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4921  CAGCCCTGGGGCCGGCCGCCCTGCGCGGTCCAGCTGCCTGCAGCTGCCGTCCCTGGCTAACAGAGGAG  4980

Qy 4981  GGCCCGGCCTGTTCGCGGCCCCGCGCCCCGTGACCTTCCCTACCGCGGCGGCGCTCTTC  5040
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4981  GGCCCGGCCTGTTCGCGGCCCCGCGCCCCGTGACCTTCCCTACCGCGGCGGCGCTCTTC  5040

Qy 5041  GTGCGCAATCGCGAGAGAGACGCGCGCGCCGCTGCTACAAGAGGCACAACCTGGCCCAGGTG  5100
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 5041  GTGCGCAATCGCGAGAGAGACGCGCGCGCCGCTGCTACAAGAGGCACAACCTGGCCCAGGTG  5100

Qy 5101  CGCTGAGGGTCGCCCCGGCCACACCCTTGGTCTCCCCGGTGGGGTCGGTGCAGACGCGGC  5160
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 5101  CGCTGAGGGTCGCCCCGGCCACACCCTTGGTCTCCCCGGTGGGGTCGGTGCAGACGCGGC  5160

Qy 5161  CAATAAAAACGCACAGCCGGCGGGCGGGCGAGAAAAAAAAAAAAAAA  5207
         |||||||||||||||||||||||||||||||||||||||||||||||
Db 5161  CAATAAAAACGCACAGCCGGCGGGCGGGCGAGAAAAAAAAAAAAAAA  5207
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RESULT 2
US-10-274-978-1
; Sequence 1, Application US/10274978
; Patent No. 6670164
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui, et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL000927-CIP-DIV
; CURRENT APPLICATION NUMBER: US/10/274,978
; CURRENT FILING DATE: 2002-10-22
; PRIOR APPLICATION NUMBER: 09/858,664
; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: 09/711,134
; PRIOR FILING DATE: 2000-11-14
; SOFTWARE: FastSEQ for Windows Version 4.0
; NUMBER OF SEQ ID NOS: 34
; SEQ ID NO 1
; LENGTH: 5207
; TYPE: DNA
; ORGANISM: Human
US-10-274-978-1

Query Match     100.0%;  Score 5207;  DB 4;  Length 5207;
Best Local Similarity  100.0%;  Pred. No. 0;
Matches 5207;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

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Qy    1  CAGCACGAGGAACTCCTTCTGATCACCTGGCCAGCTGAGGTCAGGTGGGAGGTCAGTG  60
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1  CAGCACGAGGAACTCCTTCTGATCACCTGGCCAGCTGAGGTCAGAGTGGGAGGGCAGTG  60

Qy   61  GTTCCATTGAAGGAGTACTCCTAACTGTCAGAAGCCACAGTGTATCTCAGGGGTGCTGT  120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61  GTTCCATTGAAGGAGTACTCCTAACTGTCAGAAGCCACAGTGTATCTCAGGGGTGCTGT  120

Qy  121  CGCTTGGGCTGCGGGGGGGTGTTCAGTTGCCCACAGTGTATCTCAGGGTCTCACCAACCAT  180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121  CGCTTGGGCTGCGGGGGGGTGTTCAGTTGCCCACAGTGTATCTCAGGGTCTCACCAACCAT  180
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Left block (positions 1261–2400):

Db   1261  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
           GCCCACCTTCAGCGAGGAAGACGGCCAAAGACACTTCATCAAGGCTACGGTGCAGAGAGCCCTCAG   1320

Qy   1321  GGCCCGGCCAGTGCGGCCCAGTGCCTCTCCCACCCCTGGTTCCTGGAAATCCATGCTGCGG   1380
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321  GGCCCGGCCAGTGCGGCCCAGTGCCCTCTCCCACCCCTGGTTCCTGGAAATCCATGCCTGCGG   1380

Qy   1381  GAGGAGGCCCACTTCATCAACACCAAGCAGCTCAAGTTCCTCCTCCGGCCGAGTCGCTGG   1440
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381  GAGGAGGCCCACTTCATCAACACCAAGCAGCTCAAGTTCCTCCTCGGCCCGAGTCGCTGG   1440

Qy   1441  CAGCGTTCCTGATGAGCTACAAGTCCATCCTGGTGATGCGCTCCATCCCTGAGCTGCTG   1500
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441  CAGCGGTTCCTGATGAGCTACAAGTCCATCCTGGTGATGCGCTCCATCCCTGAGCTGCTG   1500

Qy   1501  CGGGGCCCACCCGACACAGCCCTCCTCCGGCGGTAGCCGGCACCTCTGCAGGGACACTGGT   1560
           ||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501  CGGGGCCCACACCGACAGCCCCTCCTCCGGCGGTAGCCCGGCACCTCTGCAGGGACACTGGT   1560

Qy   1561  GGCTCCTCCAGTTCCTCCTCCTCTGACAACGAGCTCGCCCCATTGCCCGGGCTAAG   1620
           |||||||||||||||||||||||||||||||||||||||||||||
Db   1561  GGCTCCTCCAGTTCCTCCTCCTCTGACAACGAGCTCGCCCCATTGCCCGGGCTAAG   1620

Qy   1621  TCACTGCCACCTCCCCGGTGACACTCACCACTTGCTGCTGCGGGCTTCCTGCGG   1680
           ||||||||||||||||||||||||||||||||||||||||||||||
Db   1621  TCACTGCCACCTCCCCGGTGACACTCACCACTTGCTGCGGGGCTTCCTGCGG   1680

Qy   1681  CCCTCGGCCAGCCTGCTGAGGAAGCCGAGGCCAGTGACGCGTTCACCGAGGCCCCAGCT   1740
           ||||||||||||||||||||||||||||||||||||||||||||||
Db   1681  CCCTCGGCCAGCCTGCTGAGGAAGCCGAGGCCAGTGACGCGTTCCACCGAGGCCCCAGCT   1740

Qy   1741  CCGCCTGCATCTCCCCGAGGGTGCCGGGCCACCCGCCCAGGGCTGCGTGCCCGCGGCAC   1800
           |||||||||||||||||||||||||||||||||||||||||||||
Db   1741  CCGCCTGCATCTCCCCGAGGGTGCCGGGCCACCCGCCCAGGGCTGCGTGCCGTGCCCGGCAC   1800

Qy   1801  AGCGTCATCCGCAGCCTGTTCTACCACCAGGCGGTGAGAGCCTGAGAGCCACGGGGCCTG   1860
           ||||||||||||||||||||||||||||||||||||||||||||||
Db   1801  AGCGTCATCCGCAGCCTGTTCTACCACCAGGCGGGTGAGAGCCTGAGAGCCCACGGGGCCTG   1860

Qy   1861  GCCCCCGGGAGCAGCGGGGCCACCCGCCCCCGGCGGCGGCGCCACTGCTGCCGCTACATT   1920
           |||||||||||||||||||||||||||||||||||||||||||||
Db   1861  GCCCCCGGGAGCAGCGGGGCCACCCGCCCCCGGCGGCGGCGCCACTGCTGCCGCTACATT   1920

Qy   1921  GCGGGGGCCGCTGCCAGGGCCGCTGCGGCCAGCCACTGATGGAGCACCGGTCTGGAGGAG   1980
           ||||||||||||||||||||||||||||||||||||||||||||||
Db   1921  GCGGGGGCCGCTGCCAGGGCCGCTGCGGCCAGCCACTGATGGAGCACCGGTCTGGAGGAG   1980

Qy   1981  GCCGCCAGGAGGAGCAGGCCCACCCTCCTGGCCAAAGCCCCTCATTCGAGACTGCCCTC   2040
           ||||||||||||||||||||||||||||||||||||||||||||||
Db   1981  GCCGCCAGGAGGAGCAGGCCCACCCTCCTGGCCAAAGCCCCTCATTCGAGACTGCCCTC   2040

Qy   2041  CGGCTGCCTGCCTCTGGCACCCACTTGGCCCCTGCCCACCAGCCACTCCCTGGAACATGAC   2100
           |||||||||||||||||||||||||||||||||||||||||||||
Db   2041  CGGCTGCCTGCCTCTGGCACCCACTTGGCCCCTGCCCACCAGCCACTCCCTGGAACATGAC   2100

Qy   2101  TCTCCGAGCACCCCCCCGGGGGCCCCCGGCCTGCGGAGGCCTGCGGTGAGGCACTGCCTTCA   2160
           ||||||||||||||||||||||||||||||||||||||||||||||
Db   2101  TCTCCGAGCACCCCCCCGGGGGCCCCCGGCCTGCGGAGGCCTGCGGGTGAGGCACAGCGCCTTCA   2160

Qy   2161  GCCCCTCCGGGGGCCCTATCAGGGACATGGGCACCCTCAGGGCTCCAAGCAGCTT   2220
           |||||||||||||||||||||||||||||||||||||||||||||
Db   2161  GCCCCTCCGGGGGCCCTATCAGGGACATGGGCACCCTCAGGGCTCCAAGCAGCTT   2220

Qy   2221  CCATCCACTGTGGCCAGGCACTGCTTCAGCCAGGCACTGCTTCCGGACACAGCCCT   2280
           |||||||||||||||||||||||||||||||||||||||||||||
Db   2221  CCATCCACTGTGGCCACCCAGGCACTGCTTCAGCCAGGCACTGCTTCCCGGACACAGCCCT   2280

Qy   2281  TGGGGGCAGCCAGCCCCTTTCTGCCACCCCAAGCAGGGTTCTGCCCCCCCAGGAGGGCTGC   2340
           |||||||||||||||||||||||||||||||||||||||||||||
Db   2281  TGGGGGCAGCCAGCCCCTTTCTGCCACCCCAAGCAGGGTTCTGCCCCCCCAGGAGGGCTGC   2340

Qy   2341  AGCCCCCACCCAGCAGTGCCCCATGCCCTCCTGGCTCCTTCCCTCCGAGGATCTTGCAAA   2400
           ||||||||||||||||||||||||||||||||||||||||||||||

Right block (positions 2341–3480):

Db   2341  AGCCCCCACCCAGCAGTGCCCATGCCCTCCTCCTGGCTCCTTCCCTCCGAGGATCTTGCAAA   2400

Qy   2401  GAGGCCCCTTAGTACCCTCAAGCCCCTTCTTGGACAGCCCTGGAGCAGCCCTGCCCT   2460
           ||||||||||||||||||||||||||||||||||||||||||||
Db   2401  GAGGCCCCTTAGTACCCTCAAGCCCCTTCTTCTTGGACAGCCCTGCCCT   2460

Qy   2461  GCCAAAGCAAGCCCCCATTGGACTCTAAGATGGGCCTGAGACATCTCTTCCTGGG   2520
           |||||||||||||||||||||||||||||||||||||||||||||
Db   2461  GCCAAAGCAAGCCCCCATTGGACTCTAAGATGGGCCTGAGACATCTCTTCCTGGG   2520

Qy   2521  AGGCCAAAACCCGGCCCCTGCAGTTCCCCAGGGTCAGCCTCCCAGGGAGCTCTTCCCAA   2580
           ||||||||||||||||||||||||||||||||||||||||||||||
Db   2521  AGGCCAAAACCCGGCCCCTGCAGTTCCCCAGGGTCAGCCTCCCAGGGAGCTCTTCCCAA   2580

Qy   2581  GTGAGCTCCTCAGGGTGGCTCTCCCAGGTGGCACAGAGCCTGGCACAGAGGCCTGGGAT   2640
           |||||||||||||||||||||||||||||||||||||||||||||
Db   2581  GTGAGCTCCTCAGGGTGGCTCTCCCAGGTGGCACAGAGCCTGGCACAGAGGCCTGGGAT   2640

Qy   2641  GCGGAGGGGTGGACCCAGGAGGCTGAGGATCTGCCGACTCCACACCCAGCGAGGGC   2700
           |||||||||||||||||||||||||||||||||||||||||||||
Db   2641  GCGGAGGGGTGGACCCAGGAGGCTGAGGATCTGCCGACTCCACACCCTTGCAGGCG   2700

Qy   2701  CCTCAGGAACAGAGTGACCATGGCAAGTTCTCCCTGGGTGGTCGGGGACGAGGC   2760
           ||||||||||||||||||||||||||||||||||||||||||||||
Db   2701  CCTCAGGAACAGAGTGACCATGGCAAGTTCTCCCTGGGTGGTCGGGGTACGGCAGGC   2760

Qy   2761  GTGGCTGGCTATGGCACCTTTGCCTTTGGCTGTGAGATGCGGCAGGTCGGCAGAGCT   2820
           |||||||||||||||||||||||||||||||||||||||||||||
Db   2761  GTGGCTGGCTATGGCACCTTTGCCTTTGGCTGTGAGATGCGGCAGGTCGGCAGAGCT   2820

Qy   2821  CCCATGTGGGCCAGGATAGCCTGGCTGTGTCCCAGTCGGAGGAGGAGCAGGAGGAGGAG   2880
           ||||||||||||||||||||||||||||||||||||||||||||||
Db   2821  CCCATGTGGGCCAGGATAGCCTGGCTGTGTCCCAGTCGGAGGAGGAGCAGGAGGAGGAG   2880

Qy   2881  GCCAGGGCTGAGTCCCAGTCGGAGGAGCAGGAGAGCCCAGGCCCACTGCCC   2940
           |||||||||||||||||||||||||||||||||||||||||||||
Db   2881  GCCAGGGCTGAGTCCCAGTCGGAGGAGCAGGAGAGCCCAGGCCCACTGCCC   2940

Qy   2941  CAGGTCAGTGCAAGCCTGTGCCTGAGGTCGGCAGGGTCCCACCAGAGCTCTCCAGAG   3000
           |||||||||||||||||||||||||||||||||||||||||||||
Db   2941  CAGGTCAGTGCAAGCCTGTGCCTGAGGTCGGCAGGGTCCCACCAGAGCTCTCCAGAG   3000

Qy   3001  CCCACCCATGGAGGACATCGGGCAGCTCTCCCTGTGCAGATCCGGGACCTGTCAGGT   3060
           |||||||||||||||||||||||||||||||||||||||||||||
Db   3001  CCCACCCATGGAGGACATCGGGCAGCTCTCCCTGGTGCAGATCCGGGACCTGTCAGGT   3060

Qy   3061  GATGCGGAGGCGGCCGACACAATATCCCTTCATTCGAGACTGCCCTC   3120
           |||||||||||||||||||||||||||||||||||||||||||||
Db   3061  GATGCGGAGGCGGCCGACACAATATCCCTTGGACATTTCCGAGTGGCCCGCCTACCTC   3120

Qy   3121  AACCTCTCAGACCTGTACGATATCAAGTACCTCCCATTCGACTTTATGATCTTCAGGAAA   3180
           |||||||||||||||||||||||||||||||||||||||||||||
Db   3121  AACCTCTCAGACCTGTACGATATCAAGTACCTCCCATTCGAGTTTATGATCTTCAGGAAA   3180

Qy   3181  GTCCCGAGCACCCCCAAGGTCCGCTCAGCGAGCCGCCCCATGGCCGGAGCTGGCCGAG   3240
           |||||||||||||||||||||||||||||||||||||||||||||
Db   3181  GTCCCCAAGTCCGCTCAGCCGCCAGAGCCGCCCCATGGCCGGAGCTGGCCGAG   3240

Qy   3241  TTCCCGAGCCACGTGGCCCTGCCCTGGAACTGGCCCCCCAGGGCTCTGGAGATC   3300
           |||||||||||||||||||||||||||||||||||||||||||||
Db   3241  TTCCCGAGCCACGTGGCCCTGCCCTGGAACTGGCCCCCCAGGGCTGGAGATC   3300

Qy   3301  ACAGAGGAGTCAGAGGATGTGGACGCGCTGCTCGGCAGGAAGCGC   3360
           |||||||||||||||||||||||||||||||||||||||||||||
Db   3301  ACAGAGGAGTCAGAGGATGTGGACGCGCTGCTCGGCAGGAAGCGC   3360

Qy   3361  AAGTGGTCCTCGCCGTCACGCAGCCTGGGAGGCACCCGCCTGGAT   3420
           |||||||||||||||||||||||||||||||||||||||||||||
Db   3361  AAGTGGTCCTCGCCGTCACGCAGCCTTCCACTTCCTGGGAGGCACCCGCCTGGAT   3420

Qy   3421  GAGCCTGCAGAGCTGGGGCTGCCGTGAGAGAGTGAAGGCTCCGG   3480
           |||||||||||||||||||||||||||||||||||||||||||||
Db   3421  GAGCCTGCAGAGCTGGGGCTGCCGTGAGAGAGTGAAGGCTCCGG   3480
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Qy  3481 ATCCTTGAAGGCAGGCCGGAAGGTCTGGAGAAGAAGGAGGGGCCCCCCAGGAAGAAGCCAGGC 3540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3481 ATCCTTGAAGGCAGGCCGGAAGGTCTGGAGAAGAAGGAGGGGCCCCCCAGGAAGAAGCCAGGC 3540

Qy  3541 CTTGTTCCTTCCGGCTCTCAGGTCTGAAGAGCTGGACACCGAGCGCGCACATTCCTAAGG 3600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3541 CTTGTTCCTTCCGGCTCTCAGGTCTGAAGAGCTGGACACCGAGCGCGCACATTCCTAAGG 3600

Qy  3601 GAGCTCTCAGATGAGACTGTGGTGCCTCGGGCCAGTCAGTGACACTGGCCTGCCAGTGTCA 3660
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3601 GAGCTCTCAGATGAGACTGTGGTGCCTCGGGCCAGTCAGTGACACTGGCCTGCCAGGTGTCA 3660

Qy  3661 GCCCAGCCAGCTGCCCAGGCCACCTGGACAAAGACCGAGCCCCCTGGAGAGCAGCAGC 3720
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3661 GCCCAGCCAGCTGCCCAGGCCACCTGGACAAAGACCGGAGCCCCCTGGAGAGCAGCAGC 3720

Qy  3721 CGTGTCCTCATCTCTGCCACCCTCAAGAACTTCCAGCTTCTGACCATCCTGGTGGTGGTG 3780
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3721 CGTGTCCTCATCTCTGCCACCCTCAAGAACTTCCAGCTTCTGACCATCCTGGTGGTGGTG 3780

Qy  3781 GCTGAGGACCTGGGTGTGTACACCTGCGTGAGCAATGCGCTGGGGACAGTGACCACC 3840
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3781 GCTGAGGACCTGGGTGTGTACACCTGCGTGAGCAATGCGCTGGGGACAGTGACCACC 3840

Qy  3841 ACGGGCGTCCTCCGGAAGGCAGAGCGCCCCTCATCTTCGCCATGCCGGAATCCTACGGCCCTGTGACC 3900
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3841 ACGGGCGTCCTCCGGAAGGCAGAGCGCCCCTCATCTTCGCCATGCCGGAATCCTACGGCCCTGTGACC 3900

Qy  3901 GTGTACGCCGGATGGGCTGCTGGTCTCAGCCTAGAAGGCGGCAGCTGGACCACACTGGCCTCCGACATCTTT 3960
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3901 GTGTACGCCGGATGGGCTGCTGGTCTCAGCCTAGAAGGCGGCAGCTGGACCACACTGGCCTCCGACATCTTT 3960

Qy  3961 TACATTGTGCAGTGCAGGCTAGCAAGCTCTCCCGGGGTGCACCTACACCTTCCGCACGGCA 4020
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3961 TACATTGTGCAGTGCAGGCTAGCAAGCTCTCCCGGGGTGCACCTACACCTTCCGCACGGCA 4020

Qy  4021 GACTGCTGCTACCTGACCAGCAGGAATGGGTCCCTACAGCAGCCCCTCGGAGCAAGTCTCCTCGGGA 4080
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4021 GACTGCTGCTACCTGACCAGCAGGAATGGGTCCCTACAGCAGCCCCTCGGAGCAAGTCTCCTCGGGA 4080

Qy  4081 TGTGTCAAGGCAGGAATGGGTCCCTACAGCAGCCCCTCGGAGCAAGTCTCCTCCGGA 4140
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4081 TGTGTCAAGGCAGGAATGGGTCCCTACAGCAGCCCCTCGGAGCAAGTCTCCTCTGGGA 4140

Qy  4141 GGGCCCAGCCACCTGGCCTCTGAGGAGGAGACCCAGGAGCCCAGGGCGGTCAGCCCACCCCTGCCC 4200
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4141 GGGCCCAGCCACCTGGCCTCTGAGGAGGAGACCCAGGAGCCCAGGGCGGTCAGCCCACCCCTGCCC 4200

Qy  4201 AGCACAAAGACCTTCGCATTCCAGACACAGATCCAGACACAGATCCAGAGGGCCGCTTCAGCGTGGTGCGG 4260
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4201 AGCACAAAGACCTTCGCATTCCAGACACAGATCCAGACACAGATCCAGAGGGCCGCTTCAGCGTGGTGCGG 4260

Qy  4261 CAATGCTGGGAGAAGGCCAGCGGCGGCGCTGCCCGCCCAAGATCATCCCCTACCACCCCC 4320
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4261 CAATGCTGGGAGAAGGCCAGCGGCGGCGCTGCCCGCCCAAGATCATCCCCTACCACCCCC 4320

Qy  4321 AAGGACAAGACAGACAGTGCTGCGCCGAATACGAGGCCCTCAAGGGCTCCCACCCGCAC 4380
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4321 AAGGACAAGACAGACAGTGCTGCGCCGAATACGAGGCCCTCAAGGGCTCCCACCCGCAC 4380

Qy  4381 CTGGCCCAGCTGCACGCAGCCTACCTCAGCGCCCCCCGGCACCCCGCTCATCTTGGAGCTG 4440
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4381 CTGGCCCAGCTGCACGCAGCCTACCTCAGCGCCCCCCGGCACCCCGCTCATCTTGGAGCTG 4440

Qy  4441 TGTCTGGGCCCGAGCTGCTCCCCGGCCCGGCTTCAGCGTGGTCGCGG 4500
         |||||||||||||||||||||||||||||||||||||||||||||
Db  4441 TGTCTGGGCCCGAGCTGCTCCCCGGCCCGGCTTCAGCGTGGTCGCGG 4500

Qy  4501 GTGAAGGACTACCTGGCCAGATGTTGAGTGCCACCCAGTACCTGCACAACCAGCACATC 4560
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4501 GTGAAGGACTACCTGTGGCAGATGTTGAGTGCCACCCAGTACCTGCACAACCAGCACATC 4560
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Qy  4561 CTGCACCTGGACCTGAGGTCCGAGAACATGATCATCACCGAATACAACCTGCTCAGGTC 4620
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4561 CTGCACCTGGACCTGAGGTCCGAGAACATGATCATCACCGAATACAACCTGCTCAGGTC 4620

Qy  4621 GTGGACCTGGGCAATGCACAGAGCCTCAGCCAGGAGAAGGTGCTGCCCTCAGACAAGTTC 4680
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4621 GTGGACCTGGGCAATGCACAGAGCCTCAGCCAGGAGAAGGTGCTGCCCTCAGACAAGTTC 4680

Qy  4681 AAGGACTACCTAGAGACCATGGCTCCAGAGCTCCTGGAGGGGCTGTTCCACAG 4740
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4681 AAGGACTACCTAGAGACCATGGCTCCAGAGCTCCTGGAGGGGCTGTTCCACAG 4740

Qy  4741 ACAGACATCTGGGCCATCGGTGTGACAGCCTTCATCATGCTGGCAGGGCCGAGTACCCGGTG 4800
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4741 ACAGACATCTGGGCCATCGGTGTGACAGCCTTCATCATGCTGGCAGGGCCGAGTACCCGGTG 4800

Qy  4801 AGCAGCGAGGGTGCACGGACCTGCAGAGGAGACTGGCCAAGGGGCTGGTCCGGCTGAGC 4860
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4801 AGCAGCGAGGGTGCACGGACCTGCAGAGGAGACTGGCCAAGGGGCTGGTCCGGCTGAGC 4860

Qy  4861 CGTGCTACGCGGGGCTGTCCGGGGCCGGCCCGTGGCCTTCCTGCGCAGCACTTCTGTCGCGCC 4920
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4861 CGTGCTACGCGGGGCTGTCCGGGGCCGGCCCGTGGCCTTCCTGCGCAGCACTCTGTCGCGCC 4920

Qy  4921 CAGCCCTGGGCCGGCCCGTCCAGCTGGCCTGCTGCCAGTGGCTAACAGAGGAG 4980
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4921 CAGCCCTGGGCCGGCCCGTCCAGCTGGCCTGCTGCCAGTGGCTAACAGAGGAG 4980

Qy  4981 GGGCCGGCCTGTTCGCGGCGTACCACCGGCGCGGGCTGCGCGCGGTCTTC 5040
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4981 GGGCCGGCCTGTTCGCGGCGTACCACCGGCGCGGGCTGCGCGCGGTCTTC 5040

Qy  5041 GTGGGCAATCGCCGAGAGAGAGCGCGGCCACAACCTGGCCCAGGTG 5100
         ||||||||||||||||||||||||||||||||||||||||||||||
Db  5041 GTGGGCAATCGCCGAGAGAGAGCGCGGCCACAACCTGGCCCAGGTG 5100

Qy  5101 CGCTGAGGGTCGCCCCGCAGACGCGCACCCCTGGTCTCCCCGCTGGGGGTTCGCGCGACGCGC 5160
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5101 CGCTGAGGGTCGCCCCGCAGACGCGCACCCCTGGTCTCCCCGCTGGGGGTTCGCGCGACGCGC 5160

Qy  5161 CAATAAAAACGACAGCGGGCGGAGAAAAAAAAAAAAAAAAAA 5207
         ||||||||||||||||||||||||||||||||||||||||||
Db  5161 CAATAAAAACGACAGCGGGCGGAGAAAAAAAAAAAAAAAAAA 5207
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RESULT 3
US-10-274-978-3
; Sequence 3, Application US/10274978
; Patent No. 6670164
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui, et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL000927-CIP-DIV
; CURRENT APPLICATION NUMBER: US/10/274,978
; CURRENT FILING DATE: 2002-10-22
; PRIOR APPLICATION NUMBER: 09/858,664
; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: 09/711,134
; PRIOR FILING DATE: 2000-11-14
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 5207
; TYPE: DNA
; ORGANISM: Human
US-10-274-978-3

Query Match             100.0%;  Score 5207;  DB 4;  Length 5207;
Best Local Similarity   100.0%;  Pred. No. 0;
Matches  5207;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

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Qy      1 CAGCACGAGGAGGAACTCCTTCTGATCACCTGGCCAGCTGAGGTCAGAGTGGGAGGAGGCAGTG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 CAGCACGAGGAGGAACTCCTTCTGATCACCTGGCCAGCTGAGGTCAGAGTGGGAGGAGGCAGTG 60

Qy     61 GTTCCATTGAAGGAGTACTCCTAACTGTCAGAAGCCTGGCGGTCAGGATGGGGTGCTGT 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GTTCCATTGAAGGAGTACTCCTAACTGTCAGAAGCCTGGCGGTCAGGATGGGGTGCTGT 120

Qy    121 CGCTTGGGCTGCGGGGGGTGTTCAGTTGCCCACAGTGTATCTCAGGGTCTCACCAACCAT 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 CGCTTGGGCTGCGGGGGTGTTCAGTTGCCCACAGTGTATCTCAGGGTCTCACCAACCAT 180

Qy    181 CCAAGCATGGTAGGCTGTGGCTGGCACCCCAGGGTGTCTGGGGAGGTGGTGTCTCCAC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CCAAGCATGGTAGGCTGTGGCTGGCGACCCCAGGGGTGTCTGGGGAGGTGGTGTCTCCAC 240

Qy    241 AGTTCCCTCCGCCCTCCCAGGGCCCCATCCATGCAGTAACCATCGAGGATGTGCAG 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 AGTTCCCTCCGCCCTCCCAGGGCCCCATCCATGCAGTAACCATCGAGGATGTGCAG 300

Qy    301 GCACAGACAGGCGGAACGGCCCAATTCGAGGCTATCATTGAGGGCGCACCCACAGCCCTCG 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 GCACAGACAGGCGGAACGGCCCAATTCGAGGCTATCATTGAGGGCGCACCCACAGCCCTCG 360

Qy    361 GTGACCTGGTACAAGACAGCGTCCAGCTGTGGACAGCACCCGGCTTAGCCAGCAGCAA 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GTGACCTGGTACAAGACAGCGTCCAGCTGTGGACAGCACCCGGCTTAGCCAGCAGCAA 420

Qy    421 GAAGGCACCACATACTCCCTGGTGTGCTGAGGCATGTGGCCTTCGAAGGATGCCGGCGTTTAC 480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 GAAGGCACCACATACTCCCTGGTGTGCTGAGGCATGTGGCCTTCGAAGGATGCCGGCGTTTAC 480

Qy    481 ACCTGCCTGGCCCAAAACACTGGTGCCCAGTGCCTCGAAGGCAGAGCTGCTGGTGCTT 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 ACCTGCCTGGCCCAAAACACTGGTGCCCAGTGCCTCGAAGGCAGAGCTGCTGGTGCTT 540

Qy    541 GGGGGGGACAATGAGCCGGACTCAGAGACGCAAAGCCACCGGAGGAAGCTGCACTCCTTC 600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GGGGGGGACAATGAGCCGGACTCAGAGACGCAAAGCCACCGGAGGAAGCTGCACTCCTTC 600

Qy    601 TATGAGGTCAAGGAGGAGATTGGAAGGGGCGTGTTTGGCTTCGTAAAAAGAGTGCAGCAC 660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 TATGAGGTCAAGGAGGAGATTGGAAGGGGCGTGTTTGGCTTCGTAAAAAGAGTGCAGCAC 660

Qy    661 AAAGGAAAACAAGATCTTGTGCGCTGCCAAGTTCATCCCCTACGGAGCAGAACTCGGGCC 720
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 AAAGGAAAACAAGATCTTGTGCGCTGCCAAGTTCATCCCCTACGGAGCAGAACTCGGGCC 720

Qy    721 CAGGCATACAGGGAGCGGAGACATCCTGGCCGGCGCACCCGGCTGTCACGGGGCTG 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 CAGGCATACAGGGAGCGGAGACATCCTGGCCGGCGCACCCGGCTGTCACGGGGCTG 780

Qy    781 CTGGACCAGTTTGAGACCGCCGCTACAGGAAGGGGCCATGCGCGTTCTCTCCACCTGGAC 840
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 CTGGACCAGTTTGAGACCGCCGCTACAGGAAGGGGCCATGCGCGTTCTCTCCACCTGGAC 840

Qy    841 GAGCTGCTGGACCGCCGTACAGGAAGGGGCGTGGTGACGGAGGCCGGAGGTCAAGGTCTAC 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 GAGCTGCTGGACCGCCGTACAGGAAGGGGCGTGGTGACGGAGGCCGGAGGTCAAGGTCTAC 900

Qy    901 ATCCAGCAGCTGGTGAGGGGCTGACTACCTGCGACTCACTGCGT TCTCCACCTGGAC 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 ATCCAGCAGCTGGTGAGGGGCTGACTACCTGCGACTCACTGCGT TCTCCACCTGGAC 960

Qy    961 ATAAAGCCCTCTAACATCCTGATGGTGCATCCGCCCGGGAAGACATTAAAATCTGCGGAC 1020
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 ATAAAGCCCTCTAACATCCTGATGGTGCATCCGCCCGGGAAGACATTAAAATCTGCGGAC 1020

Qy   1021 TTTGGCTTTGGCCCAGAACATCACCCCAGCTGCAGTTCAGCCAGTTACGGGCTCCCCT 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 TTTGGCTTTGGCCCAGAACATCACCCCAGCTGCAGTTCAGCCAGTTACGGGCTCCCCT 1080

Qy   1081 GAGTTCGTCTCCCCCGAGATCATCCCGACTGCTGCTCATCCCGTGAGCGAAGCCTTCGACACCAAC 1140
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 GAGTTCGTCTCCCCCGAGATCATCCCGACTGCTGCTCATCCCGTGAGCGAAGCCTTCGACACCAAC 1140
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Qy   1141 GCCATGGGTGTCATCTCCACCTGCTCATCCCGACTGCTGCTCATCCCGGAGGAGT 1200
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 GCCATGGGTGTCATCTCCACCTGCTCATCCCGACTGCTGCTCATCCCGGAGGAGT 1200

Qy   1201 GACCGTGCCACCCTGCTGGAGGGTCTGGAGCGGGCGGTGTCATGGAGCAGCCCCATGGCT 1260
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 GACCGTGCCACCCTGCTGGAGGGTCTGGAGCGGGCGGTGTCATGGAGCAGCCCCATGGCT 1260

Qy   1261 GCCCACCTCAGCGAGACCGCCAAAGACTTCATCAAGGTACGCTGCAGAGACCCCCAG 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 GCCCACCTCAGCGAGACCGCCAAAGACTTCATCAAGGTACGCTGCAGAGACCCCCAG 1320

Qy   1321 GCCCGGCCTAGTGCGGCGCCCAGTGCCTCTCCCACCCCTGGTTCCTGAAATCATGCCTGCG 1380
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 GCCCGGCCTAGTGCGGCGCCCAGTGCCTCTCCCACCCCTGGTTCCTGAAATCATGCCTGCG 1380

Qy   1381 GAGGAGGCCACTTCATCAACACCAAGTCAAGTTCCTCCTGCCCGAAGTCGCTGG 1440
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Db   1381 GAGGAGGCCACTTCATCAACACCAAGTCAAGTTCCTCCTGCCCGAAGTCGCTGG 1440

Qy   1441 CAGCGTTCCTGATGAGCTACAAGTCATCCTGGTGATGGCGCTCATCCTGAGCTGCTG 1500
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 CAGCGTTCCTGATGAGCTACAAGTCATCCTGGTGATGGCGCTCATCCTGAGCTGCTG 1500

Qy   1501 CGGGGCCACCCGACAGCCCCTCCCTCGGCGTAGCCCGGCACCCTGCAGGGACACTGT 1560
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 CGGGGCCACCCGACAGCCCCTCCCTCGGCGTAGCCCGGCACCCTGCAGGGACACTGT 1560

Qy   1561 GGCTCCTCAGTTCCTCCTCTCTGACAACGAGCTCGCCCCATTGCCCGGGCTAAG 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 GGCTCCTCAGTTCCTCCTCTCTGACAACGAGCTCGCCCCATTGCCCGGGCTAAG 1620

Qy   1621 TCACTGCCACCCTCCCGGTGACACTCACCACTGCTGCTGCGTCCACCCCGGGCTTCCTGCGG 1680
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Db   1621 TCACTGCCACCCTCCCGGTGACACTCACCACTGCTGCTGCGTCCACCCCGGGCTTCCTGCGG 1680

Qy   1681 CCCTCCGCCAGCCTCCCGAGGAGCGTGCGGGCCGCCCAGGCGCTCCACCGAGCCCCAGCT 1740
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Db   1681 CCCTCCGCCAGCCTCCCGAGGAGCGTGCGGGCCGCCCAGGCGCTCCACCGAGCCCCAGCT 1740

Qy   1741 CCGGCTGCATCCCCGAGGGTGCCGGGCACCAGGCGGGTGAGAGCCCTGAGAGCCCCGGCAC 1800
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 CCGGCTGCATCCCCGAGGGTGCCGGGCACCAGGCGGGTGAGAGCCCTGAGAGCCCCGGCAC 1800

Qy   1801 AGCGTCATCCGCAGCCTGTTCTACCACCAGGCCGGGGCACGGGCCCTGAGAGGCGGCCCTG 1860
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 AGCGTCATCCGCAGCCTGTTCTACCACCAGGCCGGGGCACGGGCCCTGAGAGGCGGGGCTG 1860

Qy   1861 GCCCCGGGGAGCGGCCTGCCAGGCCTGCGCGGGCCACTGATGAGCCAAAGCCCCGGCTACATT 1920
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Db   1861 GCCCCGGGGAGCGGCCTGCCAGGCCTGCGCGGGCCACTGATGAGCCAAAGCCCCGGCTACATT 1920

Qy   1921 GCGGGGGCGCTGCCAGGCGGCCGTGGTGACGGAGGCCGGTGCTGGAGGAGGAG 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 GCGGGGGCGCTGCCAGGCGGCCGTGGTGACGGAGGCCGGTGCTGGAGGAGGAG 1980

Qy   1981 GCCGCAGGGAGGAGCAGGCCACCCTGGCCAAAGCCCCTCATTCGAGACTGCCCTC 2040
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 GCCGCAGGGAGGAGCAGGCCACCCTGGCCAAAGCCCCTCATTCGAGACTGCCCTC 2040

Qy   2041 CGGCTGCCTCGCTGCCCGAGCACCACTTGGCCCTGGAGGCTGCGGTGAGCCACATGAC 2100
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041 CGGCTGCCTCGCTGCCCGAGCACCACTTGGCCCTGGAGGCTGCGGTGAGCCACATGAC 2100

Qy   2101 TCTCCGAGCACCCCCGCCCCTCCTCGGAGGCTACGGCCTTCA 2160
          ||||||||||||||||||||||||||||||||||||||||
Db   2101 TCTCCGAGCACCCCCGCCCCTCCTCGGAGGCTACGGCCTTCA 2160

Qy   2161 GCCCCTCCGGGGGCCCCTATCAGGGACATGGGCACCCTCAGGGCTCCAGCAGCTT 2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy 3301 ACAGGAGGAGTCAGAGGATGTGACGCGCTCGTGCGGTCGGCGGTGGGCAGGAAGCGC 3360
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Db 3301 ACAGGAGGAGTCAGAGGATGTGGACGCGCTCGTGCGGTCGGCGGTGGGCAGGAAGCGC 3360

Qy 3361 AAGTGGTCCTCGCCGTCACGCAGCCTCTTCCACTTCCTCGGGAGGCACCTGCCGCGTGGAT 3420
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Db 3361 AAGTGGTCCTCGCCGTCACGCAGCCTCTTCCACTTCCTCGGGAGGCACCTGCCGCGTGGAT 3420

Qy 3421 GAGGCTGCAGAGCTGGGCGTCGGTGCGGCGTGAGAGTGAAGGCCTCCGTGGAGCACATCTCCCGG 3480
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3421 GAGGCTGCAGAGCTGGGCGTCGGTGCGGCGTGAGAGTGAAGGCCTCCGTGGAGCACATCTCCCGG 3480

Qy 3481 ATCTGAAGGCAGGCCGGAAGGTCTGGAAGGAGGAGGGGCCCCCAGGAAGGAAGCCAGGC 3540
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3481 ATCTGAAGGCAGGCCGGAAGGTCTGGAAGGAGGAGGGGCCCCCAGGAAGGAAGCCAGGC 3540

Qy 3541 CTTGCTTCCTTCCGGTCTCAGGTCTGAAGAGCTGGACCGGACGGCCGCGACATTCCTAAGG 3600
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3541 CTTGCTTCCTTCCGGTCTCAGGTCTGAAGAGCTGGACCGGACGGCCGCGACATTCCTAAGG 3600

Qy 3601 GAGCTCTCAGATGAGACTGTGGTCCTGGGCCAGTCAGTCAGTGACACTGGCCTGCCAGGTGTCA 3660
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Db 3601 GAGCTCTCAGATGAGACTGTGGTCCTGGGCCAGTCAGTCAGTGACACTGGCCTGCCAGGTGTCA 3660

Qy 3661 GCCCAGCCAGCTGCCCAGGCCACCTGAGCAAAGACGAGCCCCTGGAGCAGCAGCAGC 3720
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Db 3661 GCCCAGCCAGCTGCCCAGGCCACCTGAGCAAAGACGAGCCCCTGGAGCAGCAGCAGC 3720

Qy 3721 CGTGTCCTCATCTCTGCCACCCTCAAGAACTTCCAGCTTCGACCATCCTCGTGGTGGTGTG 3780
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3721 CGTGTCCTCATCTCTGCCACCCTCAAGAACTTCCAGCTTCGACCATCCTCGTGGTGGTGTG 3780

Qy 3781 GCTGAGACCTGGTGTGTACACCTGCAGGTGAGCAATGCGCTGGGACAGTGACCACC 3840
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Db 3781 GCTGAGACCTGGTGTGTACACCTGCAGGTGAGCAATGCGCTGGGACAGTGACCACC 3840

Qy 3841 ACGGGCCGTCCTCCGGAAGGCAGAGCCGGCCCTCATCTTCGGCCATGCCGGATATCGGGGAG 3900
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Db 3841 ACGGGCCGTCCTCCGGAAGGCAGAGCCGGCCCTCATCTTCGGCCATGCCGGATATCGGGGAG 3900

Qy 3901 GTGTACGGCGGATGGGGGTGCTGGTCTGGAAGCCCGTGAAGTCCTACGGCCCTGTGACC 3960
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Db 3901 GTGTACGGCGGATGGGGGTGCTGGTCTGGAAGCCCGTGAAGTCCTACGGCCCTGTGACC 3960

Qy 3961 TACATTGTGCAGTGCAGCCTAGAAGGCGGCAGCGGCCTTCCGGACATCTTT 4020
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Db 3961 TACATTGTGCAGTGCAGCCTAGAAGGCGGCAGCGGCCTTCCGGACATCTTT 4020

Qy 4021 GACTGCTGCTACCTGACAGCAGCAAGCTCTCCCGGGGTGGCACCTACACCTTCCGGCACGGCA 4080
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4021 GACTGCTGCTACCTGACAGCAGCAAGCTCTCCCGGGGTGGCACCTACACCTTCCGGCACGGCA 4080

Qy 4081 TGTGTCAGCAGGCAGGAATGGGTCCCTACAGCAGCCCGTGGAGCCAAGTCCTCCTGGGA 4140
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4081 TGTGTCAGCAGGCAGGAATGGGTCCCTACAGCAGCCCGTGGAGCCAAGTCCTCCTGGGA 4140

Qy 4141 GGGCCCAGCCACCTGGCCTCTCCAGTGGAGGAGGCGGTCAGCGCCCTGCCC 4200
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4141 GGGCCCAGCCACCTGGCCTCTCCAGTGGAGGAGGCGGTCAGCGCCCTGCCC 4200

Qy 4201 AGCACAAAGACCTTCCATTCGAGTTTATGATCTTCAGGAAA 4260
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Db 4201 AGCACAAAGACCTTCCATTCGAGTTTATGATCTTCAGGAAA 4260

Qy 4261 CAATGCTGGGAGAAGGCCAGCGGCGCGCGGCCCAAGATCATCCCCTACCACCCC 4320
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Db 4261 CAATGCTGGGAGAAGGCCAGCGGCGCGCGGCCCAAGATCATCCCCTACCACCCC 4320

Qy 4321 AAGGACAAGACAGCAGTGCTCGCCGGAATACGAGGGCCTCAAGGGACATCTTGAGATC 4380
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Db 4321 AAGGACAAGACAGCAGTGCTCGCCGGAATACGAGGGCCTCAAGGGACCCCAGGATC 4380


Db 2161 GCCCCTCCGGGGGGCCCTATCAGGGACATGGGCACCCTCAGGGCTCCAAGCAGCTT 2220

Qy 2221 CCATCCACTGTGGCCACCAGGCACTGCTCAGCCAGAGAGGCCATCCCGGACAGCCCT 2280
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Db 2221 CCATCCACTGTGGCCACCAGGCACTGCTCAGCCAGAGAGGCCATCCCGGACAGCCCT 2280

Qy 2281 TGGGGCAGCCAGCAGCCCCTTCTGCCACCCAAGCAGAGGTTCTGCCCACCCAGGAGGGCTGC 2340
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Db 2281 TGGGGCAGCCAGCAGCCCCTTCTGCCACCCAAGCAGAGGTTCTGCCCACCCAAGGAGGGCTGC 2340

Qy 2341 AGCCCCCACCCAGAGTTGCCCCATGCCCCTGGCCTCTTCCCTCCCTCCAGGATCTTGCAAA 2400
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Db 2341 AGCCCCCACCCAGAGTTGCCCCATGCCCCTGGCCTCTTCCCTCCCTCCAGGATCTTGCAAA 2400

Qy 2401 GAGGCCCCCTTAGTACCCTCAAGCCCCTTCTTGGGACAGCCCAGCCCTGCCCCT 2460
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2401 GAGGCCCCCTTAGTACCCTCAAGCCCCTTCTGGGACAGCCCAGCCCTGCCCCT 2460

Qy 2461 GCCAAAGCAAGCCCCCATTGGACTCTAAGATGGGGCCTGGAGACATCTCTTCTTCCTGGG 2520
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Db 2461 GCCAAAGCAAGCCCCCATTGGACTCTAAGATGGGGCCTGGAGACATCTCTTCTTCCTGGG 2520

Qy 2521 AGGCCAAAACCCGGCCCCTGCCAGTTCCCCAGGGTCAGCCTCCCAGGCGAGTCTTCCCAA 2580
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Db 2521 AGGCCAAAACCCGGCCCCTGCCAGTTCCCCAGGGTCAGCCTCCCAGGCGAGTCTTCCCAA 2580

Qy 2581 GTGAGCTCCCTCAGGGTGGCTCTCCCAGGTGGGCACAGAGCCTGCCCCTCCCTGGAT 2640
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2581 GTGAGCTCCCTCAGGGTGGCTCTCCCAGGTGGGCACAGAGCCTGCCCCTCCCTGGAT 2640

Qy 2641 GCGAGGGGCTGGACCCAGGAGGCTGAGGATCTGTCCGACTCCACACCCACCTTGCAGCGCG 2700
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2641 GCGGAGGGGCTGGACCCAGGAGGCTGAGGATCTGTCCGACTCCACACCCACCTTGCAGCGCG 2700

Qy 2701 CCTCAGGAACAGGTGACCATGCGCAAGTTCTCCCTGGGTGGTCGCGGGGCTACCGAGGC 2760
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Db 2701 CCTCAGGAACAGGTGACCATGCGCAAGTTCTCCCTGGGTGGTCGCGGGGCTACCGAGGC 2760

Qy 2761 GTGGCTGGCTATGGCACCTTGCCCTTTGGTGAGATGCAGGGGGCATGCTGGGGCAGGGG 2820
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Qy 2821 CCCATGTGGGCCAGGATAGCCTGGGGCTGTGTCCCAGTCGCAGGAGCAGGAGGAGGAGGAG 2880
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Qy 2881 GCCAGGGCTGAGTCCCAGTCGGAGGAGCAGGAGCCCAGGGCCTGAGAGCCCACTGCCC 2940
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Db 2881 GCCAGGGCTGAGTCCCAGTCGGAGGAGCAGGAGCCCAGGGCTGAGAGCCCACTGCCC 2940

Qy 2941 CAGGTCAGTGCAAGGCCTGTGCCTCGAGTCGGCAGGTCGGCTCCCACCAGAGTCTTCCAGAG 3000
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Db 2941 CAGGTCAGTGCAAGGCCTGTGCCTCGAGTCGGCAGGTCGGCTCCCACCAGAGTCTTCCAGAG 3000

Qy 3001 CCCACCCCATGGGAGGACATCGGGCAGTTCTCCTGCTCGTGTCAGATCCGGGACTCGTCAGGT 3060
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Db 3001 CCCACCCCATGGGAGGACATCGGGCAGTTCTCCTGCTCGTGTCAGATCCGGGACTCGTCAGGT 3060

Qy 3061 GATGCGGAGGGCGGCCGACCAGTTCCTGGAGTGACCCCGCTACCTC 3120
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Db 3061 GATGCGGAGGGCGGCCGACCAGTTCCTGGAGTGACCCCGCTACCTC 3120

Qy 3121 AACCTCTCAGACCGTACGATATCAAGTACCCCCATTCGAGTTTATGATCTTCAGGAAA 3180
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3121 AACCTCTCAGACCGTACGATATCAAGTACCCCCATTCGAGTTTATGATCTTCAGGAAA 3180

Qy 3181 GTCCCCAAGTCGGGAGAAGGCCTCAGCCGAGGAGCTGGCCGAG 3240
        |||||||||||||||||||||||||||||||||||||||||||
Db 3181 GTCCCCAAGTCGGGAGAAGGCCTCAGCCGAGGAGCTGGCCGAG 3240

Qy 3241 TTCCCGGAGCCTGGCCACGTGGCCCACGTGCGCGGAATGGGCCCCCAAGGGCCTCGGAGATC 3300
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3241 TTCCCGGAGCCTGGCCACGTGGCCCACGTGCGCGGAATACGAGGGCCTCAAGGGCCTCGGAGATC 3300
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Tue Apr 27 10:11:33 2004　　　　us-10-697-263-1.rni

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;  LENGTH: 1429
;  TYPE: DNA
;  ORGANISM: Mus musculus
;  FEATURE:
;  NAME/KEY: CDS
;  LOCATION: (10)..(1353)
US-09-159-385-4

Query Match    3.4%;   Score 178.2;  DB 2;  Length 1429;
Best Local Similarity  53.5%;  Pred. No. 7.9e-27;
Matches  437;  Conservative  0;  Mismatches 353;  Indels  27;  Gaps  2;

Qy   601  TATGAGGTCAAGAAGGAGGAGATTGGAAGGGCCGTGTTGGCTTCGTAAAAAGAGTGCAGCAC  660
                ||| |||  | |||||  ||| || | ||||  ||||| |||   ||||  |||
Db    46  TATGAGATGGGAGGAGGAGCTTGCAGTGGCCAATTTGCCATCGTGCGCAAGTGCCAGCAG  105

Qy   661  AAAGGAAACAAGATCTTGTGCGCTGCCAAGTTCATCCCCTACGGCGAGCAGAACT------  714
                ||  |||  | || | || ||||| || ||||| | | ||||  || || |
Db   106  AAGGGCACGGCACGGCATGGCAGTATGCAGCCAAGTTCATCAAGAACGGCGGCCGTCCATCCAGC  165

Qy   715  ----------CGGGCCCAGGCATACAGGGAGGGAGGACATCCTGGCCGCGCTGAGC  759
                          ||| || | | ||  |||  |||  |  || |||
Db   166  CGGCGCGGTGTGAGCCGGGAGAGAAGATCGAACGCGAGTGAGCATCCTGCGCGGAGATCCGC  225

Qy   760  CACCCGCTGCTCACGGCGGCTGCTGACGCCAGTTGAGACCGCAAGACCCTCATCCTCATC  819
                || || |||| ||| | ||| | |  |  ||  ||   | ||| | |  || ||
Db   226  CACCCCAACATCATAACACTGCATGACGTGTTCGAGACAAGAACAAGACAGATGTGGTGCTGATC  285

Qy   820  CTGGAGCTGTGCTCATCCGAGAGAGCTGCTGAGGAGGGCTGGTCCGGCTGAGC  879
                || || ||  | ||||  |  | |  ||  | | | || |||| | | |
Db   286  CTGGAGCTGGTGTCGGTGGCGGAGCTTTTCGACTTCGTGGCCGAGAGAGGAGTCATTGACG  345

Qy   880  GAGGCCAGGTAACGGGCTGTGTCCTTCCTGGGGCGCCGTGGTGGAGGGGCTGCACTACCTGCACAGC  939
                ||| ||  ||| |||||  | || | |||| ||  ||| || || || |
Db   346  GAGGATGAGGCCACGCACAGTTCCTCAAACAAATCCTAGACGGTGTCCTCAACTACTGCACTCC  405

Qy   940  CATGGCGTTCTCCACCTGGACATAAAGCCCTCTAACAATCCTCATGGT------GCATCCT  993
                 ||  || |  | ||  | || || || | || | || | | |
Db   406  AAGGCCATCGACACTTTGACCCGAAGGCCGAGAACATCATGTTGCTGGACAAGCACGCA  465

Qy   994  GCCCGGGAAGACATTAAAAATCTGCACTTTGGCTTTGCCCAGAACATCACCCCAGCAGAG  1053
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Db   466  GCCAGCCCCGGCATTAAGCTCATCGACTTTGGCATGCGCGCACAGGATCGACGCTGGCAGC  525

Qy  1054  CTGCAGTTCAGCCAGTACGGCTCTCCCCGGGATCATCCAGCAGTG  1113
                || |||| | |||  || | ||| ||  ||| | ||||
Db   526  GAGTTCAAGAAACATCTTTGGCACACCCGAGTTTGTCGCCCCGAGGTG  585

Qy  1114  CCTGTGAGCGAAGCCTCCGACATTGGGCCATGGGGTGTCATCTCCACCTGAGCCTTCAGCCTGACC  1173
                ||  || ||||  || | ||  ||| || | |  ||| | |  || ||||
Db   586  CCACTTGGCTTGGAGGCTGACATGGCATGTGGCGTCATCACCTACATCCTCCTGGAGC  645

Qy  1174  TGCTCATCCCATTGCGCGAGGATGACCGTGCACCCTCTGAACGTCCTGGAGGGG  1233
                | | |||  ||  ||| ||  || | | |||  |  | | ||| || | |
Db   706  AACTATGACTTTGATGAGAATACTTCAGCAGCACCGAGCTGGCCAAGGACTTCATC  765

Qy  1234  CGGCTGTGTCATGGAGCAGCCCACGTGCCCACCTGCGAAGACGCCAAAGACTTCATC  1293
                || | ||  | |  ||||  |||  ||  ||  || | |  | ||| |||| ||||
Db  1294  AAGGCTACGCTGCAGAGAGCCCCTCAGGCCCGGCCTAGTGCGGCCCAGTGCCTCTCCCAC  1353

Qy  1354  CCCTGGTTCCTGAAATCCATGCCTGCGGGAGGAGGGCCC  1390
                || |  || || ||  | || | ||  ||  || || |
Db   766  CGCAGGCGTGCTGTGTCAAAGACACCCCAAGGAGGAGGAGGATGATGACCATCGCGCACAGAGCGCACTGGGAGCAT  825
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Qy  4381  CTGGCCCAGCTGACGCAGCAGCCTACCTCAGCCCCCGGCACCTGGTGCTCATCTTGGAGCTG  4440
                ||||||||||||||||||||||||||||||||||||| |||||||| |||  ||||
Db  4381  CTGGCCCAGCTGCACGCAGCACCTACCTCCTCAGCCCCCGGCACCTGTGCTGCTCATCTTGGGAGCTG  4440

Qy  4441  TGCTCTGGGGCCGAGCTGCTCCCCTGGCCGCGCGAGAGGGCCTTCCTACTCAGAATCTGAG  4500
                |||||||||||| |||  |||| |||||||| | ||| |  || |||| | || ||
Db  4441  TGCTCTGGGCCGAGCTGCTCCCCTGGCCCGAGAGGGCCTCCTACTCAGAATCTGAG  4500

Qy  4501  GTGAAGGACTACCTGTGCAGATGTTGAGTGCCACCCAGTACCTGACAACCAGCACATC  4560
                ||||||||||||  ||||| ||||| |||||||| |||||| ||| || |||||||||
Db  4501  GTGAAGGACTACCTGTGGCAGATGTTGAGTGCCACCCCAGTACCTGACAACCAGCACATC  4560

Qy  4561  CTGCACCTTGGACCTGAGCTCCGAGAACATGATCATCACCGAATACAACAACCTGCTCAAGGTC  4620
                ||||||||||||| |||||||| |||||| ||| ||||||| |||||||| ||| |||||||
Db  4561  CTGCACCTTGGACCTGAGCTTCCGAGAACATGATCATCACCGAATACAACAACCTGCTCAAGGTC  4620

Qy  4621  GTGGACCTGGGCAATGCACAGAGCCTCAGCCAGGAGAAGGTGTGCCCTCAGACAGTTC  4680
                |||||||||||||||  ||||||||||||||||||||||||| |||||||| |||||||
Db  4621  GTGGACCTGGGCAATGCACAGAGCCTCAGCCAGGAGAAGGTGTGCTGCCCTCAGACAGTTC  4680

Qy  4681  AAGGACTACTAGAGACCATGGCTCCAGAGCTCCTGGAGGGCCAGGGGGTGTTCCACAG  4740
                ||||||||||||||||||||||||||||||||||||||||||||  ||||  |||||||
Db  4681  AAGGACTACTAGAGACCATGGCTCCAGAGCTCCTGGAGGGCCAGGGGCTGTTCCACAG  4740

Qy  4741  ACAGACATCTGGGCACCATGCGTGTGACAGCCTTCATCATGTCGAGCGCCAGTACCCGGTG  4800
                |||||||| |||| |||||| | |  ||||||||||||||||||  || ||||| || |||
Db  4741  ACAGACATCTGGGCCATGGCCATGTGTGACAGCCTTCATCATGTCGAGCGCCAGTACCCGGTG  4800

Qy  4801  AGCAGCGAGGGTGCACGGACCTGCAGAGAGACTGCCAAGGGGTTGGTCCGGCTGAGC  4860
                ||||||||||| ||| ||||||||||||||||  || ||||||||| ||||||||||
Db  4801  AGCAGCGAGGGTGCACGGCACCTCCAGAGAGACTGCCAAGGGGTTGGTCCGGCTGAGC  4860

Qy  4861  CGCTGCTACGCGGGGCTGTCCGGGGGCGCGCCGTGGCCTTCCTGCGCAGCACTCTGTGCGCC  4920
                |||||||||||||||||||||| ||||||||||||||||||| ||||||||| || ||||||
Db  4861  CGCTGCTACGCGGGGCTGTCCGGGGGCGCGCCGTGGCCTTTCCTGCGCAGCACTCGTGCGCC  4920

Qy  4921  CAGCCCTGGGGCCGGCCGGGCCTGCCCAGCTGCCCAGTGCCCGTGGCTAACAGAGGAG  4980
                ||||||||||||||||||||||||||||||||||||||||| |||||||| || ||||||
Db  4921  CAGCCCTGGGGCCGGCCGGGCCTGCCCAGCTGCCCAGTGCCCGTGGCTAACAGAGGAG  4980

Qy  4981  GGCCCGGCCGCTGTTCGCGGCCCCGGCCCGTGACCTTCGCGCCTACCGCGGGGGCGTCGCGGCTTC  5040
                ||||||| |||||||||||||||||||| ||||||||||| || ||||||| ||||||| |||||
Db  4981  GGCCCGGCCGCTGTTCGCGGCCCCGGCCCGTGACCTTCGCGCCTACCGCGGGGGCGTCGCGCTTC  5040

Qy  5041  GTGGCCAATCGCGAGAAGACGACGCGCGCTGCGCTGCTGCTACAAGAGGCACAACCTGGCCCAGGTG  5100
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  5041  GTGGCCAATCGCGAGAAGACGACGCGCGCTGCGCTGCTGCTACAAGAGGCACAACCTGGCCCAGGTG  5100

Qy  5101  CGCTGAGGGTCGCCCCGGCCACACCCTTGGTCTCCCCGCTGGGGTCGCTGCGACGCGGC  5160
                |||||||||||||||||||| ||||||||||||||| || ||||| ||||||||||||||
Db  5101  CGCTGAGGGTCGCCCCGGCCACACCCTTGGTCTCCCCGCTGGGGTCGCTGCGACGCGGC  5160

Qy  5161  CAATAAAAACGCACAGCCCGGCGGAAAAAAAAAAAAAAAA  5207
                ||||||||||||||||||||||||||||||||||||||||
Db  5161  CAATAAAAACGCACAGCCCGGCGGAGAAAAAAAAAAAAAAA  5207
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RESULT 4
US-09-159-385-4
;  Sequence 4, Application US/09159385
;  Patent No. 5958748
;  GENERAL INFORMATION:
;  APPLICANT: AKIRA, SHIZUO
;  APPLICANT: KAWAI, TARO
;  TITLE OF INVENTION: DNA CODING FOR SERINE/THREONINE KINASE
;  FILE REFERENCE: PH-569
;  CURRENT APPLICATION NUMBER: US/09/159,385
;  CURRENT FILING DATE: 1998-09-23
;  EARLIER APPLICATION NUMBER: JP97/261589
;  EARLIER FILING DATE: 1997-09-26
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: PatentIn Ver. 2.0
;  SEQ ID NO 4

RESULT 5
US-09-186-277-4
;  Sequence 4, Application US/09186277
;  Patent No. 6171841

GENERAL INFORMATION:
;  APPLICANT: AKIRA, SHIZUO
;  APPLICANT: KAWAI, TARO
;  TITLE OF INVENTION: DNA CODING FOR SERINE/THREONINE KINASE
;  FILE REFERENCE: 081356/0128
;  CURRENT APPLICATION NUMBER: US/09/186,277
;  CURRENT FILING DATE: 1998-11-05
;  EARLIER APPLICATION NUMBER: JP97/261589
;  EARLIER FILING DATE: 1997-09-26
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4
;  LENGTH: 1429
;  TYPE: DNA
;  ORGANISM: Mus musculus
;  FEATURE:
;  NAME/KEY: CDS
;  LOCATION: (10)..(1353)
US-09-186-277-4

Query Match             3.4%;    Score 178.2;  DB 3;   Length 1429;
Best Local Similarity  53.5%;    Pred. No. 7.9e-27;
Matches  437;  Conservative  0;  Mismatches 353;  Indels 27;  Gaps  2;

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Qy    601  TATGAGGTCAAGGAGGAGGAGGATTGGAAGGGGCGTGTTTGGCTTCGTAAAAAAGAGTGCAGCAC  660
           ||||||   ||||||||||||||   |||| |||||||||  ||||||
Db     46  TATGAGATGGGAGGAGGAGCTTGGCAGTGGCCAATTTGCCATCGTGCGCAAGTGCCAAGCAG  105

Qy    661  AAAGGAAACAGAGATCTTGTGCGCTGCCAAGTTCATCCCCTACGGAGCAGAACT------  714
           ||||| |||
Db    106  AAGGGCACGGCACGGCCATGCATGGAGTATGCAGCCAAGTTCATCAAGAAGCGCGGCGCCTGCCATCAGC  165

Qy    715  ----------CGGGCCCAGGCATACAGGGAGCGAGACATCCTTCGGCCCGCTGAGC  759
                     ||||||||||  ||||  ||  ||||| | |||||
Db    166  CGGCGGCGGTGTGAGCCGGGAGGATCGAACGCGAGGTGAGCATCCTGCGCGAGATCCGC  225

Qy    760  CACCCGCTGGTCACGGGCGCTGCTGACCAGTTGAGACCCTCAAGACCCTCATCCTCATC  819
           |||||  |  |||| | ||||||| |||||||||||
Db    226  CACCCCAACATCATAACACTGCATGCAGTGTGTTCGAGAACAAGACAGATGTGTTGCTGATC  285

Qy    820  CTGGAGCTGTGTCATCCGAGGAGGACTGTGGACACCGCCTGTACAGGGAGGGGCGTGGTGACG  879
           |||||||||||| |||| |||||||| | ||
Db    286  CTGGAGCTGGTGTCCGGTGCGGAGCTTTTCATCGGACTTCCTGCCGAGAAGGAGTCATTGACG  345

Qy    880  GAGGGCGAGGTCAAGGTCTACATCCGAGCAGCTGTGTGAGGGGCTGCACTACCTGCACAGC  939
           ||||||  ||  |||||||||||||||| | ||| ||||||||
Db    346  GAGGATGAGGCCACGCAGTTCCTCAAACAAATCCTAGACGCGGTGTCCACTACCTGCACTCC  405

Qy    940  CATGGCGTTCTCCACCTGGACATAAAGCCCTCAAACATCCTGATGGT------GCATCCT  993
           |||| |||| |||||||||||| |||| ||| |||| ||| || |     ||||||
Db    406  AAGCGGCATCGCACACTTTGACCTGAAGCCCGAGACACTTCATCATGTTGCTGGACAAGCACGCA  465

Qy    994  GCCCGGGAAGACATTAAAATCTGCGGACTTGGCTTGCCCAGAACATCACCCCAGCAGAG  1053
           | |||||||| || |    ||||  |||||||||||||   |||||  |||  |||||||
Db    466  GCCAGCCCCGCCATTAAGCCATTAAGCTTCATCGATCGGCTCATTGGGCATCGGGATCGCTGGCAGC  525

Qy   1054  CTGCAGTTCAGCCAGTACGGCTCCCCGAGTTCGTCTCCCCGAGATCATCCAGCAGAAC  1113
           |||||| |  ||| |||||   |||||||||||  |   ||||   |||||||||||  |||
Db    526  GAGTTCAAGAACATCTTTGGCACACCCGGAGTTTGTGCCCGAGATCGTGAACTATGAG  585

Qy   1114  CCTGTGAGCGGAAGCCTCCGACATTTGGGCCATGGGCGTGTCATCCTCAGCCTTGACC  1173
           ||||||  ||| |||||||| |||||||||| | |  || ||||||||||
Db    586  CCACTTGGCTTGGAGGCTGACATGTGGAGCATTGGCGTCATCCTCTACATCCTCCTGAGC  645

Qy   1174  TGCTCATCCCCATTTGCCGGCGAGATGACCGTGCCACCTCCTGAACGTCCTGGAGGGGG  1233
           |||||||||  |||||||
Db    646  GGAGCCTCCCCATTCCTGGGCGACAGCGGGAGACGTCGCGGAGAACATCTCAGCAGTG  705

Qy   1234  CGCGTGTCATGGAGCAGCCCCATGCTGCGAAGACGGCAAAGACTTCATC  1293
           ||||  ||    ||||||
Db    706  AACTATGACTTTGATGAGGAATACTTCAGCGAGCCACCAGCCAAGGACTTCATC  765

Qy   1294  AAGGCTACGCGTGCAGAGAGCCCCTCAGGGCCCTAGTGCGCGCCCTAGTGCGCGTC  1353
           ||||| |  |  ||  ||||||||
Db    766  CACAAGATCGAGGCGGGGAACCAGTTCAAGAACATCTTCGGCCCGAGTTTGTGGCC  825
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Db    766  CGCAGGCTGCTGCTCAAGACCCCAGAGAGGAGGATGACCATCGCACAGAGCCTGGAGCAT  825
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          |||||| |||| ||| |||| |||||||  |||| ||||| ||||| |||||||||||||
Qy   1354  CCCTGGTTCCTGAAATCCATCGCCTGCGGAGGAGCCC  1390
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Db    826  TCCTGGATCAAGGTGCCGCAGGGCGAGGCGAGGACGCGGCGCCC  862

RESULT 6
US-09-159-385-3
; Sequence 3, Application US/09159385
; Patent No. 5958748
; GENERAL INFORMATION:
;  APPLICANT: AKIRA, SHIZUO
;  APPLICANT: KAWAI, TARO
;  TITLE OF INVENTION: DNA CODING FOR SERINE/THREONINE KINASE
;  FILE REFERENCE: PH-569
;  CURRENT APPLICATION NUMBER: US/09/159,385
;  CURRENT FILING DATE: 1998-09-23
;  EARLIER APPLICATION NUMBER: JP97/261589
;  EARLIER FILING DATE: 1997-09-26
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
;  LENGTH: 2132
;  TYPE: DNA
;  ORGANISM: Homo sapiens
;  FEATURE:
;  NAME/KEY: CDS
;  LOCATION: (94)..(1455)
US-09-159-385-3

Query Match             3.3%;    Score 173.4;  DB 2;   Length 2132;
Best Local Similarity  53.3%;    Pred. No. 8.1e-26;
Matches  431;  Conservative  0;  Mismatches 351;  Indels 27;  Gaps  2;

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Qy    580  CGGAGGAAGCTGCACTCCTTCTATGAGGTCAAGGAGGAGATTGGAAGGGGCGTGTTTGGC  639
           ||||||| ||||| ||||||  |||||| ||     ||||  || || ||| |||||||||
Db    109  CAGGAGGACGTGGAGGACCATTATGAGAGGGGGGAGGAGCTGGGCAGCGGCGGCCAGTTTGCG  168

Qy    640  TTCGTAAAAAGAGTGCAGCACAAAGGAAACAGATCTTGTGCGCTGCCAAGTTCATCCC-  698
           ||||| ||||  |||| | |||||||| | |  ||  || |||||||||||||||
Db    169  ATCGTGCGGAAGTGCCGGCAGAAGGGCACCGGCAAGGGCAAGGAGTACGCAGCCAAGTTCATCAAG  228

Qy    699  ------------CCTACGGAGCAGCAGATCCGGGTGGGGGTGAGCGAGCGGGAGGA  738
                       || |  | | |||  |  ||| ||||| |||| |||||   ||||
Db    229  AAGCGCCGGCCGCTGTCATCCGCCGGGGTGTGGGTGAGCGTGCACGGGCGTGCTGGACAGTTGAGACC  288

Qy    739  GCATCCTGGCCGCGCTGAGCCACCCGCTGGTCACGGGCGTCACGGGCGTTGAGACC  798
           ||  ||  |   |  |  || ||||| ||  || || ||| |  | | ||| ||||
Db    289  AACATCCTCGGGAGATCCGGCACCCCAACATCATCACCCGCACGACATCTTCGAGAAC  348

Qy    799  CGCAAGACCCTCATCCTCCGAGAGGTGTGTCTCATCCGCGAGGAGTGCTGCTGGACACCGGCTG  858
           |||||  | |||||| | | ||| |||| |  | |||||||  || | ||||||||
Db    349  AAGAGCAGACGTGGGTCCTCATCCTGGAGCTGGTGTCGGCGGGAGCTTTGACTTCCTG  408

Qy    859  TACAGGGAAGGGCGTTGGTGACGGCCGCAGGTCAAGGTCACATCCAGCAGCGTGGTGGAG  918
           ||| || |||| || | || | || ||||||  |||||| | |||| | | |  || |||
Db    409  GCGGAGAAAGAGTGCTGACGGAGGACGAGGCCACCCAGTTCCTCAAGCAGATCCTGGAC  468

Qy    919  GGGCTGCACTACCTGCACAGCCATGGCGTGTCATCCTCCACCTGGACATAAAGCCCTCTAACATC  978
           |||||||| |||||||||| ||||  |||||||||  ||||| | ||||  || ||   ||||||
Db    469  GGCGTTCACTACCTGCACTCGCACTCAAGCCTACCATCCTCCTGAGCGGAGCCTCCATC  528

Qy    979  CTGATGGTGTCATCCTGCCCGGGAAGAC------ATTAAAATCTGGCTTTGGCTTGCC  1032
           || || ||||| || || ||||  |  |        |||| ||| |  ||||||  |
Db    529  ATGCTGCTGGACAAGCACGTGCCCACCACCAATCAGAATCAAGCTTCATCGACTTCGGCATCGCG  588

Qy   1033  CAGAACATCACCCCAGAGCTCAGCGAAGACGCAGAGCTCAGCCAGTACGGGTCGTCTCC  1092
           ||||| || | || | | |||||| |  || |||||||||||| |||   ||||| || |
Db    589  CACAAGATCGAGGCGGGGAACCAGTTCAAGAACATCTTCGGCCCGAGTTTGTGGCC  648

Qy   1093  CCCGGAGATCATCCAGCAGAACCCTGTGAGCGGAACCCTCCGACATTTGGGCCATGGGCGTGTC  1152
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Db 469 GGCGTTCACTACCTGCACTCTAAGCCATCCACATTTGACCTGAAGCCGGAAAAACATC 528
        |||  ||  |||       |||||  |||||||||||||||||||||||||
Qy 979 CTGATGGTGCATCCTGCCCGGGAAGAC-----ATTAAAATCTGGACTTTGGCTTTGCC 1032

Db 529 ATGCTGCTGGACAAGAACGTGCCAACCACGAATCAAGCTCATCGACTTCGGCATCGCG 588
        ||||||||||||||||||||||||||||
Qy 1033 CAGAACATCACCCCAGCAGAGCTGCAGTTCAGCCCAGTACGGCTCCCCTGAGTTCGTCTCC 1092

Db 589 CACAAGATCGAGCGGCGGGAACGAGTTCAAGAACATCTTCGGCACCCCGGAGTTTGTGGGCC 648
        |||||||||||||||||||||||||||||||
Qy 1093 CCCGGATCATCCAGCAGAACCCTGTGAGGAGGAAGCCTCCACATTGGGCCATGGTGTC 1152

Db 649 CCAGAGATTGTGAACTATGAGCGCGTGGGCGTGGACGCGGACATCGGAGCATCGTGTC 708
        |||||||||||||||||||||||||||||||
Qy 1153 ATCTCCTACCTCAGCCTGACTTCGCTCATCCCATTGCCGGCGGAGAGTGACCGTGCCACC 1212

Db 709 ATCACCTATATCCTCTGAGCCGGTGCATCCCCGTTCGTGGGCGACCAAGCAGGAGACG 768
        ||||||||||||||||||||||||||||||||
Qy 1213 CTCCTGAACGTCCTGGAGGGGCGGTGTCATGGAGCAGCCCATGGCTGCCACCTCAGC 1272

Db 769 CTCACCACACATCTCAGCCGTGAACTACGACTTCGACGAGGAGTACTTCAGCAACACCAGC 828
        |||||||||||||||||||||||||||||||
Qy 1273 GAAGACGCCAAAGACTTCATCAAGGTCACGTGCAGAGAGCCCCTCAGGCCCGGCCTAGT 1332

Db 829 GAGCTGGCCAAGGACTTCATTCGCCGGCTGCTCGTCAAAGATCCCAAGATCCCAAGCGGAGAATGACC 888
        ||||||||||||||||||||||||||||||
Qy 1333 GCGGCCCAGTGCCTCTCCCACCCCTGTT 1361
        ||||||||||||||||
Db 889 ATTGCCCAGAGCCTGGAACATTCCTGGAT 917

RESULT 8
US-08-826-267-1
; Sequence 1, Application US/08826267
; Patent No. 5994070
; GENERAL INFORMATION:
; APPLICANT: Streuli, Michel
; TITLE OF INVENTION: No. 5994070e1 TRIO Molecules and Uses Related Thereto
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/826,267
; FILING DATE: 1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/014,214
; FILING DATE: 27 MARCH (1996)
; ATTORNEY/AGENT INFORMATION:
; NAME: Amy E. Mandragouras
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: DFN-010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8906 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA

Db 649 CCAGAGATTGTGAACTATGAGCGCGTGGGCGTGGACGCGGACATCGGAGCATCGTGTC 708
        |||||||||||||||||||||||||
Qy 1153 ATCTCCTACCTCAGCCTGACTTCGCTCATCCCATTGCCGGCGGAGAGTGACCGTGCCACC 1212

Db 709 ATCACCTATATCCTCTGAGCCGGTGCATCCCCGTTCGTGGGCGACCAAGCAGGAGACG 768
        |||||||||||||||
Qy 1213 CTCCTGAACGTCCTGGAGGGGCGGTGTCATGGAGCAGCCCATGGCTGCCACCTCAGC 1272

Db 769 CTCACCACACATCTCAGCCGTGAACTACGACTTCGACGAGGAGTACTTCAGCAACACCAGC 828
        |||||||||||||||
Qy 1273 GAAGACGCCAAAGACTTCATCAAGGTCACGTGCAGAGAGCCCCTCAGGCCCGGCCTAGT 1332

Db 829 GAGCTGGCCAAGGACTTCATTCGCCGGCTGCTCGTCAAAGATCCCAAGCGGAGAATGACC 888
        |||||||||||||||
Qy 1333 GCGGCCCAGTGCCTCTCCCACCCCTGTT 1361
        |||||||||||||
Db 889 ATTGCCCAGAGCCTGGAACATTCCTGGAT 917

RESULT 7
US-09-186-277-3
; Sequence 3, Application US/09186277
; Patent No. 6171841
; GENERAL INFORMATION:
; APPLICANT: AKIRA, SHIZUO
; APPLICANT: KAWAI, TARO
; TITLE OF INVENTION: DNA CODING FOR SERINE/THREONINE KINASE
; FILE REFERENCE: 081356/0128
; CURRENT APPLICATION NUMBER: US/09/186,277
; CURRENT FILING DATE: 1998-11-05
; EARLIER APPLICATION NUMBER: JP97/261589
; EARLIER FILING DATE: 1997-09-26
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 2132
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (94)..(1455)
US-09-186-277-3

Query Match       3.3%;    Score 173.4;   DB 3;   Length 2132;
Best Local Similarity  53.3%;   Pred. No. 8.1e-26;
Matches 431;   Conservative  0;   Mismatches 351;   Indels 27;   Gaps  2;

Qy 580 CGGAGGAAGCTGCACTCCTTCTATGAGGTCAAGGAGGAGATTGAAGGGGCGTGTTGGC 639
        |||||||||||||||||||||||
Db 109 CAGGAGGACGTGGAGGACCATTATGAGATGGGGGAGGAGCTGGGCAGCGGCCCAGTTTGCG 168

Qy 640 TTCGTAAAAGAGTGCAGCACAAAGGAAACAAGATCTTGTGCGCTGCCAAGTTCATCCC- 698
        ||||||||||||||||||||||
Db 169 ATCCTGCCGGAAGTGCCCGGCACGGGAGACGGCCAAGGAGTACGCAGCCAAGTTCATCAAG 228

Qy 699 ----------CCTACGGAGCAGAACTCGGCGCCCAGGCATACAGGGAGCGA 738
        |||||||||||
Db 229 AAGCGCCCGCCTGTCATCAGCCGGCGTGGGGTGAGCCGGAGGAGGAGATCGAGCGGGAGGTG 288

Qy 739 GACATCCTGGCCGGCGCCGCTGAGCCACCCGTCACGGGAGTCTGCCACCAGTTGAGACC 798
        |||||||||||||||
Db 289 AACATCCTGCGGGAGATCGGCACCCCAAACATCATCACCCTGCACGACACATCTTCGAGAAC 348

Qy 799 CGCAAGACCCTCATCCTCATCCTGAGCTGTGTGCTCATCCGAGGAGCTGCTGGACCCGCCTG 858
        |||||||||||||||
Db 349 AAGACGGACGTGGTCATCCTCCATCCTGGAGTGACGGAGGGTCTTTGACTTCCTG 408

Qy 859 TACAGGAGGGGCGTGGTGACGGACCGAGGTCAAGGTCAAGGTCACCAGCTCGGTGGAG 918
        |||||||||||||||
Db 409 GCGGAGAAAGAGTGCGTGACGGAGGACGAGCACCCAGTTCCTCAAGCAGATCCTGGAC 468

Qy 919 GGGCTGACTACCTGCACAGCCATGGCGTTCCCACCTGGACATAAAGCCCTCTAACATC 978

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;  FEATURE:
;    NAME/KEY: CDS
;    LOCATION: 67..8647
US-08-826-267-1

Query Match             2.9%;   Score 153.6;  DB 2;  Length 8906;
Best Local Similarity  49.4%;   Pred. No. 1.2e-21;
Matches  461;  Conservative    0;  Mismatches  464;  Indels   9;  Gaps   2;

Qy     435 CTCCCTGGTGCTGAGGCATGTGAGCCTGAAGGATGCCGGGCTTTACACCTGCCTGGCCCA 494
           |||||||  ||||| ||||||  ||  ||  | ||||  | ||||||| || |||||
Db    7584 CACGCTGAAGATTGTGGGCGTGACCACGGAAGATGACGGCATCTTACACGTGCATCGCTGT 7643

Qy     495 AAACACTGGTGCCAGTGCTTCTGCAAGGCAGAGAGCTGCTGGTGTCTTGGGGGGACAATGA 554
           ||   ||   |||||  |   ||  ||||  ||||| |||   ||   |||   | |
Db    7644 CAATGACATGGTTCAGCTGCTCATCATCGGCCAGTCCGCACCCGAGGGTCCAGGGATGGA 7703

Qy     555 GCCGGACTCAGAGAAGCAAAGCCACCGGAGGAAGCTGCACTCCTTCTTCTATGAGGTCAAGA 614
           | ||  | ||||  ||  || ||  |||||||| |  |  |  ||     |||||||||
Db    7704 TGGGATCATGTGACCTGGAAAGAC-----AACTTGACTCCTTCTACAGTGAAGTGGC 7757

Qy     615 GGAGATTGGAAGGGGCGTGTTTGGCTTCGTGTAAAAGAGTGCAGCACAAAGGAAACAAGAT 674
           |  |||||   ||    ||   |  |  | || ||  ||  || |||||| || ||
Db    7758 TGAGCTTGGCAGCGGGGCAGATTCCTGTCGTTAAGAAATGTGATCAGAAAGGAACCAAGCG 7817

Qy     675 CTTGTGCGCTGCCAAGTTCATCCCCTACGGAGCCAGAACTCGGGCCCAGGCATACAGGGGA 734
           | ||||   || |||  | |||  ||| | ||||  |  |  ||  ||||||| | |
Db    7818 AGCAGTGCGCCACTAAGTTTGTGAACAAGAAGTTGATGAAGCCGCGAACCAGGTCACCCATGA 7877

Qy     735 GCGAGAACATCTGGCCCGCGCCTGGTCACCCCGGCGTGCTGACCAGTTTGA 794
           ||   |||||  | ||    || ||     ||  |  |  | ||||||||||
Db    7878 GCTTGGGCATCTGCAGAGCCTCCAGCACCCCTGCTTGTCGGCTTCTGACACACCTTTGA 7937

Qy     795 GACCCGCAAGACCCTCATCCTGTCGTGCTCATCCGAGCGTGCTGCTGGACCCG 854
           |||| |||||  |  ||||  | |||  |||| | || ||||  ||  | ||
Db    7938 GACCCCCCAGCCAGCTACATCCTGTCTTTAGAAATGGCTGACCAGGGTGCGTCCTCTGCCTG 7997

Qy     855 CCTGTACAGGAAGGGCCGTGGTGACGGAGGCCCAGGTCAAGGTCTACATCCAGCAGCTGGT 914
           ||| | |||| |||  |||||| ||||   | ||||  ||| ||| || | ||||  ||||
Db    7998 CGTGGTGCCGATGGGAGGAGCCTCACTGAAGGAAGAATCAGGGCGCACCTGGGGAGGTTCT 8057

Qy     915 GGAGGGGCTGCGACTACCTGCACAGCCATGGCCGTTCTCCACCTGGACATAAAGCCCTCTAA 974
           |||   |||||  || |||  |||    | || |||| |||  ||||  |||||| |||||
Db    8058 GGAAGCTGTCCGGTACCTCCGGTAGGATAGCAGGATAGCACCTGGACCTAAAGCCTGAGAA 8117

Qy     975 CATCCTGATG---GTGCATCCGTCGCCCGGGAACGACATTAAAATCTGCGACTTTGGCTTTGC 1031
           |||||     |  ||  | |   | | |  |  || | |  ||  | | ||  |||| |
Db    8118 TATCCTGGTGGATGAGAGTTAGCCAAGCAACCATCGGCTGCTGACTTTGGAGGATGC 8177

Qy    1032 CCAGAACATCACCCCAGCAGAGCTCAGTTCAGCCAGTACGGCTCCCCTGAGTTCGTCTC 1091
           ||| | || | |||| ||||||  |||  | ||  ||| | ||| |    |||| | |||
Db    8178 TGTTCAGCTCAACACGACCTACTACATCCACCAGTTACTGGGAACCCTGAATTCCAGAGC 8237

Qy    1092 CCCGGAGATCATCCAGCAGACCCTGTGAGCGAAGCCTCCGACATTTGGGCCATGGGTGT 1151
           |||  |  | ||||||||| | ||| | || ||| |  |||||  ||||| ||| || |
Db    8238 CCCTGAAATCATCCTGGGAACCCTGTCTCCCTGACCCGGATACGGTGGAGTGTTGAGT 8297

Qy    1152 CATCTTCCTACCTCAGCCTGCTCATCCCCATTTGCCGGCGAGTGACCGGTGCCAC 1211
           |||  | |||  || || | || || ||||| ||| | | | ||||  || ||  |
Db    8298 GCTCACATACGTACTTCTTAGTGCGTGTTCCCCTTCCTGAATGACAGTGTGGAAGAGAC 8357

Qy    1212 CCTCCTGAACGTCCTGGAGGGGCGGCGGTGTGTCATGGAGCAGCCCCATGGCTGCCACCTCAG 1271
           |||| | || ||||   || |   ||  | |  | ||| ||||   ||||| |  | || |
Db    8358 CTGCCTGAACATTTGCCGCCTTAGACTTTAGCTTCCCAGATGACTACTTTAAAGGAGTTGAG 8417

Qy    1272 CGAGACGGCCAAAGACTTCATCAAGGCTACGCTTGCAGAGAAGCCCCTCAGGCCCCGGCCTAG 1331
           |||| | ||||| |  |||||| | |  | |  | || ||||   |  | ||||| | |||
Db    8418 CCAGAGGCCAAGGAGTTTCGTGCTTCCTCCTCGCAGGAGGACGGCGCGGCTTCCACAGAGAAGGATGCCCAGCCA 8477

Qy    1332 TGCGGCCCAGTGCCTCTCCACCCCTGGTTCCTG 1365
           | | |||||| ||  |   | || || || |
Db    8478 GGCTCGCGTTCGGCCCTGCAGGAGCAGTGGCTGCAG 8511
```

```
Query Match             2.3%;   Score 122.2;  DB 2;  Length 1282;
Best Local Similarity  49.2%;   Pred. No. 1.4e-15;
Matches  319;  Conservative    0;  Mismatches  329;  Indels    0;  Gaps    0;

Qy     717 GGCCCAGGCATACAGGGAGGAGGAGACATCCTGGCCGCGCTGGCCGGCTGGTCACGGG 776
           |||||||||  ||  |||| |||||| ||||||||  | || ||  | |||  ||  |
Db     365 GGCCCTGGTGCTGAGGAACGAGAGATCGCAGTGTGCTGTAGGATCAGTCACCCACCAACATCGTCGC 424

Qy     777 GCTGCTGGACCAGTTTGAGACCCCGCAAGACCCTCATCCTCTCGGAGCGTGTGCTCATC 836
           |||||| || ||||||| || ||||  ||||  | || | || ||||| ||| | |||
Db     425 TCTGGAGGATGTCCACGAGACGCCCTTCCCACCTCACCCTGCCATGGAGCCATGGGTGACGGG 484

Qy     837 CGAGGAGCTGCTGGACCGCCTGTACAGGAGGGCGTGGTGTGAACGGCCGAGGTCAAGGT 896
           | ||||| ||||| ||| ||| |||| || |  |||||| ||| |  |||||||||||
Db     485 TGGCGAGCTGTTTGACCGACATCATGGAGCCTCCTACAGAGAAGGATGCCCAGCCA 544

Qy     897 CTACATCCAGCAGCTGGTGTGGAGGGGCTGCACTACCTGCACAGCCTGGTTCTCCACCT 956
           |||| | |||||| ||| ||| |  |  | ||||||||||||| | ||  | |||||| |
Db     545 TCTGGTGGTCAGGTCCTTGGCCCTGCAGGAGCAGTGGCTGCAG 604
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SEQUENCE CHARACTERISTICS:
    LENGTH: 1282 base pairs
    TYPE: nucleic acid
    STRANDEDNESS: single
    TOPOLOGY: linear
IMMEDIATE SOURCE:
    LIBRARY: PROSNOT06
    CLONE: 827431
US-09-272-796-12

Query Match          2.3%;    Score 122.2;  DB 3;   Length 1282;
Best Local Similarity 49.2%;  Pred. No. 1.4e-15;
Matches 319;  Conservative  0;  Mismatches 329;  Indels  0;  Gaps  0;

```
Qy   717 GGCCCAGGCATACAGGGAGCGAGGAGACATCCTGGCCGCGCTGAGCCACCCGTGGTCACGGG 776
             ||||| ||              |  |||| |
Db   365 GGCCCTGGTCGAGAACGAGATCGGACGTGCTTCCGTAGGATCAGTCACCCAACATCGTCGC 424

Qy   777 GCTGCTGGACCAGTTTGAGACCCGCAAGACCCTCATCCTCATCCTGGAGCTTGTCTCATC 836
             |||||| || || | |
Db   425 TCTGGAGGATGTCACGAGACCCTTCCCACCTCTACCTGCCATGGAACTGGTGACGGG 484

Qy   837 CGAGGAGCTGCTGGACCGCCTGTACAGGAAGGCGGTGGTGACGGAGGGCCGAGGTCAAGGT 896
             |            |||||                       |
Db   485 TGGCCAGCTGTTTGACCGCATCATGGAGGCGGCGGTCCTACACAGAAGAAGGATGCCAGCCA 544

Qy   897 CTACATCCAGCAGCTGGTGTGGAGGGGCTGCACTACCTGCACAGCCATGGCGTTCTCCACCT 956
             |              |||||
Db   545 TCTGGTGGGTCAGGTCCTTGGCGCCGTCCTTGGGGATCGTGCACCG 604

Qy   957 GGACATAAAGCCCTCAACATCCTGATGGTGCATCCTGCCCGGGAAGACATTAAAATCTG 1016
             ||||   || ||
Db   605 GGACCTCAAGCCCGAAAACCTCCTGTATGCCACGCCCTTTGAGGACTCGAAGATCATGGT 664

Qy  1017 CGACTTTGGCTTTGCCCAGAACATCACCCCAGCAGAGCTGCAGTTCAGCCAGTACGGCTC 1076
             ||| |||||         |  |||  |                     |
Db   665 CTCTGACTTTGGACTCTCCAAAATCCAGGTGGGAACATGCTAGGCACCGCCTGTGGGAC 724

Qy  1077 CCCTGAGTTCGTCTCCCCGAGATCATCCAGCAGAACCTGTGAGCGAAGCTCCGACAT 1136
             ||| |  | |  ||||||
Db   725 CCCTGGATATGTGGCCCCAGAGTCTTGGACAGAAACCCTACGGGAAGGCCGTAGAATGT 784

Qy  1137 TTGGGGCCATGGGTGTCATCTCCTACCTCAGCCTGACCTGCTCATCCCCATTTGCCGGCGA 1196
             ||||| ||||  ||||||||||||||| |||  |||
Db   785 GTGGGCCCTGGGCGTCATCTCCTACATCCTGTGTGGGTACCCCCCTTCTACGACGA 844

Qy  1197 GAGTGACCGTGCCACCTCCTGAACGTCCTGGAGGGGGCGCCTGTCATGGAGCAGCCCCAT 1256
             ||| ||||  ||  ||| | ||| || || ||||| ||
Db   845 GAGCGACCCCTGAGCGTCTTCAGCCAGATCCTGAGGGCCAGCTATGATGAGTTTGACTNTCCTTT 904

Qy  1257 GGCTGCCCACCTCAGCGAAGACGCCAAAGACTTCATCAAGGCTACGGTCGCAGAGAGCCCC 1316
             |||||||| || |||| |||| |||||||||  ||  |||  || ||   |||  |   ||
Db   905 CTGGGATGACATCTCAGAATCAGGCAAAGACTTTATTCGGCACCTTTCTGGAGCGAGACCT 964

Qy  1317 TCAGGCCCGGCCTAGTGCGGCCCAGTGCCTTCTCCCACCCCTGGTTCCT 1364
             |||   |  |||  |    ||| |||  |||  |||| ||| |||  ||
Db   965 TCAGAAGAGGTTCACCTGCCAACAGCCCTTGCGGGACCCTTTGGATCTT 1012
```

RESULT 10
US-09-272-796-12
; Sequence 12, Application US/09272796
; Patent No. 6207148
GENERAL INFORMATION:
    APPLICANT: Bandman, Olga
    APPLICANT: Hillman, Jennifer L.
    APPLICANT: Corley, Neil C.
    APPLICANT: Guegler, Karl G.
    APPLICANT: Lal, Preeti
    APPLICANT: Goli, Surya K.
    APPLICANT: Shah, Purvi
    TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
    TITLE OF INVENTION: KINASES
    NUMBER OF SEQUENCES: 21
    CORRESPONDENCE ADDRESS:
        ADDRESSEE: Incyte Pharmaceuticals, Inc.
        STREET: 3174 Porter Drive
        CITY: Palo Alto
        STATE: CA
        COUNTRY: USA
        ZIP: 94304
    COMPUTER READABLE FORM:
        MEDIUM TYPE: Diskette
        COMPUTER: IBM Compatible
        OPERATING SYSTEM: DOS
        SOFTWARE: FastSEQ for Windows Version 2.0
    CURRENT APPLICATION DATA:
        APPLICATION NUMBER: US/09/272,796
        FILING DATE:
        CLASSIFICATION:
    PRIOR APPLICATION DATA:
        APPLICATION NUMBER: 08/878,989
        FILING DATE:
    ATTORNEY/AGENT INFORMATION:
        NAME: Billings, Lucy J J
        REGISTRATION NUMBER: 36,749
        REFERENCE/DOCKET NUMBER: PF-0321 US
    TELECOMMUNICATION INFORMATION:
        TELEPHONE: 415-855-0555
        TELEFAX: 415-845-4166
        TELEX:
INFORMATION FOR SEQ ID NO: 12:

RESULT 11
US-09-016-434-953
; Sequence 953, Application US/09016434
; Patent No. 6500938
GENERAL INFORMATION:
    APPLICANT: Janice Au-Young
    APPLICANT: Jeffrey J. Seilhamer
    TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
    TITLE OF INVENTION: PATHWAY GENE EXPRESSION
    NUMBER OF SEQUENCES: 1490
    CORRESPONDENCE ADDRESS:
        ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
        STREET: 3174 PORTER DRIVE
        CITY: PALO ALTO

Query Match    2.3%;    Score 122.2;    DB 4;    Length 1282;
Best Local Similarity  49.2%;    Pred. No.1.4e-15;
Matches  319;    Conservative   0;    Mismatches 329;    Indels   0;    Gaps   0;

Qy   717 GGGCCAGGCATACAGGGAGGCGAGACATCCTGGCCGCGGCTGAGCCACCCGCTGGTCACGGGG 776
          ||||||  ||   ||   ||  ||||
Db   365 GGGCCTGCTGGGAGGAACGAGATCGGCAGTCGTCCGTAGGATCAGTCAGTCACCCCAACATCGTCGC 424

Qy   777 GCTGCTGGACCAGTTGAGACCCGGCCAAGACCCTCATCCTCTGGAGCTGTGCTCATC 836
          ||| ||   |   |||   |||||||
Db   425 TCTGGAGGATGTCCACGAGAGCCCTTCCACCTCTACCTGGCCATGGAACTGGTGACGGGG 484

Qy   837 CGAGGAGCTGCTGACCGGCCTGTACAGGAAGGGCGTGGTGACCGAGGCCGAGGTCAAGGT 896
          |   |||  || ||
Db   485 TGGGGAGCTGTTGACCGCCATCATGAGGCCGCCTCCTACACAGGAAGGATGATGCCAGCCA 544

Qy   897 CTACATCCAGCAGCTGGTGGAGGGCTGCACTACCTGCACAGCCATGGCGTTCTCCACCT 956
          ||||
Db   545 TCTGGTGGGTCAGGTCCTTGGCGCCGTCCTACCTGCACAGCGCTGGGGATCGTGCACCG 604

Qy   957 GGACATAAAGCCCTAACATCCTGATGGTGCATCCTGCCCGGGAAGACATTAAAATCTG 1016
          ||||
Db   605 GGACCTCAAGCCCGAAAACCTCCTTTGTATGCCACGCGCCCTTTGACGACTCGAAGATCATGGT 664

Qy  1017 CGACTTGGCTTTGCCCAGACAATCACCCCAGCAGAGCTGCAGTTCAGCCAGTACGGCTC 1076
          || |||
Db   665 CTCTGACTTTGGACTCTCCAAAAATCCAGGCTGGGAACAATGCTAGGCACCGCCGTGTGGGAC 724

Qy  1077 CCCTGAGTTCGTCTCCCCCGAGATCATCCAGCAGCATCATCCAGCACGTGTGAGCGAAGCCTCCGACAT 1136
          ||||
Db   725 CCCTGGATATGTGGCCCCAGAGCTCTTGGAGCAGCAGAAACCCTACGGGAGGCCGTAGATGT 784

Qy  1137 TTGGGCCATGGGTGTCATCTCCTACCTCAGCCTGACCTGCCTCATCCCCATTTGCCGGCGA 1196
          |||||||    ||||||||||||||
Db   785 GTGGGCCCCTGGGGCGTCATCTCCTACACTCCTGCTGTGTGGTGTACCCCCCCCTTCACGACGA 844

Qy  1197 GAGTGACCGTGCCACCCTCTGAACGTCCTGGAGGGGGCGCGTGTCATGGAGCAGCCCCAT 1256
          |||  ||||   ||||||| |  |||||||| | || ||| |||
Db   845 GAGCGACCCCTGAGCTCTTCAGCCAGATCCTGAGGCGCCACGCTATGAGTTTGACTNTCCTTT 904

; OTHER INFORMATION: disclosed in Figure 30."
US-07-951-715A-20

Query Match              2.3%;     Score 122.2; DB 1;    Length 1349;
Best Local Similarity   51.5%;     Pred. No. 1.4e-15;
Matches 333; Conservative    0;  Mismatches 308;    Indels    6;    Gaps     2;

Qy   758 GCCACCCCTGGTCACGGGCGTCGTGGACCAGTTTGAGACCCGCAAGACCCTCATCCTCA 817
         ||||    ||||  |||  || |||||||||  |||||| ||||||
Db    25 GCCAGCCCAACGTGGTGGGCCTCCGCGGCGGCCGTACGAGGACAAGCAGAGCGTGCACCTCG 84

Qy   818 TCCTGGAGCTGTGCTCATCCGAGGAGCTGCTGGACCGCGCTGCTGGAGGAGGGGCGTGGTGA 877
         ||||||||||||||||||||| ||| |||  ||||||||   |||||||||||||||
Db    85 TCATGGAGCTGTCGCCGGCGGGGAGCTCTTCGACCGCCATCATCGCCCGGGGCCCAGTACA 144

Qy   878 CGGAGGCCGAGGTCAAGGTCTACATCCAGCAGCTGGTGGAGGGGCTGCTGACTACTGCACA 937
         ||||||||  |||    |||    ||
Db   145 CGGAGGCGGCGGCCGCCGGAGCTGCTGCGCGCCATCGTGCAGATCGTGCAGCACCTGCCACT 204

Qy   938 GCCATGGCGTTCCACCTGGACATAAAGCCCTCAACATCCTGATGGTGCATCCTGCCC 997
         ||||||||||||||||  ||||||||||  ||||||||||||||||||
Db   205 CCATGGGGTGATGCACCGGGACATCAAGCCCGAGAACTTCCTGCTGCTCAGCAAGGACG 264

Qy   998 GGGAAG--ACATTAAAATCTGCGACTTTGCCTTTGCCCAGAACATCACCCCAGCAGAGC 1054
         |||||      ||     |||| |||||||   ||||||||||||||||||||||
Db   265 AGGACGCGCGCCTCAAGGCCACCGACTTCGGCCCTCCGCTCTTCTTCAAGGAGGGCGAGC 324

Qy  1055 TGCAGTTCAGCCAGTACGGCTCCCCGTGAGTTCGTCTCCCCGAGATCATCCAGCAGAACC 1114
         |||||||||||||||  |||||||||    |||||||||||||||
Db   325 TGCTCAGGGACATCGTCGGCAGCGCCTACTACATCGCCCGAGGTGCTCAAGAGGAAGT 384

Qy  1115 CTGTGAGCGAAGCCTCCGACATTTGGCCATGGGTGTCATCTCCTACCTCAGCCTGACCT 1174
         |||||||||||||||||||||||||  |||
Db   385 ACG---GCCCGGAGGCCGACATCGGAGCGTCGGCGCTCATGTCCGCCCATCCTCCTCGCCG 441

Qy  1175 GCTCATCCCATTTGCCGGCGAGGTGACCGTGCCACCCTCCTGAACGTCCTCGGAGGGGC 1234
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Db   442 GGCTGCCTCCCTTCGCGGCAGAGAACGGCATCTTCACCGCCATCCTGCCGAGGGC 501

Qy  1235 GGCGTGTCATGGAGCAGCCCCATGGTGCCCACCTCAGCGAAGACGCCAAAGACTTCATCA 1294
         ||    ||||    ||||||| |||||||||||||||||
Db   502 AGCTTGACCTCTTCCAGCGAGCCATGCCACACATCTCGCCGGAGCCCAAGGATCTCGTCA 561

Qy  1295 AGGCTACGCTGCGAGAGAGCCCCTAGCGCCGGCCCAGTTCCCACCGTTGCGTCCTCCCACC 1354
         |||    ||||||  |||||||||   |||||||||  |||
Db   562 AGAAGATGCTCAACATCAACCCCCAAGGAGCGGCTCACGGCGTTCACGGCGCGCTCCAATCACC 621

Qy  1355 CCTGGTTCCTGAAATCCATGCCTGCGGAGGAGGCCCACTTCATCAAC 1401
         ||||||||||||| ||||||||||||||||||||
Db   622 CATGGAATCAAAGAAGACGGAGACGCGGCCGCCTGACACGCCCGTTGACAAC 668

RESULT 13
US-08-459-448A-20
; Sequence 20, Application US/08459448A
; Patent No. 5889336
; GENERAL INFORMATION:
;  APPLICANT: Koziel, Michael G.
;  APPLICANT: Desai, Nalini M.
;  APPLICANT: Lewis, Kelly S.
;  APPLICANT: Kramer, Vance C.
;  APPLICANT: Warren, Gregory W.
;  APPLICANT: Evola, Stephen V.
;  APPLICANT: Crossland, Lyle D.
;  APPLICANT: Wright, Martha S.
;  APPLICANT: Merlin, Ellis J.
;  APPLICANT: Launis, Karen L.
;  APPLICANT: Rothstein, Steven J.
;  APPLICANT: Bowman, Cindy G.
;  APPLICANT: Dawson, John G.
;  APPLICANT: Dunder, Erik M.
;  APPLICANT: Pace, Gary M.
;  APPLICANT: Suttie, Janet L.

---

TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
NUMBER OF SEQUENCES:   94
CORRESPONDENCE ADDRESS:
  ADDRESSEE: No. 5889336artis Corporation
  STREET: Patent & Trademark Dept., 520 White Plains
  STREET: Rd., POB 2005
  CITY: Tarrytown
  STATE: New York
  COUNTRY: USA
  ZIP: 10591-9005
COMPUTER READABLE FORM:
  MEDIUM TYPE: Floppy disk
  COMPUTER: IBM PC compatible
  OPERATING SYSTEM: PC-DOS/MS-DOS
  SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/08/459,448A
  FILING DATE: 02-JUN-1995
  CLASSIFICATION: 800
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US 07/951,715
  FILING DATE: 25-SEP-1992
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US 07/772,027
  FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
  NAME: Pace, Gary M.
  REGISTRATION NUMBER:   40403
  REFERENCE/DOCKET NUMBER:   CGC 1577/CIP/DIV4
TELECOMMUNICATION INFORMATION:
  TELEPHONE:  (919)541-8582
  TELEFAX:    (919)541-8689
INFORMATION FOR SEQ ID NO:   20:
SEQUENCE CHARACTERISTICS:
  LENGTH:  1349 base pairs
  TYPE:  nucleic acid
  STRANDEDNESS:  single
  TOPOLOGY:  linear
MOLECULE TYPE: cDNA
HYPOTHETICAL:  NO
FEATURE:
  NAME/KEY:  CDS
  LOCATION:  3..1226
  OTHER INFORMATION:  /note= "cDNA sequence for maize
  OTHER INFORMATION:  pollen-specific calcium dependent protein kinase gene as
  OTHER INFORMATION:  disclosed in Figure 30."
US-08-459-448A-20

Query Match              2.3%;     Score 122.2; DB 2;    Length 1349;
Best Local Similarity   51.5%;     Pred No. 1.4e-15;
Matches 333; Conservative    0;  Mismatches 308;    Indels    6;   Gaps     2;

Qy   758 GCCACCCCTGGTCACGGGCGTCGTGGACCAGTTTGAGACCCGCAAGACCCTCATCCTCA 817
         ||||    ||||  |||  || |||||||||  |||||| ||||||
Db    25 GCCAGCCCAACGTGGTGGGCCTCCGCGGCGGCCGTACGAGGACAAGCAGAGCGTGCACCTCG 84

Qy   818 TCCTGGAGCTGTGCTCATCCGAGGAGCTGCTGGACCGCGCTGCTGGAGGAGGGGCGTGGTGA 877
         ||||||||||||||||||||| ||| |||  ||||||||   |||||||||||||||
Db    85 TCATGGAGCTGTCGCCGGCGGGGAGCTCTTCGACCGCCATCATCGCCCGGGGCCCAGTACA 144

Qy   878 CGGAGGCCGAGGTCAAGGTCTACATCCAGCAGCTGGTGGAGGGGCTGCTGACTACTGCACA 937
         ||||||||  |||    |||    ||
Db   145 CGGAGGCGGCGGCCGCCGGAGCTGCTGCGCGCCATCGTGCAGATCGTGCAGCACCTGCCACT 204

Qy   938 GCCATGGCGTTCCACCTGGACATAAAGCCCTCAACATCCTGATGGTGCATCCTGCCC 997
         ||||||||||||||||  ||||||||||  ||||||||||||||||||
Db   205 CCATGGGGTGATGCACCGGGACATCAAGCCCGAGAACTTCCTGCTGCTCAGCAAGGACG 264

Qy   998 GGGAAG--ACATTAAAATCTGCGACTTTGGCTTTGCCCAGAACATCACCCCAGCAGAGC 1054
         |||||      ||     |||| |||||||   ||||||||||||||||||||||
Db   265 AGGACGCGCGCCTCAAGGCCACCGACTTCGGCCCTCCGCTCTTCTTCAAGGAGGGCGAGC 324

NAME:: Pace, Gary M.
REGISTRATION NUMBER:: 40403
REFERENCE/DOCKET NUMBER:: CGC 1577/CIP/DIV3
TELECOMMUNICATION INFORMATION:
TELEPHONE:: (919)541-8582
TELEFAX:: (919)541-8689
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH:: 1349 base pairs
TYPE:: nucleic acid
STRANDEDNESS:: single
TOPOLOGY:: linear
MOLECULE TYPE:: cDNA
HYPOTHETICAL:: NO
FEATURE:
NAME/KEY:: CDS
LOCATION:: 3..1226
OTHER INFORMATION:: /note= "cDNA sequence for maize
OTHER INFORMATION:: pollen-specific calcium dependent protein kinase gene as
OTHER INFORMATION:: disclosed in Figure 30."
US-08-459-595A-20

Query Match        2.3%;  Score 122.2;  DB 3;  Length 1349;
Best Local Similarity  51.5%;  Pred. No. 1.4e-15;
Matches  333;  Conservative  0;  Mismatches 308;  Indels  6;  Gaps  2;

```
Qy    758 GCCACCCGCTGGTCACGGGCGTGCTGGACCAGTTGAGACCCGCAAGACCCTCATCCTCA 817
          || |||||||||| |||  | ||||||  ||||||| ||||   ||  ||| | ||| |
Db     25 GCCAGCCCAACGTCGTGGGGCCTCCGCGGCGGCGTACGAGCAAGCAGAGCGTGCACCTCG 84

Qy    818 TCCTGGAGTGTGCTCATCCGAGGAGCTGCTGGACGCCTGTACAGGAAGGCGTCGGTGA 877
          |||||||||||||||  | || |||||||||| ||||| |  | |||||||||||| ||
Db     85 TCATGGAGCTGTGCGCGGCGGGAGCTCTTCACCGGCATCATCGCCCGGGGCCAGTACA 144

Qy    878 CGGAGGCCGAGGTCAAGGTCTACATCCAGCAGCTGGTGGAGGGGCTGCACTACCTGCACA 937
          |||| |||||||| | |||||||| ||||| |||||||| |||||||||||||| || |
Db    145 CGGAGCGGCGGCCGCGGAGCTGCTGCGCGCCATCGTGCAGATCGTGCACACTGCCACT 204

Qy    938 GCCATGGCGTTCTCCACCTGGACATAAAGCCCTTAACATCCTGATGGTGCATCCTGCCC 997
          |||||| | |  || || ||  | |||| |||  ||| |  |||||| ||| ||||
Db    205 CCATGGGGTGATGCACCGGAGCATCAAGCCCGAGAACTTCCTGCTGCTCAGCAAGGACG 264

Qy    998 GGGGAG--ACATTAAAATCTGGGACTTTGGCTTGCCAGACACATCACCCCAGCAGAGC 1054
          || ||    | |||   |||  |||| || | ||  |||| ||| |||| ||||||||
Db    265 AGGACGCGCGGCCTCAAGGCCACCGACTTTCGGCCTCTCCGGTCTTCTTCAAGGAGGGGCGAGC 324

Qy   1055 TGCAGTTCAGCCAGTACGGCTCCCCTGAGTTCGTCTCCCCCGAGATCATCCAGCAGAACC 1114
          ||||||| |||||| |||||| |||| |||| || | | |||||||||||||||||||
Db    325 TGCTCAGGGACATCGTCGGCAGCCGCCTACTACATCGCGCGCCAGGGTGCTCAAGAGGAAGT 384

Qy   1115 CTGTGAGCGAAGCCTCCGACATTTGGGCCATGGTGTCATCTCCTACACTCCAGCCGCTGACCT 1174
          ||| ||| ||||||| ||| |||||  |||| |||| |  | || ||| | |||||||||
Db    385 ACG--GCCCGGAGGCCGACATCTGGAGCGTCGGCGGCTCATGGTCATCATCTTTCCTCGCCG 441

Qy   1175 GCTCATCCCATTTGCCGCGGAGAGTGACCGTGCCACCCTCCTGAACGTCCTGGACGGGGC 1234
          |||||||||||| || ||||||||| || ||| ||| | || ||  ||||||||| || |
Db    442 GCGTGCCTCCCTTCTGGGGCAGAGAACGAGAGACGGCCATCTTCACCGGCCATCCTGCGAGGGGC 501

Qy   1235 GCGTGTCATGGAGCAGCCCCATGGCTGCCACCTGCCGAGACGCCAAAGACTTCATCA 1294
          ||| ||||| || ||||| |||| || ||| | ||||| || |||||||| ||| ||
Db    502 AGCTTGACCTCTCCAGCGAGCCATGGCCACACATCTCGCCCGGGAGCCAAGGATCTCGTCA 561

Qy   1295 AGGCTACGCTGCGAGAGAGCCCCTCAGGCCGCGGCCCAGTGCCTCTCCACC 1354
          ||||| | ||| |||| | |||||||||||| ||||||| |||||||||||
Db    562 AGAAGATGCTCAACATCAACCCAAGGAGCGGCGTCACGCGGCGTTCCAGGTCCTCAATCACC 621

Qy   1355 CCTGGTTCCTGAAATCCATAGCCTGCGGAGGAGGCCCACTTCATCAAC 1401
          ||| |||||||||   || ||| ||||| ||||||||  ||  |||||
Db    622 CATGGATCAAAGAAGACGGAGACGGAGACGCCGCCTTGACACGCGCGCTTGACAAC 668
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RESULT 14
US-08-459-595A-20

; Sequence 20, Application US/08459595A
; Patent No. 6018104
GENERAL INFORMATION:
APPLICANT:: Koziel, Michael G.
APPLICANT:: Desai, Nalini M.
APPLICANT:: Lewis, Kelly S.
APPLICANT:: Kramer, Vance C.
APPLICANT:: Warren, Gregory W.
APPLICANT:: Evola, Stephen V.
APPLICANT:: Crossland, Lyle D.
APPLICANT:: Wright, Martha S.
APPLICANT:: Merlin, Ellis J.
APPLICANT:: Launis, Karen L.
APPLICANT:: Rothstein, Steven J.
APPLICANT:: Bowman, Cindy G.
APPLICANT:: Dawson, John L.
APPLICANT:: Dunder, Erik M.
APPLICANT:: Pace, Gary M.
APPLICANT:: Suttie, Janet L.
TITLE OF INVENTION:: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
TITLE OF INVENTION:: INSECTICIDAL ACTIVITY IN MAIZE
NUMBER OF SEQUENCES:: 94

RESULT 15
US-08-459-504B-20

; Sequence 20, Application US/08459504B
; Patent No. 6075185
; GENERAL INFORMATION:
;; APPLICANT: Koziel, Michael G.
;; APPLICANT: Desai, Nalini M.
;; APPLICANT: Lewis, Kelly S.
;; APPLICANT: Kramer, Vance C.
;; APPLICANT: Warren, Gregory W.
;; APPLICANT: Evola, Stephen V.
;; APPLICANT: Crossland, Lyle D.
;; APPLICANT: Wright, Martha S.
;; APPLICANT: Merlin, Ellis J.
;; APPLICANT: Launis, Karen L.
;; APPLICANT: Rothstein, Steven J.
;; APPLICANT: Bowman, Cindy G.
;; APPLICANT: Dawson, John L.
;; APPLICANT: Dunder, Erik M.
;; APPLICANT: Pace, Gary M.
;; APPLICANT: Suttie, Janet L.
;; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
;; TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
;; NUMBER OF SEQUENCES: 94
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: No. 6075185artis Corporation
;; STREET: 3054 Cornwallis Road
;; CITY: Research Triangle Park
;; STATE: NC
;; COUNTRY: USA
;; ZIP: 27709
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC Compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/459,504B
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/459,595
;; FILING DATE: 02-JUN-1995
;; APPLICATION NUMBER: US 07/951,715
;; FILING DATE: 25-SEP-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/772,027
;; FILING DATE: 04-OCT-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Meigs, J. Timothy
;; REGISTRATION NUMBER: 38,241
;; REFERENCE/DOCKET NUMBER: CGC1577/CIP/DIV
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (919)541-8587
;; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 20:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1349 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: cDNA
;; HYPOTHETICAL: NO
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 3..1226
;; OTHER INFORMATION: /note= "cDNA sequence for maize
;; OTHER INFORMATION: pollen-specific calcium dependent protein kinase gene as
;; OTHER INFORMATION: disclosed in Figure 30."
US-08-459-504B-20

Query Match      2.3%;    Score 122.2;  DB 3;  Length 1349;
Best Local Similarity  51.5%;   Pred. No. 1.4e-15;
Matches 333;  Conservative  0;  Mismatches 308;  Indels  6;  Gaps  2;

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Qy    758 GCCACCCCTGGTCACGGGGCTGCTGACCAGTTTGAGACCCGCAAGACCCTCATCCTCA  817
              ||| ||| | ||| ||  ||  ||||| |        | | || |||  |||| ||||
Db     25 GCCAGCCCAACGTGGTGGCCTCCGCGGCGGCGTACGAGGACAAGCAGAGCGTGCACCTCG  84

Qy    818 TCCTGGAGCTGTCGTCATCCGAGGAGCTGCTGGACCGCC---TGTACAGGAAGGGCGTGGTGA  877
              || ||||||||| | |   ||||| ||| ||||||||||     |||| |
Db     85 TCATGGAGCTGTGCGCGGGCGGGGAGCTCTTCGACCGCATCATCGCCCGGGGCCAGTACA  144

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Qy    938 GCCATGGCGTTCTCCACCTGACATAAAGCCCTCTAACATCCTGATGGTGCATCCTGCCC  997
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Qy    998 GGGAAG--ACATTAAAATCTGCGACTTTGGCTTTGCCCAGAACATCACCCCAGCAGAGC  1054
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Db    265 AGGAGCGCCGCTCAAGGCCACCGACTTCGGCCTCTTCGGTCTTCTTCAAGGAGGGCGAGC  324

Qy   1055 TGCAGTTCAGCCAGTACGGCTCCCCTGAGTTCGTCTCCCCGGAGATCATCCAGCAGAACC  1114
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Db    325 TGCTCAGGGACATCGTGCGAGCGCCTACTACATCGCGCCCGAGGGTGCTCAAGGAGAAGT  384

Qy   1115 CTGTGAGCGAAGCCTCCGACATTTGGGCCATGGGTGCATCCTCCACCTCAGCCTGACCT  1174
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Qy   1235 GCGTGTCATGGAGCAGCCCATGGCTGCCCACCTGCCGAAGACGGCCAAAGACTTCATCA  1294
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Db    502 AGCTTGACCTCCAGCGAGCCATGGCCACACATCTCGCCGGGAGCCAAGGATCTCGTCA  561

Qy   1295 AGGCTACGCTGCAGAGAGCCCCTCAGCCCGCCGTAGTGCGGCCCAGTGCTCTCCCACC  1354
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Db    562 AGAAGATGCTCAACATCAACCCCAAGGAGCGGCTCACGCGGGTTCCAGGTCCTCAATCACC  621

Qy   1355 CCTGGTTCCTGAAATCCATGCGTGCGGGAGGAGGCCCACTTCATCAAC  1401
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Db    622 CATGGATCAAAGAAGAGACGGAGACGCGCCTGACACCGCGCTTGACAAC  668
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Search completed: April 26, 2004, 15:05:06
Job time : 248 secs